54 54 54 55 56 57 57 57 57 57 57 57 57 57 57	rred. No. score gree and is der no. Score M	Post-processing: Database:	Relea Copyr Psrch_pp pro n on: abular output itle: escription: escription: erfect Score: equence: coring table:	
74.0 400 3 Q26648 74.0 735 3 Q17750 72.2 485 3 Q17750 71.2 485 3 Q16873 71.2 1312 2 Q92878 71.2 2475 11 Q08358 69.9 242 8 P93468 69.9 257 8 Q40700 69.9 317 4 Q19037 69.9 317 4 P79328 69.9 385 3 Q24250 69.9 385 3 Q24250 69.9 1200 9 P73340 69.9 1648 2 Q15938 68.5 334 3 Q17970 68.5 336 9 Q34130	er of results proequal to the scallysis of the total SUMMARIES	Minimum Match 0% Listing first 45 summaries sptremb15 1:sp_fung1 2:sp_human 3:s 5:sp_mhc 6:sp_organelle 7 9:sp_bacteria 10:sp_roden 13:sp_unclassified Mean 24 067: Variance 30 3	1A John F. Collins, (c) 193-1998 University of the protein database s Jul 30 11:11:19 199 (enerated.) 9-08-817-547A-31 10) from USO8817547A RKKLQDVHN 10 150	
TEXTIN B1.  C10663 9 PROTEIN.  SIMILAR TO SACCHAROMYC C13A2.5 PROTEIN.  PUTATIVE N6-ADEININE S 5.94e+00 RAD50.  POLYPROTEIN PP220.  MADS-BOX FAMILY TRANSC PUTATIVE MADS-BOX FAMILY TRANSC PUTATIVE MADS-BOX FAMI POTEIN.  MC1-R PROTEIN.  MC1	icted by chance to have a e of the result being printed, score distribution.	sp_invertebrate 4:sp_mammal 7:sp_phage 8:sp_plant nt 11:sp_virus 12:sp_vertebrate	puting Research Unit. of Edinburgh, U.K. d Molecular Ltd using Smith-Waterman algori using Time 3.79 Seconds 1.077 Million cell updates/s	

45	44	43	42	41	40	39	38 8	37	36	35 5	34	33	32	31	30	29	28	27	26	25	24	23	22	21
48	48	48	48	48	48	48	48	48	48	48	48	48	48	48	48	49	49	49	49	49	49	50	50	50
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2510	2346	2325	2024	1625	1459	1091	1038	1034	951	943	914	481	400	164	133	3212	1914	1583	991	899	257	1972	1938	621
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Q94658	001385	Q41743	Q15154	Q08367	Q21874	Q18082	Q12532	017117	014527	030320	000291	Q18255	000328	P96113	P73917	Q94010	Q15746	015045	Q14844	Q06132	Q44871	008638	008639	Q63339
EXPORTED SERINE/THREON	TPR HOMOLOG.	ACETYL-COENZYME A CARB	PERICENTRIOL MATERIAL	ACETYL-COA CARBOXYLASE	R09E10.5.	SIMILARITY TO MYOSIN H	HYPOTHETICAL 119.1 KD	×	KIAA0291 (FRAGMENT).	ATP-DEPENDENT RNA HELI	HUNTINGTIN INTERACTING	COSMID C27D9.	HUNTINGTIN INTERACTING	POLYPEPTIDE DEFORMYLAS	HYPOTHETICAL 15.4 KD P	T08G11.1.	MYOSIN LIGHT CHAIN KIN	KIAA0336.	MYOSIN LIGHT CHAIN KIN	8	PLASMID, ORFA, B, C, D	MYOSIN.	MYOSIN.	MYCSIN HEAVY CHAIN 21
		3.54e+01			:_	3.54e+01						•	•			2.29e+01	٠	١.	2.29e+01	. 29	2.29e+01	1.47e+01	1.47e+01	1.47e+01

ALIGNMENTS

# RESULT 1 ID Q63473 AC Q63473; AC Q63473; DT 01-NOV-1996 (TREMBLREL 01, LGREATED) DT 01-NOV-1996 (TREMBLREL 01, LAST SEQUENCE UPDATE) DT 01-NOV-1996 (TREMBLREL 05, LAST SEQUENCE UPDATE) DT 01-NAN-1998 (TREMBLREL 05, LAST ANNOTATION UPDATE) DT 01-VAN-1998 (TREMBLREL 05, LAST ANNOTATION UPDATE) DT 01-VAN-1996 (TREMBLREL 07, LAST ANNOTATION UPDATE) DT 01-VAN-1996 (TREMBLREL 07, LAST ANNOTATION UPDATE) DT 01-VAN-1996 (TREMBLREL 07, LAST ANNOTATION UPDATE) DE RATTUS NORVEGICUS (RAT). CO EUTHERIA; MORENTIA. ROC EUTHERIA; MOTENTIA. ROC EUTHERIA; RODENTIA. ROC EUTHERIA; RODENTIA. ROC EUTHERIA; RODENTIA. ROC EUTHERIA; RODENTIA. ROC TISSUE-THYROID, AND PARATHYROID; RA SCHWELZER H.J., GROSS G., MAYER H.; RC TISSUE-THYROID, AND PARATHYROID; RA SCHWELZER H.J., GROSS G., MAYER H.; RC TISSUE-THYROID, AND PARATHYROID; RA SCHWELZER H.J., GROSS G., MAYER H.; RC TISSUE-THYROID, AND PARATHYROID; RA SCHWELZER H.J., GROSS G., MAYER H.; RC TISSUE-THYROID, AND PARATHYROID; RA SCHWELZER H.J., GROSS G., MAYER H.; RC TISSUE-THYROID, AND PARATHYROID; RA SCHWELZER H.J., GROSS G., MAYER H.; ROC EUTHERIA; RODENTIA. ROC EUTHERIA; TETRAPODA; MAMMALIA; ROC EUTHERIA; TETRAPODA; MAMM

Gaps

0

RESULT 2
ID Q26648
AC Q26648;
AC Q26648;
DT 01.NOV-1996 (TREMBLREL. 01, CREATED)
DT 01.NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT TEXTIN B1.
OS STRONGYLOCENTROTUS PURPURATUS (PURPLE SEA URCHIN).
CC EUCECHINOIDEA.
RN [1]
RN [1]
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE-EMBRYO;
RX MEDLINE; 94140942.
RA CHEN R., PERRONE C.A., AMOS L.A., LINCK R.W.;

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DR SEMEL; L138; G471949; 75400E80 CRC32;
SOS SENDENCE 400 AA; 46147 MR; 75400E80 CRC32;
SOET MARCHES 400 AA; 46147 MR; 75400E80 CRC32;
SOET MARCHES 6; CONSERVATIVE 74.08; SCORE 54; DB 3; Length 400;
MARCHES 6; CONSERVATIVE 0; MISMATCHES 2; Indels 0; Gaps 0;
DB 325 LEEKLODANN 334
Oy 1 LEKLODVIN 10
Search completed 7th Jul 30 11:11:48 1998
Job time: 29 secs.
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3	
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	(TM)

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

n on: Thu Jul 30 10:00:59 1998; MasPar time 4.06 Seconds 83.029 Million cell updates/sec

bular output not generated.

Title:
Description:
Perfect Score: >US-08-817-547A-3 (1-8) from US08817547A.pep 54 1 SVSEIQLM 8

Sequence:

Scoring table: PAM 150 Gap 15

Searched: 140542 segs, 42109429 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb15
1.sp\_fung1 2.sp\_human 3.sp\_invertebrate 4.sp\_mammal
5.sp\_mhc 6.sp\_organelle 7.sp\_phage 8.sp\_plant
9.sp\_bacteria 10.sp\_rodent 11.sp\_virus 12.sp\_vertebrate
13.sp\_unclassified

Statistics: Mean 21.157; Variance 18.924; scale 1.118

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	Score 50	26   BA	Length	10 B	ID Q63473	tion ROID HORMC	Pred. No. 5.43e-02
ω κ	45	83.3 83.3	1405 1405	100	P70366 Q61202	STEROID RECEPTOR COACT	1.44e+00 1.44e+00
4	45	83.3	1441	N	000150	STEROID RECEPTOR COACT	1.44e+00
, UI	45	83.3	1447	10	P70365		1.44e+00
76	434	79.6	167	<b>9</b> 9	P96578	ACETYLGLUTAMATE KINASE YDAE PROTEIN.	4.96e+00
89	43	79.6	910	11	011421	HEXON PROTEIN.	4.96e+00
9	43	79.6	911	11	Q83905	TERMINAL PROTEIN.	4.96e+00
10	42	77.8	418	w	Q26662	VERY EARLY BLASTULA PR	9.08e+00
;::	4 :	75.9	248	œ	004682		1.64e+01
13	41	75.9	373	س ص	049979	CORA.	1.64e+01
14	41	75.9	481	10	Q60823	THYMOMA VIRAL PROTO-ON	1.64e+01
15	41	75.9	591	N	Q13026		1.64e+01
10 17	4 L	75.4	100	0 K	055544	HYDOTHETTOM: 100 3 KD	1.646+01
18	41	75.9	1371	ø	P73337	SENSORY TRANSDUCTION H	1.64e+01
19	41	75.9	3456	1	P89201		1.64e+01
20	40	74.1	99	9	Q58911	HYPOTHETICAL 11.5 KD P	2.93e+01

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21
39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	40	40	40	40	40	40	40	40	40	40
•	72.2	•	72.2	72.2	72.2	72.2	72.2	72.2	72.2	72.2	72.2	72.2	72.2	Ν	74.1	74.1		74.1	74.1	74.1	74.1	74.1	74.1	74.1
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μ,	ω	w	5	2	12	2	ω	ω	w	ω				6	w	w	₩	ω	ω	ω	9	9	ω	ω
Q06116	Q18038	Q27448	Q90413	Q91743	Q91288	Q91742	017179	001625	Q19506	017822	Q90841	Q02529	Q49717	Q60482	Q20456	Q19285	Q02511	Q07995	Q27064	Q27063	006164	034472	002074	Q19478
CHROMOSOME XVI COSMID	CODED FOR BY C. ELEGAN	GLUTAMINE-DEPENDENT CA	FIBROBLAST GROWTH FACT	FIBROBLAST GROWTH FACT	FIBROBLAST GROWTH FACT	FIBROBLAST GROWTH FACT	COSF1.1 PROTEIN.	COSMID ZC196.	F17A2.9.	F17A2.9.	HYPOTHETICAL PROTEIN (	FIBROBLAST GROWTH FACT	B1549_F2_87.	CGRP-RECEPTOR COMPONEN	F46C3.3.	HYPOTHETICAL PROTEIN F	HYPOTHETICAL 133.0 KD	RNA-DIRECTED DNA POLYM	SIALIDASE.	SIALIDASE (FRAGMENT).	MMGC.	YRRI PROTEIN.	SIMILAR TO MYOSIN HEAV	F15B9.1.
5.17e+01	5.17e+01	5.17e+01	5.17e+01	٠	5.17e+01	5.17e+01	٠	5.17e+01	5.17e+01	5.17e+01	5.17e+01	5.17e+01	5.17e+01	5.17e+01	•			2.93e+01	2.93e+01	2.93e+01	2.93e+01	2.93e+01	2.93e+01	2.93e+01

R R R R	2888		RESUL	Qy Qy	X B O	SO PRO	8888	22222	RESULT
SEQUENCE FROM N.A. SEQUENCE FROM N.A. YAO T.P., KU G., ZHOU N., SCULLY R., LIVINGSTON D.M.; PROC. NATL. ACAD. SCI. U.S.A. 93:10626-10631(1996).	MUSKULUS (MOUSE). MUS MUSCULUS (MOUSE). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; RODENTIA.	01-FEB-1997 (TREMBLREL. 02, CREATED) 01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE) 01-MAY-1997 (TREMBLREL. 03, LAST ANNOTATION UPDATE) STEROID RECEPTOR COACTIVATOR-1.	LT 2 P70366. PRELIMINARY; PRT; 1405 AA.	22 AISEIOLM 29 ::       1 SVSEIOLM 8	Query Match 92.6%; Score 50; DB 10; Length 105; Best Local Similarity 75.0%; Pred. No. 5.43e-02; Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  SECHMELZER H.J., GROSS G., MAYER H.;  ADV. GENE TECHNOL. 21:228-229(1984).  EMBL; M54875; G601933;  NON_TER 1 1  NON_TER 1 1  SEQUENCE 105 AA; 11746 MW; 6AC3163E CRC32;	PTH. RATTUS NORVEGICUS (RAT). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; RODENTIA.	0034/3; 01-NOV-1996 (TREMBLREL. 01, CREATED) 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE) 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE) PARATHYROID HORMONE (FRAGMENT).	LT 1

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***	(ME)	

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

n on: Thu Jul 30 10:05:09 1998; MasPar time 2.56 Seconds 41.911 Million cell updates/sec

bular output not generated.

Title: Description: Perfect Score: >US-08-817-547A-4 (1-7) from US08817547A.pep 43 1 SVSEIQL 7

Sequence:

Scoring table: PAM 150 Gap 15

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 13.853; Variance 40.505; scale 0.342

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

11111111111111111111111111111111111111	Sult No.
44444444444444444444444444444444444444	Score
	Query
12 C C C C C C C C C C C C C C C C C C C	Length
7222 8839977933335544	BB
W21948 W21947 P82176 P82176 W17949 W24793 W08131 W08131 W08130 R58232 R34356 R34356 R34356 R34357 R581054	Ü
Fusion protein compri Sequence of parathyroid hor Human parathyroid hor Wild type parathyroid Human pHH derivative, Human pHH derivative, Human pHH derivative, [Lys3]-hPH(1-34)-H Human parathyroid hor Human parathyroid hor Human parathyroid hor [L8, A17,Q18, A19, R22,T [S14, 115,Q16,D17,L18, Sequence of methionin [D-Ser3]hPH (1-34).H [Thr16]hPH (1-34). Cyclised human parath Human parathyroid hor Brathyroid hor Human parathyroid hor Human parathyroid hor Human parathyroid hor	Description
9.43e+01 9.43e+01 9.43e+01 9.43e+01 9.43e+01 9.43e+01 9.43e+01 9.43e+01 9.43e+01 9.43e+01 9.43e+01 9.43e+01 9.43e+01 9.43e+01 9.43e+01 9.43e+01 9.43e+01	Pred. No.

43 100.0 35 14 R/450 Parathyroid hormone p 43 100.0 35 14 R7450 Parathyroid hormone p 43 100.0 35 14 R74426 Parathyroid hormone p 43 100.0 35 14 R74426 Parathyroid hormone p 43 100.0 35 14 R74426 Parathyroid hormone p 43 100.0 35 9 R58212 [Alai7]-hpTH(1-36)-NH 43 100.0 36 9 R58278 [LB,A16,D17,L18,A19]- 43 100.0 36 9 R58277 [NLe18]-hpTH(1-36)-NH 43 100.0 36 9 R58277 [NLe18]-hpTH(1-36)-NH 43 100.0 36 9 R58277 [D-Gln29]-hpTH(1-36)-NH 43 100.0 36 9 R58272 [D-Gln29]-hpTH(1-36)-NH 43 100.0 36 9 R58213 [D-earl7]-hpTH(1-36)-NH 43 100.0 36 9 R58214 [Ala19]-hpTH(1-36)-NH 43 100.0 36 9 R58214 [Leu21]-hpTH(1-38)-OH 43 100.0 38 9 R58141 [Leu21]-hpTH(1-38)-OH 43 100.0 38 9 R58141 [Leu21]-hpTH(1-38)-OH 43 100.0 38 9 R58158 [Ala19]-hpTH(1-38)-OH 43 100.0 38 9 R58159 [Vail4]-hpTH(1-38)-OH 43 100.0 44 26 P30015 Human parathyroid hor 43 100.0 84 27 W25487 Human parathyroid hor 43 100.0 84 27 W25487 Human parathyroid hor 43 100.0 84 27 R29365 Oxidation resistant p 43 100.0 84 5 R29563 Oxidation resistant p	45	44	43	42	41	40	39	38	37	36	ω 5	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20
35 14 K745U3 PARTACHYPOID NORMONE  36 14 K745U3 PARTACHYPOID NORMONE  35 14 K74450 PARTACHYPOID NORMONE  35 14 K74426 PARTACHYPOID NORMONE  35 14 K74426 PARTACHYPOID NORMONE  36 9 K58212 [Ala17]-hPTH(1-36)-  36 9 K58277 [M.e18]-hPTH(1-36)-  36 9 K58213 [M.e18]-hPTH(1-36)-  36 9 K58213 [M.e18]-hPTH(1-38)-  36 9 K58214 [M.e19]-hPTH(1-38)-  37 9 K5814 [M.e19]-hPTH(1-38)-  38 9 K5815 [M.e19]-hPTH(1-38)-  38 9 K5814 [M.e19]-hPTH(1-38)-  38 9 K5815 [M.e19]-hPTH(1-38)-  39 K5815 [M.e19]-hPTH(1-38)-  30 M.e19]-HPTH(1-38)-  30 M.e19]-HPTH(1-36)-  30 M.e19]-HPTH(1-36)-  31 M.e19]-hPTH(1-36)-  32 M.e19]-hPTH(1-36)-  33 M.e19]-HPTH(1-36)-  34 M.e19]-hPTH(1-36)-  35 M.e19]-hPTH(1-36)-  36 M.e19]-HPTH(1-36)-  37 M.e19]-HPTH(1-36)-  38 M.e19]-HPTH(1-36)-  39 M.e19]-HPTH(1-36)-  30 M.e19]-HPT	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	4
5 14 K74503  Parathyroid hormone 5 14 K74509  Parathyroid hormone 5 14 K74426  Parathyroid hormone 6 9 R58212  [Ala17] hPTH(1-36) 6 9 R58277  [Net18] hPTH(1-36) 6 9 R58277  [Net18] hPTH(1-36) 6 9 R58196  [LB,A16,D1-hPTH(1-36) 6 9 R58277  [D-Sha4, D-Ala36] 6 9 R58277  [D-Sha4, D-Ala36] 6 9 R58227  [D-Gln29] hPTH(1-36) 6 9 R58227  [D-Sar17] hPTH(1-36) 6 9 R58214  [Ala19] hPTH(1-36) 6 9 R58214  [Ieu21] hPTH(1-36) 9 R58134  [Ieu21] hPTH(1-38) 9 R58134  [Ieu21] hPTH(1-38) 9 R58134  [Val14] hPTH(1-38) 9 R58135  [Ala27] hPTH(1-38) 9 R58145  [Val14] hPTH(1-38) 9 R58105  [Ala27] hPTH(1-38) 9 R58134  [Leu21] hPTH(1-													•	٠	٠			٠		٠	•	٠				٠
4 K/4503 4 K/4503 4 K/4504 4 K/4509 4 R74510 6 Parathyroid hormone 4 K74426 6 Parathyroid hormone 4 K74426 6 Parathyroid hormone 6 R58212 6 [Ala17]-hpTH(1-36) 9 R58046 9 R58278 [D-Met.18]-hpTH(1-36) 9 R58277 [N1e18]-hpTH(1-36) 9 R58227 [D-Gln29]-hpTH(1-36) 9 R58227 [D-Gln29]-hpTH(1-36) 9 R58214 [Ala19]-hpTH(1-36) 9 R58214 [Ala19]-hpTH(1-38) 9 R58114 [Leu21]-hpTH(1-38) 9 R58115 [Val14]-hpTH(1-38) 9 R58165 PK58115 [Val14]-hpTH(1-38) 9 R58167 Human parathyroid provine parathyroid provine parathyroid R2378 8 R29565 C Oxidation resistant 5 K29563 C Oxidation resistant 6 CANACO C C C C C C C C C C C C C C C C C C	84	84	84	84	84	84	47	44	3 8	3 8	38	38	36	36	36	36	36	36	36	36	3 6	35	ω S	35	35	S.C
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	resistant	resistant	<ul> <li>enhanced</li> </ul>	ne parathyroid	parathyroid	parathyroid	protien con	parathyroid	7]-hPTH(1-38)-	4]-hPTH(1-38)-	l]-hPTH(1-38)-	9]-hPTH(1-38)-	9]-hPTH(1-36)-	c17]-hPTH(1-36)	G1n29]-hPTH(1-36)	,Q18]-hPTH(1-36)-	Phe34, D-Ala36].	]-hPTH(1-36)-	Met18]-hPTH(1-36	, A16, D17, L18, A19	7]-hPTH(1-36)-	id hormone	id hormone	id hormone	id hormone	normone

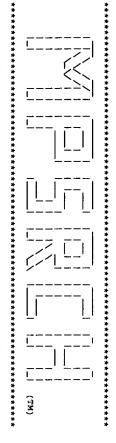
88	88	88	S	င္ပ	င္ပ	8	36	36	200	PS	T T	P	DR	DR	ΡI	PA	PR	ΡF	8	D F	1 to	4) H	1 1	1	FT	80	SO	KΨ	KW	X t	1 5	Ä	Ü	RESULT
material was incubated with tobacco etch virus (TEV) NIa protease and the PTH 1-37 fragment released, recovered by SA fragment		and isolated inclusion bodies solubilised in guanidine hydrochloride, and renatured by dilution in pH 7 phosphate buffer.	containing kanamycin and ampilcilin. Cells were harvested, lysed	The transformants were grown, with IPTG induction, in medium	repressor plasmid pUBS500 were used to transform E. coli K12 RM82.	(SA) sequence, to give psa-TEV-PTH, psa-TEV-PTH and the LacIq	opermised for an econe, which contains the Met(13-139) streptayidin	che parachyroid normone 1-3/ (Fin 1-3/) pebride with codon usage	The DNA encoding the present sequence, a linker and residues 1-7 of	Example 4; Fig 3; 37pp; German.	parathyroid hormone production	de(s) as rusions with str		WPI; 97-289290/26.	Kopetzki E;	מל		06-NOV-1996; E04850.	22-MAY-1997.	W00718314-81	/potes "parathuroid homone 1-37	Dentide 10 16	"libbo closuphic by TEN NTO			Homo sapiens.	Synthetic.		production; TEV	Linker; parathyroid hormone 1-37; PTH 1-37; streptavidin;	and DTU 1-37		W21948 standard; Protein; 16 AA.	ii l

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Search completed: Thu Jul 30 10:05:25 1998 Job time : 16 secs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PT Recombinant production of peptide(s) as fusions with streptavidin pri attached via cleavable linker - especially for urotropin and production productin
                                                                                                                                                                                                         Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
ID W2
AC W2
DT 3(
DE F)
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Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                         14 svseigl 20
||||||||
1 SVSEIQL 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; T73911.
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WPI; 97-289290/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-NOV-1996; E04850.
16-NOV-1995; DE-042702.
(BOEF) BOEHRINGER MANNHEIM GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W21947 standard; Protein; 20 AA. W21947; W21947; 30-JAN-1998 (first entry) 30-JAN-1998 (first entry) Fusion protein comprising linker and PTH 1-37 (residues 1-7). Linker; parathyroid hormone 1-37; PTH 1-37; streptavidin; fusion protein; recombinant production; thrombin. Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
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|||||||
1 SVSEIQL 7
                                                                                                                                                                                                                                                                                                                        20 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Met(13-139) streptavidin residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "parathyroid homone 1-37 (residues 1-7)"
                                                                                                                                                                                           Score 43; DB 25; Length 20;
Pred. No. 9.43e+01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 43; DB 25; Length 16;
Pred. No. 9.43e+01;
0; Mismatches 0; Indels
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

bular output not generated. n on: Thu Jul 30 10:04:35 1998; MasPar time 3.05 Seconds 83.806 Million cell updates/sec

Title: Description: Perfect Score: >US-08-817-547A-4 (1-7) from US08817547A.pep

Scoring table: PAM 150 Gap 15 Sequence:

1 SYSEIQL 7

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 19.518; Variance 19.793; scale 0.986

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

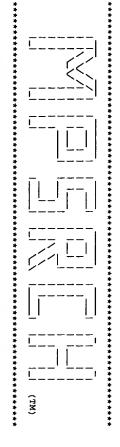
## SUMMARIES

22210000000000000000000000000000000000	No. S
377377444433333344443333333444433333333	Score
100.0 100.0 100.0 100.0 100.0 95.3 95.3 95.3 95.7 90.7 90.7 90.7 90.7 90.7 90.7 90.7 90	Query Match
34 34 37 37 37 37 31 31 36 36 36 36 36 36 31 36 31 31 43 43 43 43 43 43 43 43 43 43 43 43 43	Length
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11HTH 11HTH 11HPH 11HPH 17PG PTHU AG5091 \$76064 \$59990 12MB 151851 G69611 A35694 14179 A40020 866952 866952 866952 1MING2 2MING2 2MING2 2MING2 2MING2 2MING2	ID
cyclic parathyroid ho parathyroid hormone ( parathyroid hormone f parathyroid hormone p parathyroid hormone p parathyroid hormone p parathyroid hormone p parathyroid hormone of parathyroid hormone of parathyroid hormone of parathyroid hormone of parathyroid hormone p parathyroid hormone p parathyroid hormone p hypothetical protein collagen alpha 1(xii) hypothetical protein collagenase protein collagenase protein collagenase (EC 1.18. nitrogenase (EC 1.18. nitrogenase (EC 1.18. nitrogenase (EC 1.18. nitrogenase (EC 1.18. nitrogenase (EC 1.18.	Description
2.97e+00 2.97e+00 2.97e+00 2.97e+00 2.97e+00 9.26e+00 9.26e+00 9.27e+01 2.77e+01 2.77e+01 2.77e+01 4.72e+01 4.72e+01 4.72e+01 7.96e+01 7.96e+01 7.96e+01 7.96e+01 7.96e+01 7.96e+01 7.96e+01 7.96e+01 7.96e+01 7.96e+01 7.96e+01 7.96e+01	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	ω G	32	<u>α</u>	30	29	28	27	26	25	24
3 6	3 6	36	36	36	36	36	36	36	36	36	36	3 6	37	37	37	37	37	37	37	37	37
83.7	83.7	83.7	83.7	83.7	83.7	83.7	83.7	83.7	83.7	83.7	83.7	83.7	86.0	86.0	86.0	86.0	86.0	86.0	86.0	86.0	86.0
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S49956	A54600	I56333	G1BPSV	E33282	865212	D64716	I39649	139518	B39364	S35126	S22553	JC4202	JC4127	S41915	A49448	A05269	S36592	NIAVMA	1N2CA	1N2CC	A55070
probable membrane pro	phosphatidylinositol	apolipoprotein B - ra	gene 1 protein - spir	DNA-binding protein (	hypothetical protein	regulatory protein Dn	lipoprotein - Actinob	lipoprotein - Actinob	GDF-1 embryonic growt	anthranilate phosphor	Ig heavy chain V regi	parathyroid hormone -	protein-tyrosine kina	DNA-directed RNA poly	irregular chiasm C-ro	collagen alpha 1(III)	El protein - human pa		nitrogenase molybdenu	nitrogenase molybdenu	DNA primase (EC 2.7.7
1.32e+02	1.32e+02	1.32e+02	1.32e+02	1.32e+02	1.32e+02	1.32e+02	1.32e+02	1.32e+02	1.32e+02	1.32e+02	1.32e+02	1.32e+02	7.96e+01	7.96e+01	7.96e+01	7.96e+01	7.96e+01	7.96e+01	7.96e+01	7.96e+01	7.96e+01

COMMENT Res	#book	#authors	#CIOSS-IEIE	#submission	#authors	REFERENCE	ORGANISM	PDB_TITLE	ALTERNATE_NAMES	TITLE	RESULT 2	Qy 1 SVSEIQL	Db 1 SVSEIQL	Query Match Best Local S Matches	SUMMARY	) 4 ) ) )	FEATURE	Ø	COMMENT Det	SS-I	#submission	#authors	REFERENCE	PUBLITIES	I II E	RESULT 1 ENTRY	
pp.U, Bayreutn : University of Bayreutn (Inesis), 1990 Resolution: not applicable Determination: NMR	ren Verschiedener Parathormonfragmente in	Marx, U.C.	#CTOSS-TETETENCES PUB:12WA ERENCE TN001717	submitted to the Brookhaven Protein Data Bank, June 1996	Roesch, P.; Marx, U.C.		structures #formal_name Homo sapiens #common_name man	st	HPTH(1-34)	Ω.	12WA #type complete	IQL 7	IQL 7	h 100.0%; Score 43; DB 5; Length 34; Similarity 100.0%; Pred. No. 2.97e+00; 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	#region nelix (right hand alpha) #length 34 #molecular-weight 4146 #checksum 5768	nelix (right han	talle delete tale	cyclic; human parathyroid hormone; norleucine NMR structure; ornithine	Determination: NMR	reterences PUB: LHTH	submitted to the Brookhaven Protein Data Bank, April 1997	Roesch, P.; Seidel, G.; Schaefer, W.; Esswein, A.; Hofmann,		fragment 1 - 34, NMR, 10 structures	or macane no	_	

	Qy 1 SVSEIQL 7  Search completed: Thu Jul 30 10:04:51 1998  Job time: 16 secs.	100.0%; Score 43; DB 5; Length 34; arity 100.0%; Pred. No. 2.97e+00; Conservative 0; Mismatches 0; Indels 0; 7	KEYWORDS hormone  FEATURE	
		); Gaps ();	629	
		Gaps		



MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

n on: Thu Jul 30 10:03:18 1998; MasPar time 2.05 Seconds 85.496 Million cell updates/sec

bular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-817-547A-4 (1-7) from US08817547A.pep 43 1 SVSEIQL 7

Scoring table: PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 20.233; Variance 16.121; scale 1.255

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

esult No.	Score	Query Match	Length	B	Ħ	Description	Pred. No.
1	43	100.0	115	ָב ב	NAMUH_XHTG	PARATHYROID HORMONE PR	3.67e-01
2	43	100.0	115	Н	11	HORMONE	3.67e-01
ω	41	95.3	115	<b>-</b>	PTHY_RAT		1.46e+00
4	41	95.3	896	ب	APCE_SYNY4	PHYCOBILISOME 100.5 KD	
տ	39	90.7	567	μ	CYDC_BACSU	TRANSPORT ATP-BINDING	5.55e+00
on	39	90.7	1827	ш	CUT1_SCHPO	CUT1 PROTEIN.	5.55e+00
7	38	88.4	119	Ц	PTHY_CHICK	PARATHYROID HORMONE PR	1.06e+01
8	38	88.4	3124	μ	CA1C_CHICK	COLLAGEN ALPHA 1(XII)	1.06e+01
9	37	86.0	407	۲	Y090_METJA	PUTATIVE PROTEASE MJ00	1.98e+01
10	37	86.0	438	ب	PRI1_DROME	DNA PRIMASE 50 KD SUBU	1.98e+01
11	37	σ	491	بر	NIFD_AZOVI	NITROGENASE MOLYBDENUM	1.98e+01
12	37	86.0	605	۲	VE1_HPV09	REPLICATION PROTEIN E1	1.98e+01
13	37	86.0	615	μ	CA13_CHICK	COLLAGEN ALPHA 1(III)	1.98e+01
14	37	86.0	675	_	VPS5_YEAST	VACUOLAR PROTEIN SORTI	1.98e+01
15	37	86.0	764	$\vdash$	ICCR_DROME	IRREGULAR CHIASM C-ROU	1.98e+01
16	37	86.0	1116	μ	RPOB_HETCA	DNA-DIRECTED RNA POLYM	1.98e+01
17	37	86.0	1132	$\vdash$	JAK2_RAT	TYROSINE-PROTEIN KINAS	1.98e+01
18	37		1145	۲	DPOG_DROME	DNA POLYMERASE GAMMA (	1.98e+01
19	36	83.7	115	۳	PTHY_CANFA	PARATHYROID HORMONE PR	3.66e+01
20	36		282	$\vdash$	DAAA_STAHA	D-ALANINE AMINOTRANSFE	3.66e+01
21	36	83.7	335	$\vdash$	TRPD_LACLA	ANTHRANILATE PHOSPHORI	3.66e+01
22	36	83.7	350	ب	UOG1_MOUSE	HYPOTHETICAL UOG-1 PRO	3.66e+01
23	36	83.7	392	<b>-</b>	HRC2_CHLTR	HEAT-INDUCIBLE TRANSCR	3.66e+01

45	43	42	41	40	39	38	37	36	35 5	34	<u>ω</u>	32	31	30	29	28	27	26	25	24
ω u G U	ω 1 (5	35	35	3 5	S	ω 5	35	3 5	35	35	35	36	36	ω	36	36	36	3 6	36	36
81.4	81.4	81.4	81.4	81.4	81.4	81.4	81.4	81.4	81.4	81.4	81.4	83.7	83.7	83.7	83.7	83.7			83.7	83.7
2109	1036	890	853	760	679	500	464	325	314	303	262	1150	1070	1047	859	857	832	553	537	393
<b>-</b> -	. р	Ь	ب	Н		۳	<u>س</u>	_	_	ب	<u></u>	بر	_	<u>, , , , , , , , , , , , , , , , , , , </u>	_	_	Ц	_	Ц	ь
RRPL_VSVSJ	P200_MYCPN	YOJN_ECOLI	PXA2_YEAST	YCE5_YEAST	PBP2_STRPN	ZIPP_DROME	WCAM_ECOLI	SYK3_ECOLI	REPE_STAAU	Y367_HAEIN	FLGG_CAUCR	YIC6_YEAST	P11B_HUMAN	YBDE_ECOLI	YQD3_CAEEL	CLPB_ECOLI	KLP1_SCHPO	VG1_SPV4	ZO29_XENLA	THIL_RHIME
RNA POLYMERASE BETA SU	ı	PROBABLE SENSOR PROTEI	PEROXISOMAL LONG-CHAIN	HYPOTHETICAL 87.2 KD P	PENICILLIN-BINDING PRO	ZIPPER PROTEIN PRECURS	COLANIC ACID BIOSYNTHE	HYPOTHETICAL LYSYL-TRN	REPLICATION INITIATION	HYPOTHETICAL PROTEIN H	FLAGELLAR BASAL-BODY R	HYPOTHETICAL 133.0 KD	PHOSPHATIDYLINOSITOL 3	HYPOTHETICAL 114.7 KD	HYPOTHETICAL 96.7 KD P	CLPB PROTEIN (HEAT SHO	KINESIN-LIKE PROTEIN 1	CAPSID PROTEIN.	OOCYTE ZINC FINGER PRO	ACETYL-COA ACETYLTRANS
6.65e+01	•	6.65e+01	6.65e+01		6.65e+01	6.65e+01	6.65e+01	6.65e+01	6.65e+01		6.65e+01	3.66e+01			3.66e+01	3.66e+01	3.66e+01	3.66e+01	٠	3.66e+01

JER M.M., HENDY G.N., O'RIOR 723-5729(1978).  D. ALL H.D., JACOBS J.W., BARLI POTTS J.T. JR.; LATING HORMONES, TALMADGE R. LA, PP.9-14, EXCERPTA MEDICA	SEQUENCE OF 26-37.  MEDLINE; 74174967.  JACOBS J.W., KEMPER B., NIALL H.D., HABENER J.F., NATURE 249:155-157(1974).  [4] SEQUENCE OF 32-68. MEDLINE; 74111656. NIALL H.D., SAUER R.T., JACOBS J.W., KEUTMANN H.T. O'RIORDAN J.L.H., AURBACH G.D., POTTS J.T. JR.; PROC. NATL. ACAD. SCI. U.S.A. 71:384-388(1974).  [5] SEQUENCE OF 61-83 AND 84-115.	SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  MEDLINE; 82150870.  HENDY G.N., KRONENBERG H.M., POTTS J.T. JR., RICH PROC. NATL. ACAD. SCI. U.S.A. 78:7365-7369(1981).  [2]  SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  MEDLINE; 83169834.  VASICEK T.J., MCCEVITT B.E., FREEMAN M.W., FENNICH HENDY G.N., POTTS J.T. JR., RICH A., KRONENBERG H. PROC. NATL. ACAD. SCI. U.S.A. 80:2127-2131(1983).	RESULT 1  ID PTHY_HUMAN STANDARD; PRT; 115 AA.  AC P01270;  DT 21-JUL-1986 (REL. 01, CREATED)  DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)  DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)  DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).  GN PTH.  OS HOMO SAPIENS (HUMAN).  CEUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA;  PN [1]
a, ż	· `	81). 81). NNICK B.J., RG H.M.;	ТН). RAPODA; MAMMALIA;

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Query Match
Best Local S
Matches
                                                                 CONFLICT
SEQUENCE
                                                                                                                           HORMONE;
SIGNAL
PROPEP
CHAIN
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MARX U.C., AUSTERMA
STICHT H., WALTER S
ROESCH P.;
                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 91009811.

ARNOLD A., HORST S.A., GARDELLA T.J., BABA H., LEVINE M.A.,

KRONENBERG H.M.;

J. CLIN. INVEST. 86:1084-1087(1990).

-I- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS

BONE AND PREVENTING THEIR RENAL EXCRETION.

-I- DISEASE: DEFECTS IN PTH ARE A CAUSE OF FAMILIAL ISOLATED

HYPODARAPHYROLDISM (FIH).

EMBL; J00301; G190704; -.

EMBL; A29146; E186700; -.
                                                                                                                                                                                                                                            VARIANT
                                                                                                                                                                                                                                                                                                                                                                PIR; A01536; PTHU.
PIR; A19339; A19339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 93345518.
BARDEN J.A., CUTHBERTSON R.M.;
EUR. J. BIOCHEM. 215:315-321(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 91299748.
KLAUS W., DIECKMANN T., WRAY V.,
BIOCHEMISTRY 30:6936-6942(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRUCTURE BY NMR OF 32-68 MEDLINE; 95318084.
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MEDLINE; 75146516.

KEUTMANN H.T., NIALL H.D., O'RIORDAN J.L.H., POTTS J.T. JR.;
BIOCHEMISTRY 14:1842-1847(1975).

[8]
100.0%;
Local Similarity 100.0%;
les 7; Conservativa
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ANDREATTA R.H., HARTMANN A., JOEHL A.,
RINIXER B., RITTEL W., SIEBER P.;
HELV. CHIM. ACTA 56:470-473(1973).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 75059220.

TREGEAR G.W., VAN RIETSCHOTEN J., GREEN E., NIALL H.D., KEUTMANN H.T., PARSONS J.A., O'RIORDAN J.L.H., POTTS J. HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 355:415-421(1974).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYNTHESIS OF 32-65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BIOL.
                                                                                                                                                                                                                                            1HPH;
1HTH;
1ZWA;
1ZWB;
1ZWC;
1ZWD;
1ZWE;
1ZWE;
                                                                                                        PS00335; PARATHYROID; 1.
SIGNAL; DISEASE MUTATION; 3D-STRUCTURE.

1 25
26 31
32 115 PARATHYROID HORMONE
18 18 C -> R (IN FIH; LEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHEM. 270:15194-15202(1995).
                                                                                                                                                                                                                             12-MAR-97.
16-JUN-97.
16-JUN-97.
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15-OCT-97.
12-MAR-97.
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115
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12-MAR-97.
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SCHMID F.-X.,
                                                                 W.
    Score 43; DB 1; 1
Pred. No. 3.67e-01;
0; Mismatches (
                                                         PARATHYROID HORMONE.
C -> R (IN FIH; LEADS TO INEF)
PROCESSING OF THE PRECURSOR).
N -> D (IN REF. 5).
; 243E87C7 CRC32;
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A POTTS J.T. JR.;
L BICCHEMISTRY 13:1994-1999(1974).
L BICCHEMISTRY 13:1994-1999(1974).
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE BONE AND PREVENTING THEIR RENAL EXCRETION.
DR EMBL; XO5722; G1839; -.
DR PIR; A01535; PTPG.
DR PIR; B26806. B26806.
DR PROSITE; PS00335; PARATHYROID; 1.
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Search completed: Thu Job time: 7 secs.
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P01269;
21-JUL-1986
01-JAN-1988
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PARATHYROID
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MEDLINE; 76018954.

CHU L.L.H., HUANG W.-Y., LITTLEDIKE
BIOCHEMISTRY 14:3631-3635(1975).
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EUKARYOTA; METAZOA;
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Pred. No. 3.67e-01
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

n on: Thu Jul 30 10:03:43 1998; MasPar time 3.80 Seconds 77.626 Million cell updates/sec

bular output not generated.

Title: Description: Perfect Score: Sequence: >US-08-817-547A-4 (1-7) from US08817547A.pep 43 1 SVSEIQL 7

Scoring table: PAM 150 Gap 15

Searched: 140542 segs, 42109429 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb15
1:sp\_fung1 2:sp\_human 3:sp\_invertebrate 4:sp\_mammal
5:sp\_mhc 6:sp\_organelle 7:sp\_phage 8:sp\_plant
9:sp\_bacteria 10:sp\_rodent 11:sp\_virus 12:sp\_vertebrate
13:sp\_unclassified

Statistics: Mean 19.611; Variance 15.404; scale 1.273

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result	Score	% Query Match	Length	B	Ħ	Description	Pred. No.
_	41	95.3	896	ø	Q55544	HYPOTHETICAL 100.3 KD	1.43e+00
2	39	90.7	105	10	Q63473	PARATHYROID HORMONE (F	5.71e+00
ω	39	90.7	764	œ	P93756	RECEPTOR-LIKE PROTEIN	5.71e+00
4	38	88.4	325	ω	016546	C35A11.2 PROTEIN.	1.12e+01
ហ	38	88.4	459	<b>,</b>	013724	HYPOTHETICAL 51.4 KD P	1.12e+01
a	38	88.4	717	11	041942	õ	1.12e+01
7	38	88.4	958	œ	Q40554	PNLA-35.	1.12e+01
8	37	86.0	287	12	Q90794	ALPHA-1 TYPE III COLLA	2.16e+01
9	37	86.0	691	10	035804	JANUS PROTEIN TYROSINE	2.16e+01
10	37	86.0	714	10	P70593	A-KINASE ANCHORING PRO	2.16e+01
11	37	86.0	930	9	Q53173	MGPS.	2.16e+01
12	37	6	1145	w	Q94906	DNA POLYMERASE GAMMA (	2.16e+01
13	37	σ	1810	ω	Q18038	CODED FOR BY C. ELEGAN	2.16e+01
14	37	86.0	2089	N	Q14676	KIAA0170 PROTEIN.	2.16e+01
15	37	86.0	3456	11	P89201	POLYPROTEIN.	2.16e+01
16	36	ω	101	ω	015625	(FRAGMENT).	4.10e+01
17	36	w	189	w	Q19478	F15B9.1.	4.10e+01
18	36	83.7	203	Н	Q03201	HYPOTHETICAL 23.4 KD P	4.10e+01
19	36	83.7	356	ဖ	031461	YBGE PROTEIN.	4.10e+01
20	36	83.7	366	9	Q44163	LIPOPROTEIN PRECURSOR.	4.10e+01

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21
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D9509.25P.	LEUKOTOXIN.	PENICILLIN BINDING PRO	PENICILLIN BINDING PRO	PENICILLIN BINDING PRO	BINDING	PENICILLIN BINDING PRO	PENICILLIN BINDING PRO	(STRAIN KAGUANE/73) PE	(STRAIN NG43/69) PENIC	(STRAIN VAL) PENICILLI	PENICILLIN-BINDING PRO	PENICILLIN-BINDING PRO	B0564.3.	F56D6.3.	PENICILLIN-BINDING PRO	PEPTIDE SYNTHETASE.	POLYPEPTIDE.	HYPOTHETICAL 133.0 KD	HYPOTHETICAL 129.9 KD	IN B (	HYPOTHETICAL 42.6 KD P	CHROMOSOME XVI READING	REGULATORY PROTEIN DNI	LIPOPROTEIN PRECURSOR.
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EUKARYOTA; METAJOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; RODENTIA. [1] SEQUENCE FROM N.A.		AN-1998 (TREMBLREL. THYROID HORMONE (FRA	(TREMBLEEL 01, LAST SEQUENCE U	ומסקשם בפון חו	JT 2 Q63473 PRELIMINARY; PRT; 105 AA.	1 SYSEIQL 7	562 SVARIQL 568	Pred. No. 1.43e+00 1; Mismatches	95.3%; Score 41;	SEQUENCE 896 AA; 100295 MW; EE614E7E CRC32;		EMRI. DE33999 (61001419) -		<b>₹</b> ;	29.	CC6803;	SEOUENCE FROM N.A.	CYANOBACTERIA; CHROOCOCCALES.	PROKARYOTA; BACTERIA; GRACILICUTES; OXYPHOTOBACTERIA;	SYNECHOCYSTIS SP.		I 100 3 KD PROTETN	O1-NOV-1996 (TREMBLEEL OI, LAST ANNOTATION UPDATE)	01, CREATED)		Q55544 PRELIMINARY; PRT; 896 AA.	

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RC TISSUE-THYROID, AND PARATHYROID;
RA SCHMELZER H.J., GROSS G., MAVER H.;
RL ADV. GERE TECHNOL. 21:228-229(1984).

DR EMBL; M54875; G601933; -.

FT NON_TER 105 AA; 11746 MW; 6AC3163E CRC32;

QUERY MATCH 90.7%; SCOORE 39; DB 10; Length 105;

MATCHES 5; CONSERVATIVE 2; Mismatches 0; Indels 0; Gaps 0;

DD 22 ALSETOL 28

QY 1 SYSETOL 7

Search completed: Thu Jul 30 10:04:16 1998

Job time: 33 secs.
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

ibular output not generated. Thu Jul 30 10:07:26 1998; MasPar time 2.53 Seconds 36.409 Million cell updates/sec

Sequence: Description: Perfect Score: >US-08-817-547A-5 (1-6) from US08817547A.pep 35 1 SVSEIQ 6

Title:

Scoring table: PAM 150 Gap 15

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 12.234; Variance 31.551; scale 0.388

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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0.0 35 14 R74503 Parathyroid hormo   0.0 35 14 R74513 Parathyroid hormo   0.0 35 14 R74418 Parathyroid hormo   0.0 35 14 R74418 Parathyroid hormo   0.0 35 14 R74417 Parathyroid hormo   0.0 36 9 R58020 [LB,A16,D17,L18,A   0.0 36 9 R58055 [LB,Q18] hPTH(1-3   0.0 36 9 R58213 [D-Ser17]-hPTH(1-3   0.0 36 9 R58214 [Ala19]-hPTH(1-3   0.0 36 9 R58141 [La12]]-hPTH(1-3   0.0 36 9 R58140 [Ala13]-hPTH(1-3   0.0 38 9 R58141 [Ala13]-hPTH(1-3   0.0 38 9 R58157 [Arg27]-hPTH(1-3   0.0 38 9 R58115 [Xrg27]-hPTH(1-3   0.	35 U	3 (d	n C	ω	35	35	35	<u>3</u> 5	35	3 5	35	ω 5	35	35	35	35	3 5	35	35	35	3 5	35	35	35	35
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R74503 Parathyrold hormo R74510 Parathyrold hormo R74418 Parathyrold hormo R74417 Parathyrold hormo R74417 Parathyrold hormo R580200 [D-His9] hPTH(1-3 R580238 [D-Ser17] hPTH(1-3 R582138 [D-Ser17] hPTH(1-3 R582131 [D-Ser17] hPTH(1-3 R582131 [Ala13] hPTH(1-3 R58103 [Ala13] hPTH(1-3 R58115 [Arg27] hPTH(1-3 R58141 [Leu21] hPTH(1-3 R58115 [Ly316] hPTH(1-3 R58116 [Ser16] hPTH(1-3 R58116 [Ser16] hPTH(1-3 R58116 [V316] hPTH(1-3 R58116 [V316																									
Parathyroid hormo Parathyroid hormo Parathyroid hormo Parathyroid hormo Parathyroid hormo [D-His9]-hPTH(1-3 [L8,A16,D17,L18,A [L8,A16,D17,L18,A [L8,A16,D17,L18,A [L8,A16,D17,L18,A [L8,A16,D17,L18,A [L8,A13]-hPTH(1-38 [A131]-hPTH(1-38 [A131]-hPTH(1-38 [A131]-hPTH(1-38 [A131]-hPTH(1-38 [L927]-hPTH(1-38 [A132]-hPTH(1-38 [A132]-hPT	<b>4</b> 0	<b>.</b>	ں -	25	່ຜ	G	27	25	26	10	9	9	9	9	9	9	9	9	ဖ	ø	Q	14	14	14	14
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	~		4 2	ទ		tion resistant	parathyroid ho	protien compr	parathyroid ho	z	6]-hPTH(1-38)-0	6]-hPTH(1-38)-	7]-hPTH(1-38)-	1]-hPTH(1-38)-	3]-hPTH(1-38)-	a19]-hPTH(1-36)-	17]-hPTH(1-36)	sp30]-hРТН	Q18]-hPTH(1-36)-	,A16,D17,L18,A19]	]-hPTH(1-36)-	roid hormone	hormone	hormone	roid hormone

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etch virus (TEV) recovered by SA 1	The solution was clarified and the supernatant concentrated and purified on a column of immobilised iminobiotin. The purified	and isolated inclusion bodies solubilised in guanidine hydrochloride, and renatured by dilution in pH 7 phosphate buffer.	containing kanamycin and ampilcilin. Cells were harvested, lysed	repressor plasmid pubs500 were used to transform E. Coli Kiz KM82.	(SA) sequence, to give pSA-TEV-PTH. pSA-TEV-PTH and the LacIq	fragment of pSAM-CORE, which contains the Met(13-139) streptavidin	optimised for E. coli, was ligated to the 2.9 kb NheI-HindIII	with codon usage	DNA encoding the present	Example 4: Fig 3: 37pp: German.	parathyroid hormone production	റ		WPI; 97-289290/26.	Kopetzki E;	Z		06-NOV-1996; E04850.	22-MAY-1997.							tide	Key Location/Qualifiers	Homo sapiens.	Synthetic.	tobacco etch virus.	fusion protein; recombinant production; TEV NIa protease;	; PTH 1-37; streptavidin	Fusion protein comprising linker and PTH 1-37 (residues 1-7).	30-JAN-1998 (first entry)		W21948 standard: Protein: 16 AA.	LT 1

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Search completed: Thu Jul 30 10:07:41 1998 Job time: 15 secs.
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ID W2
AC W2
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S Example 3; Fig 3; 37pp; German.

CC The DNA encoding the present sequence, a linker and residues 1-7 of CC the parathyroid hormone 1-37 (PTH 1-37) peptide with codon usage CC optimised for E. coli, was ligated to the 2.9 kb NheI-HindIII CC (SA) sequence, to give pSA-THRO-PTH. pSA-THRO-PTH and the LacIq repressor plasmid pUBS500 were used to transform E. coli K12 RM82. Containing kanamycin and ampilciin. Cells were harvested, lysed and isolated inclusion bodies solubilised in guanidine CC hydrochloride, and renatured by dilution in pH 7 phosphate buffer. CC The solution was clarified and the supernatant concentrated and purified on a column of immobilised inminobiotin. The purified material was incubated with thrombin and the PTH 1-37 fragment column followed by SA fragment removal on an iminobiotin phace.
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Matches 6; Conservative
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22-MAY-1997.
06-NOV-1996; E04850.
16-NOV-1995; DE-042702.
(BOEF) BOEHRINGER MANNHEIM GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant production of peptide(s) as fusions with streptavidin attached via cleavable linker - especially for urotropin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kopetzki E;
WPI; 97-289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fusion protein comprising linker and PTH 1-37 (residues 1-7). Linker; parathyroid hormone 1-37; PTH 1-37; streptavidin; fusion protein; recombinant production; thrombin. Synthetic.
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W21947 standard; Protein; 20
W21947;
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nes 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "parathyroid homone 1-37 (residues 1-7)"
                                                                                                                   Score 35; DB 25;
Pred. No. 2.24e+02;
0; Mismatches 0
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

n on: Thu Jul 30 10:06:50 1998; MasPar time 3.00 Seconds 73.160 Million cell updates/sec

bular output not generated.

Description:
Perfect Score:
Sequence: Title: >US-08-817-547A-5 (1-6) from US08817547A.pep 35 1 SVSEIQ 6

Scoring table: PAM 150 Gap 15

Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

120441 seqs, 36531193 residues

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nr13d

Statistics: Mean 17.547; Variance 15.799; scale 1.111

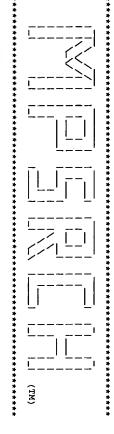
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

sult	Score	% Query Match	Length	BB	ID	Description	- Z
۱ -	35	100.0	34	5	1HTH	cyclic parathyroid ho	2.66e+01
N	35	٠	34	u	1ZWA	yroid hormone	
ω	35		37	σ	1HPH		
4	35	٠	115	N	JC4202	parathyroid hormone -	2.66e+01
5	35	٠	115	₩	PTHU	parathyroid hormone p	2.66e+01
σ	35	•	115	<b>,</b>	PTPG		
7	35	100.0	303	N	A64150	hypothetical protein	2.66e+01
æ	35	8	853	N	S34682	=	2.66e+01
9	35		1116	N	S41915	DNA-directed RNA poly	2.66e+01
10	33	94.3	37	u	12WC	parathyroid hormone (	8.67e+01
11	33		115	μ	PTBO	parathyroid hormone p	8.67e+01
12	33	94.3	115	N	A05091	hormone	8.67e+01
13	33		315	N	E69400	~	8.67e+01
14	33		424	Ŋ	139310	zinc finger protein Z	8.67e+01
15	33		428	N	A42311	O	8.67e+01
16	33		540	2	S35071	auxin-resistance prot	8.67e+01
17	33		801	N	PC6010	RNA helicase Gu - hum	8.67e+01
18	33		896	N	S59990	ī	8.67e+01
19	33	94.3	896	N	S76064	hypothetical protein	8.67e+01
20	32	91.4	270	N	B32835		
21	32		329	N	G69210	pothe	1.53e+02
22	32		422	N	A34589	lin-10 protein - Caen	1.
23	32	91.4	507	2	в69957	conserved hypothetica	1.53e+02

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JQ1662	S02711	A47474	S33664	S19011	C47017	S63221	S47329	A69474	S76437	1TOCH	LVITH	LUCYK	LUCYN	1BBRK	1TBQK	1TBQH	S76533	TUCYE	IVITG	G70133	S50344
lyprotein -	cellulase (EC 3.2.1.4	ADP-ribosyltran	flagella-associated p	endo-1,4-beta-xylanas	probable transcriptio	DNA-directed RNA poly			hypothetical protein	thrombin (EC 3.4.21.5	alpha thrombin (EC 3.	(B)	thrombin (EC 3.4.21.5	thrombin (EC 3.4.21.5	thrombin (EC 3.4.21.5	thrombin (EC 3.4.21.5	hypothetical protein	thrombin (EC 3.4.21.5	epsilon thrombin (EC	flagellar biosynthesi	aspergillopepsin homo
2.66e+02		2.66e+02	:	:	2.66e+02	•		2.66e+02	2.66e+02		2.66e+02		2.66e+02		2.66e+02	2.66e+02	2.66e+02	2.66e+02		1.53e+02	1.53e+02

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07:08 1998		Score 35; DB Pred. No. 2.66 0; Mismatche	elix (right hance) elix (right hance) ecular-weight	
		5; Length 34; se+01; s 0; Indels	dalpha)\alpha)\alpha)\alpha)	
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Thu Jul 30 10:05:44 1998; MasPar time 2.12 Seconds 70.907 Million cell update updates/sec

bular output not generated

Description: Perfect Score: Title: (1-6) from US08817547A.pep 35 1 SYSEIQ 6 >US-08-817-547A-5

Sequence:

Scoring table: PAM 150 Gap 15

Searched: 69111 segs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 18.271; Variance 12.955; scale 1.410

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description  PARATHYROID HORMON CATHERSIN B-LIKE CA-KINASE ANCHOR PE AUXIN-RESIGNANCE E PHYCOBILISOME 100. PROBABLE ABC TRANS LIN-10 PROTEIN. HYPOTHETICAL 56.4 PUTATIVE ASPARTYL
DESCRIPTION  PTHY_PIG PTHY_CANEA PARATHYROID HORMONI PTHY_HUMAN PARATHYROID HORMONI PTHY_HUMAN PARATHYROID HORMONI PTHY_HUMAN PARATHYROID HORMONI PTHY_BAST PEROXISOMAL LONG-CI RPOB_HETGA DNA-DIRECTED RNA PO GLNB_MYCTU PTHY_BAYT PHY_BAYT PHY_BAYT PHY_BOYIN PARATHYROID HORMONI CPR3_CAEEL CATHEPSIN B-LIKE CI AK75_BOVIN AK71_RAFTH AUXIM-RESISTANCE PI APCE_SYNY4 PHYCOBILISOME 100: YHBG_RHIME PHYCOB
HORMON HORMON HORMON PROTE LONG-C LONG-C LONG-C LONG-C LORMON HORMON HOR
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1 SYSEIQ

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POL1_BAYMG	YMS2_CAEEL	YS96_CAEEL	PTX3_MOUSE	YM22_YEAST	POR1_WHEAT	FAEH_ECOLI	YSCI_YEREN	CUT1_SCHPO	GUNB_CALSA	PPOL_DROME	ODO1_BACSU	CADD_STAAU	CADA_STAAU	FLHA_BACSU	XYND_BACPO	THRB_BOVIN	RDPO_SCEOB	VE1_HPV15	RBJK_DROME	CYDC_BACSU
GENOME POLYPROTEIN 1 (	$\Box$	HYPOTHETICAL 110.4 KD	PENTAXIN-RELATED PROTE	HYPOTHETICAL 38.6 KD P	OUTER MITOCHONDRIAL ME	K88 MINOR FIMBRIAL SUB	YOP PROTEINS TRANSLOCA	CUT1 PROTEIN.	ENDOGLUCANASE B PRECUR	POLY (ADP-RIBOSE) POLY	2-OXOGLUTARATE DEHYDRO	PROBABLE CADMIUM-TRANS	PROBABLE CADMIUM-TRANS	FLAGELLAR BIOSYNTHESIS	ENDO-1,4-BETA-XYLANASE	PROTHROMBIN PRECURSOR	PROBABLE REVERSE TRANS	REPLICATION PROTEIN E1	J KAPPA-RECOMBINATION	TRANSPORT ATP-BINDING
1.73e+02	1.73e+02	1.73e+02	1.73e+02	1.73e+02	1.73e+02	1.73e+02	1.73e+02	9.18e+01	9.18e+01	9.18e+01	9.18e+01	9.18e+01	9.18e+01	9.18e+01	9.18e+01	9.18e+01	9.18e+01	9.18e+01	9.18e+01	9.18e+01

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Matches 6; Conservative
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P01269;
21-JUL-1986
01-JAN-1988
01-FEB-1996
                                                                                                                                                                                  SIGNAL
PROPEP
CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (REL. 01, CREATED)
01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
PTH. SCROFA (PIG).
                                                                                                                                                                                                                                                                                                                              BIOCHEMISTRY 13:1994-1999(1974).
-I- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN BONE AND PREVENTING THEIR RENAL EXCRETION.
EMBL; X05722; G1839; -.
PIR; A01535; PTPG.
PIR; B26806; B26806.
PROSTITE; PS00335; PARATHYROID; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SAUER R.T., NIALL H.D., HOGAN M.L., KEUTMANN POTTS J.T. JR.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 32-115. MEDLINE; 74253317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 26-115.
MEDLINE; 76018954.
CHU L.L.H., HUANG W.-Y., LITTLEDIKE E.T.,
BIOCHEMISTRY 14:3631-3635(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE; 87316938
SCHWELZER H.-J., GROSS G., WIDERA G., MAYER
NUCLEIC ACIDS RES. 15:6740-6740(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EUTHERIA; ARTIODACTYLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                              HORMONE; SIGNAL.
32 SVSEIQ 37
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115
P.
12852 MW;
                                                          Score 35; DB 1; Length 115; Pred. No. 5.84e+00; 0; Mismatches 0; Indels
                                                                                                                                                                                  PARATHYROID HORMONE; 98B67F47 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O'RIORDAN J.L.H.,
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RESULT
ID PT
AC PS
Search completed: Thu Jul 30 10:05:51 1998 Job time: 7 secs.
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RY SEQUENCE FROM N.A.

RX MEDLINE; 95365966.

RX MEDLINE; 95365966.

RX MEDLINE; 95365966.

RA ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,

GENE 160:241-243(1995).

-1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN

BOME AND PREVENTING THEIR RENAL EXCRETION.

BOME AND PREVENTING THEIR RENAL EXCRETION.

PROSITE; PS00335; PARATHYROID; 1.

KW HORMONE; SIGNAL.

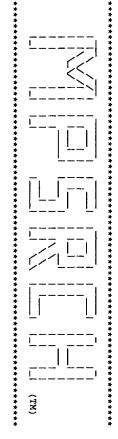
1 25 BY SIMILARITY.

FT FROPEP 26 31 BY SIMILARITY.

FT FROPEP 26 31 BY SIMILARITY.

FT FROPEP 26 31 BY SIMILARITY.

SQ SEQUENCE 115 AA; 12957 MW; 16EDDOEBC CRC32;
                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 35; DB 1; Length 115; Best Local Similarity 100.0%; Pred. No. 5.84e+00; Matches 6; Conservative 0; Mismatches 0; Indels
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PTY_CAPPA STANDARD; PRT; 115 AA.
P52212;
01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
                                                                                                                                                                                         32 SVSEIQ 37
||||||
1 SVSEIQ 6
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; CARNIYORA.
                                                                                                                                                                                                                                                                                                                                                    ,0
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Thu Jul 30 10:06:08 1998; MasPar time 3.81 Seconds 66.309 Million cell updates/sec

bular output not generated.

Title:
Description:
Perfect Score:
Sequence: >US-08-817-547A-5 (1-6) from US08817547A.pep 35

1 SVSEIQ 6

Scoring table: PAM 150 Gap 15

Searched: 140542 segs, 42109429 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: sptremb15

1:sp\_fung1 2:sp\_human 3:sp\_invertebrate 4:sp\_mammal 5:sp\_mhc 6:sp\_organe1le 7:sp\_phage 8:sp\_plant 9:sp\_bacteria 10:sp\_rodent 11:sp\_virus 12:sp\_vertebrate 13:sp\_unclassified

Statistics: Mean 17.730; Variance 12.970; scale 1.367

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result	Score	Query	Length	DB	ID	Description	Pred. No.
1	35	100.0	714	10	P70593	A-KINASE ANCHORING PRO	8.71e+00
2	35	100.0	771	ω	Q20026	CODED FOR BY C. ELEGAN	8.71e+00
ω	33	94.3	315	9	029062	3-HYDROXYACYL-COA DEHY	3.59e+01
4	ω ω	94.3	324	9	007213	HYPOTHETICAL 35.5 KD P	3.59e+01
5	33	94.3	424	N	Q15916	ZID, ZINC FINGER PROTE	3.59e+01
6	ω	94.3	484	ω	018032	TOSFIA.4.	3.59e+01
7	ω	94.3	794	4	018742	LU-ECAM-1.	3.59e+01
80	33	94.3	801	N	Q13436	NUCLEOLAR RNA HELICASE	3.59e+01
9	33	94.3	820	4	018743	LU-ECAM-1.	3.59e+01
10	33	94.3	896	9	Q55544	HYPOTHETICAL 100.3 KD	3.59e+01
11	33	94.3	905	4	018741	LU-ECAM-1.	3.59e+01
12	33	94.3	1967	11	010378	LARGE PROTEIN.	3.59e+01
13	32	91.4	43	N	Q14359	GALACTOSE-1-PHOSPHATE	7.10e+01
14	32	91.4	91	9	P72152	FLAG.	7.10e+01
15	32	91.4	131	11	P87572	E4 ORF1.	7.10e+01
16	32	91.4	239	9	P74971	PV. VESICATORIA ORF1.	7.10e+01
17	32	91.4	258	9	Q52785	ABC-TYPE PERMEASE HOMO	7.10e+01
18	32	91.4	270	9	Q53342	ORF 5' OF RPON.	7.10e+01
19	32	91.4	317	11	Q66606	VIRAL NUCLEOPROTEIN.	7.10e+01
20	32	91.4	329	9	026918	CONSERVED PROTEIN.	7.10e+01

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	ω H	30	29	28	27	26	25	24	23	22	21
3	3	<u>ω</u>	31	31	31	<u>3</u> 1	31	31	31	31	31	31	31	31	31	31	31	31	31	32	32	32	32	32
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016625	Q98902	P91304	015034	036363	Q06078	022113	P93756	Q61468	P79386	P97855	Q51919	Q47701	P71859	P74465	Q14538	007802	Q26980	Q55737	Q63473	Q44909	Q39603	Q44759	014301	Q13283
K10G6.3 PROTEIN.	NEURAL CELL ADHESION M	CODED FOR BY C. ELEGAN	KIAA0318 (FRAGMENT).	DNA POLYMERASE (EC 2.7	SIMILAR TO TRANSCRIPTI	HCR2.	RECEPTOR-LIKE PROTEIN	MEGAKARYOCYTE POTENTIA	ORPHAN NUCLEAR RECEPTO	RAS-GTPASE-ACTIVATING	PUTATIVE CHAPERONINE (	POLYSACCHARIDE CHAIN L	HYPOTHETICAL 33.9 KD P	PILIN BIOGENESIS PROTE	MACROPHAGE LECTIN 2.	HYPOTHETICAL 27.4 KD P	ZEN TC (FRAGMENT).	HYPOTHETICAL 16.4 KD P	PARATHYROID HORMONE (F	FLAGELLAR EXPORT PROTE	HEAT SHOCK PROTEIN 70B	FLHA.	BETA-TRANSDUCIN.	GAP SH3 BINDING PROTEI
1.37e+02	1.37e+02	1.37e+02	1.37e+02	1.37e+02	1.37e+02	1.37e+02	1.37e+02	1.37e+02	1.37e+02	1.37e+02	1.37e+02	1.37e+02	1.37e+02	1.37e+02	1.37e+02	1.37e+02	1.37e+02	1.37e+02	1.37e+02	7.10e+01	7.10e+01	7.10e+01	7.10e+01	7.10e+01

RA RA	RESULT AC OO	Db Ma	RESULT PACE OF COLUMN ACCURATE
SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  MEDLINE; 94150718.  MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,  WILSON R., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,  BONFIELD J., BURTON J., CONNELL M., FAVELLO A., FULTON L.,  CRAXTON M., DEAR S., DU Z., DUBBIN R., FAVELLO A., FULTON L.,  GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,  JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,	LT 2 Q20026 Q20026; Q20026; Q1-NOV-1996 (TREMBLREL. 01, CREATED) Q1-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE) Q1-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE) Q1-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE) CODED FOR BY C. ELEGANS CDNA CEESB82F. F35C8.7. CAENORHABDITIS ELEGANS. EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.	Query Match 100.0%; Score 35; DB 10; Length 714; Best Local Similarity 100.0%; Pred. No. 8.71e+00; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 4 SYSEIQ 9 11111 1 SYSEIQ 6	P70593  PRELIMINARY; PRT; 714 AA.  P70593  01-FEB-1997 (TREMBLREL. 02, CREATED)  01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)  01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)  A-KINASE ANCHORING PROTEIN AKAP150.  A-KINASE ANCHORING PROTEIN AKAP150.  RATTUS NORVEGICUS (RAT).  REUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  EUTHERIA; RODENTIA.  [1]  SEQUENCE FROM N.A.  TAKAI Y., IRIE M., TOYADA A., HATA Y.;  SUBMITTED (SEP-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.  EMBL; U67136; G1532182;  EMBL; U67136; G1532182;  SEQUENCE 714 AA; 75938 MW; OALCFC1F CRC32;

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RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M., RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R., SHALDON N., SMITH A., SONNAMER E., STADEN R., SUISTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R., RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RI NATURE 368:32-38(1994).

RN SEQUENCE FROM N.A.
RN GIJ
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11111111111111111111111111111111111111	Result No. Score Mo. Score	Database: Statistics:	Title: Description: Perfect Score: Sequence: Scoring table: Scoring table: Post-processing	Relea Copyr MPsrch_pp pro n on:	
00.0 16 25 W21948 00.0 20 25 W21947 00.0 34 2 W19997 00.0 34 22 W19997 00.0 34 22 W17967 00.0 34 22 W17960 00.0 34 9 R58228 00.0 34 9 R58228 00.0 34 7 R34353 00.0 34 7 R34353 00.0 34 22 W17947 00.0 34 22 W17947 00.0 35 14 R74415 00.0 35 14 R74415 00.0 36 9 R58047	is the number of results ter than or equal to the ived by analysis of the SUMMARI	a-geneseq31-2 1:part1 2:part2 3:part3 4:pa 8:part8 9:part9 10:part10 11 14:part14 15:part15 16:part1 19:part19 20:part20 21:part2 24:part24 25:part25 26:part2 24:part24 75:part25 26:part2	>US-08-817-547A-6 (1-5) from US08817547A.pep 28 1 SVSEI 5 PAM 150 Gap 15 124785 seqs, 15338987 residue Listing first 45 summaries	se 3.1A John F. Collins, Bioclight (c) 1993-1998 Universit Distribution rights by Oxf tein - protein database searc Thu Jul 30 10:09:42 1998; not generated.	
sion protein compri ssion protein compri man parathyroid hor r clised human parath man pri analogue [C man PTH analogue [C man pri analogue [C man pri analogue [C man pri analogue [C man parathyroid hor man parathyroid hormone p rathyroid hormone p	cted by chance to have of the result being poscore distribution.	<pre>part4 5:part5 6:part6 7:part7 11:part11 12:part12 13:part13 t16 17:part17 18:part18 t21 22:part22 23:part23 t26 27:part27</pre> 9; scale 0.429		oomputing Research Unit.  Y of Edinburgh, U.K.  Cord Molecular Ltd  Th, using Smith-Waterman algorithm  MasPar time 2.61 Seconds  29.338 Million cell updates/sec	**************************************

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	84	84	84	84	84	84	84	84	84	84	47	44	38	38	38	38	38	38	38	36	36	36	<u>ω</u>	36	36	36	
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ALIGNMENTS	56	σ	69	8	942	57	56	R21220	2	W25687	4	2	807	807	814	814	R58283	811	813	830	829	803	26	S	R58284	82	
	resistant	xidation resis	equence of variant	nce of variant	parathyroid	PTH encoded	resistar	Human parathyroid hor	Ä	parathyroid h	n protien	arathy	3]-hPTH(1-38)-	33]-hPTH(1-38)	21]-hPTH(1-38)-	hPTH(1-38)	(Pmc)23]-hPTH(1-	(1-38)-	-hPTH(1-38)-	36]-hPTH(1-	35]-hPTH(1-3	l,Q18]-hPTH(1-	]-hPTH	L-(hPTH 3-35)-	[D-Trp23]-hPTH(1-36)-	9]-hPTH(1-3	
	.96e+C	.96e+C	.96e+0	.96e+C	.96e+C	.96e+0	6e+0	.96e+0	.96e+0	.96e+0	.96e+0	.96e+0	6e+0	.96e+0	.96e+0	6e+0	7.96e+02	.96e+0	.96e+0	.96e+0	.96e+0	.96e+0	6e+0	.96e+0	.96e+0	. 9	

# ALIGNMENTS

The parathyroid hormone production

Example 4; Fig 3; 37pp; German.

The DNA encoding the present sequence, a linker and residues 1-7 of the DNA encoding the present sequence, a linker and residues 1-7 of the parathyroid hormone 1-37 (PPH 1-37) peptide with codon usage optimised for E. coli, was ligated to the 2.9 kb NheI-HindIII

Crapital to fpSAM-CORE, which contains the Met(13-139) streptavidin (SA) sequence, to give pSA-TEV-PTH. pSA-TEV-PTH and the LacIq crepressor plasmid pUBS500 were used to transform E. coli K12 RM82.

Crapital to fine transformants were grown, with IPFG induction, in medium containing kanamycin and amplicillin. Cells were harvested, lysed and isolated inclusion bodies solubilised in guanidine the fine collation was clarified and the supernatant concentrated and column of immobilised ininobiotin. The purified contactial was incubated with tobacco etch virus (TEV) NIA protease and the PTH 1-37 fragment released, recovered by SA fragment 22-MAY-1997. 06-NOV-1996; 16-NOV-1995; Synthetic 30-JAN-1998 (first entry)
Fusion protein comprising linker and PTH 1-37 (residues 1-7).
Linker; parathyroid hormone 1-37; PTH 1-37; streptavidin;
fusion protein; recombinant production; TEV NIa protease; W21948 standard; Protein; W21948; 30-JAN-1998 (first entry) Recombinant production of peptide(s) as fusions with streptavidin attached via cleavable linker - especially for urotropin and (BOEF ) BOEHRINGER MANNHEIM GMBH Kopetzki E; WPI; 97-289290/26. Peptide Peptide Key N-PSDB; T73912. WO9718314-A1. Peptide Homo sapiens. tobacco etch virus. E04850. DE-042702. /note= 2.9 /note= "linker cleavable by TEV NIa protease" 10..16 /note= "parathyroid homone 1-37 (residues 1-7) Location/Qualifiers "parathyroid homone 1-37 (residues 1-7)" "Met(13-139) streptavidin residue" 16 A A

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Search completed: Thu Job time: 16 secs.
                                                                                                                                                                                    #88888888
                                                                                                                                                                                                                                                                                                                                                           PT Recombinant production of peptide(s) as fusions with streptavidin PT Recombinant production of peptide(s) as fusions with streptavidin PT PT Recombinant production PT parathyroid hormone production

EXAMPLE 3; #19 3; 379p; German.

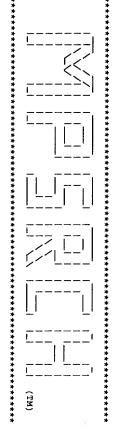
CC The DNA encoding the present sequence, a linker and residues 1-7 of CC ptimised for E. coll. was ligated to the 2.9 kb NheI-HindIII CC (SA) sequence, to give pSA-THRO-PTH. pSA-THRO-PTH and the LacIq repressor plasmid pubs500 were used to transform E. coll K12 RM82. The transformants were grown, with IPTG induction, in medium containing kanamycin and ampilcilin. Cells were harvested, lysed and isolated inclusion bodies solubilised in guanidine thydrochloride, and renatured by dilution in pH 7 phosphate buffer. CC The solution was clarified and the supernatant concentrated and cmaterial was incubated with thrombin and the PTH 1-37 fragment CC column followed by chromatography on a fractogel and reverse phase cc.
                                                                                                                 Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 5; Conservative
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Best Local Similarity 100.0%;

Matches 5; Conservative
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22-MAY-1997.
06-NOV-1995; DE-042702.
(BOEF) BOEHRINGER MANNHEIM GMBH.
                                                        14 svsei 18
|||||
1 SVSEI 5
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WPI; 97-289290/26.
N-PSDB; T73911.
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W21947 standard; Protein; 20
W21947;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-1998 (first entry) Fusion protein comprising linker and PTH 1-37 (residues 1-7). Linker; parathyroid hormone 1-37; PTH 1-37; streptavidin; fusion protein; recombinant production; thrombin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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A
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         Jul 30 10:09:58 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "linker cleavable by thrombin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Met(13-139) streptavidin residue"
2.13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "parathyroid homone 1-37 (residues 1-7)"
                                                                                                            Score 28; DB 25; Le
Pred. No. 7.96e+02;
0; Mismatches 0;
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Pred. No. 7.96e+02;
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                                                                                                                                          Length 20;
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В



MPsrch\_pp on: protein - protein database search, using Smith-Waterman algorithm

abular output not generated. Thu Jul 30 10:09:06 1998; MasPar time 2.97 Seconds 61.602 Million cell updates/sec

Title:
Description:
Perfect Score:
Sequence: >US-08-817-547A-6 (1-5) from US08817547A.pep 28 1 SVSEI 5

Scoring table: PAM 150 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 16.244; Variance 13.192; scale 1.231

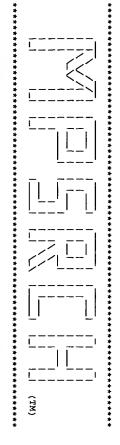
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

NO.	Score	% Query Match	Length	B	Ħ	Description	· 22
ב	28	100.0	34	5	1HTH	cyclic parathyroid ho	3.60e+02
N	28	100.0	34	σ	12WA	yroid hormone	
ω	28	100.0	37	v	1HPH	parathyroid hormone f	3.60e+02
4	28	100.0	115	N	JC4202	parathyroid hormone -	
տ	28		126	N	S75413	٣	3.60e+02
თ	28	100.0	227	N	S54466	•	•
7	28		303	N	A64150	μ	3.60e+02
8	28	•	308	N	JQ1401	glutathione synthase	3.60e+02
9	28	٠	316	ហ	10NRA		•
10	28	•	316	տ	10NRB		3.60e+02
11	28	100.0	316	u	1UCWA	transaldolase (EC 2.2	3.60e+02
12	28	100.0	316	U	1UCWB	2	•
13	28	100.0	344	N	A30544	dnaK-type molecular c	3.60e+02
14	28	100.0	362	N	S12895	polygalacturonase (EC	٠
15	28	100.0	387	N	S33517	tubulin alpha chain -	•
16	28	100.0	389	N	S20933	naringenin-chalcone s	3.60e+02
17	28	100.0	389	N	S33610	naringenin-chalcone s	3.60e+02
18	28	100.0	389	N	S35167	naringenin-chalcone s	•
19	28	•	389	N	S26414	naringenin-chalcone s	3.60e+02
20	28		405	N	A35620	coenzyme F420 hydroge	3.60e+02
21	28	100.0	408	N	A69040	F420-	
22	28		415	ν	S63221	DNA-directed RNA poly	3.60e+02
23	28	100.0	420	N	C64552	exonuclease VII, larg	٠

44 5	4 4 3	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
28 28	2 2 8 8	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0		100.0									100.0	
1332 2844	1146 1232	1116	1039	974	962	921	915	853	741	737	691	628	609	609	491	458	453	451	450
22	N	N	N	N	N	N	N	N	Ν	N	N	N	N	N	N	N	N	N	N
I48314 S28291	S07915 B39432	S41915	S02711	A44484	S58107	A55854	A43802	S34682	S50340	S63453	S54262	A69381	S29698	S55957	B69499	S44741	S07459	JC4133	A45547
homeotic protein CDP hypothetical protein	<pre>RF2 protein - yeast ( ATP-dependent deoxyri</pre>	ted R	cellulase (EC 3.2.1.4	Ď.	hypothetical protein	secA protein - Caulob	cellulase (EC 3.2.1.4	probable transport pr	CHL12 protein - yeast	probable RNA helicase	yl-accepting	type II secretion sys	dnaK-type molecular c	hypothetical protein	sodium- and chloride-	C02C2.3 protein - Cae	tubulin alpha-I chain	alpha-tubulin isoform	tubulin alpha-II chai
3.60e+02 3.60e+02	3.60e+02	3.60e+02	3.60e+02	3.60e+02	3.60e+02	3.60e+02	3.60e+02	3.60e+02	3.60e+02	3.60e+02	3.60e+02	3.60e+02	3.60e+02	3.60e+02	3.60e+02	3.60e+02	3.60e+02	3.60e+02	3.60e+02

able	#book in Strukturen Verschiedener Parathormonfragmente in ###################################	ors	REFERENCE TN001717	rences PDB:1	ion submitted to the Brookhaven Protein Data	rs	REFERENCE A67856	structures	structure of human parathyroid hormone	NATE NAMES HPTH(1-34)	TITLE parathyroid hormone (residues 1-34) - human	т 2	Oy 1 SVSEI 5	Db 1 SVSEI 5	Query Match 100.0%; Score 28; DB 5; Length 34; Best Local Similarity 100.0%; Pred. No. 3.60e+02; Matches 5; Conservative 0; Mismatches 0; Indels	20-29 #region helix (right hand alpha) SUMMARY #length 34 #molecular-weight 4146 #checksum	ביים ליים ליים ליים ליים ליים ליים ליים	ŵ	COMMENT Resolution: not applicable	#submission submitted to the Brookhaven Protein Data Bank, #cross-references PDB: HTH	#authors Roesch, P.; Seidel, G.; Schaefer, W.; Esswein, E.	E the solution structure of cyclic human fragment 1 - 34, NMR, 10 structures	ENTRY 1HTH #type complete TITLE cyclic parathyroid hormone residues 1 34 mut K130RN, S17E, M18NLE - synthetic
	ragmente in Loesung, h (Thesis), 1996				Bank, June 1996		<u> </u>		fragment 1-34, NMR 10		nan				34; dels 0; Gaps 0;	cksum 5768		ucine NMR structure;		Bank, April 1997	swein, A.; Hofmann,	parathyroid hormone	34 mutant M8NLE,



MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Jul 30 10:07:59 1998; MasPar time 2.00 Seconds 62.621 Million cell updates/sec

fabular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-817-547A-6 (1-5) from US08817547A.pep 28

1 SVSEI 5

Scoring table: PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 16.927; Variance 10.693; scale 1.583

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

1 2 3 3 4 4 4 4 7 7 7 7 8 8 8 8 11 11 11 11 11 11 11 11 11 11 1	NO.
NN	Score
11111111111111111111111111111111111111	Query
93 115 115 212 2127 227 227 3303 3316 3316 3362 3389 3389 3389 3389 3389 3389 3389 338	Length I
	DB
TRBJ_ECCLI PTHY_HUMAN PTHY_HUMAN PTHY_PIG TBAA_PNECA YMY0_YEAST YA5A_ENCI TALB_ECCLIC TBAB_CCHIC TBAB_CCHIC TGAB_CHIC CHS3_TRISU CHS4_MEDSA CHS5_MEDSA CHS5_MEDSA CHS2_PEA CHS1_PEA CHS3_PEA CHS3_PEA CHS3_PEA CHS9_MEDSA FRHA_METTH RPA3_YEAST	ID
TRBJ PROTEIN.  PRARATHYROID HORMONE PR PARATHYROID HORMONE PR PARATHYROID HORMONE PR PARATHYROID HORMONE PR PARATHYROID HORMONE PR POLEDIN ALPHA CHAIN (F TUBULIN ALPHA CHAIN (F TUBULIN ALPHA CHAIN (F HYPOTHETICAL 24.9 KD HYPOTHETICAL PROTEIN H PROTEIN ALPHA-8 CHAIN POLYGALACTURONASE II P POLYGALACTURONASE II P POLYGALACTURONASE II P POLYGALACTURONASE 3 (E CHALCONE SYNTHASE 4-2 CHALCONE SYNTHASE 4-1 CHALCONE SYNTHASE 17 (E CHALCONE SYNTHASE 17 (C CHALCONE SYNTHASE 1 (E CHALCONE SYNTHASE 3 (E CHALCONE	Description
1. 2277ee	Pred. No.

45	44	43	42	41	40	39	38 8	37	36	3 5	34	ω ω	32	31	30	29	28	27	26	25	
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100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	1000
2916	1505	1332	1146	1116	1039	974	962	921	737	644	621	609	609	493	458	453	451	451	448	447	
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YN81_CAEEL	CDP_HUMAN	CDP_MOUSE	KTXA_KLULA	RPOB_HETCA	GUNB_CALSA	SIN4_YEAST	YA4E_SCHPO	SECA_CAUCR	SUV3_YEAST	KNH_HUMAN	DNAK_MYCLE	DNAK_MYCTU	YL01_YEAST	PUR1_SYNP7	YKH3_CAEEL	TBA_PLAFK	TBA_TRYBR	TBA_TORMA	TBA_CANAL	TBA1_YEAST	+ t
HYPOTHETICAL 316.1 KD	CCAAT DISPLACEMENT PRO	CCAAT DISPLACEMENT PRO	KILLER TOXIN ALPHA AND	DNA-DIRECTED RNA POLYM	ENDOGLUCANASE B PRECUR	GLOBAL TRANSCRIPTIONAL	HYPOTHETICAL TRP-ASP R	PREPROTEIN TRANSLOCASE	MITOCHONDRIAL ATP-DEPE	KININOGEN, HMW PRECURS	DNAK PROTEIN (HEAT SHO	DNAK PROTEIN.	HYPOTHETICAL 69.8 KD P	AMIDOPHOSPHORIBOSYLTRA	HYPOTHETICAL ACETYLCHO	TUBULIN ALPHA CHAIN.	TUBULIN ALPHA CHAIN.	TUBULIN ALPHA CHAIN (A	TUBULIN ALPHA CHAIN.	TUBULIN ALPHA-1 CHAIN.	- COCHE
1.27e+02	1.27e+02	1.27e+02	1.27e+02	1.27e+02	1.27e+02	1.27e+02	1.27e+02	1.27e+02	1.27e+02	1.27e+02	1.27e+02	1.27e+02	1.27e+02	1.27e+02	1.27e+02	1.27e+02	1.27e+02	1.27e+02	1.27e+02	1.27e+02	F . C . C .

SECTOR	RESULT	Qy	M B Q u	SQ	X	DR DR	DR	88	P R	RX	R P	2 2	R.	쫎	RC	공 :	로 S	გ	ន	000	3 1	ij	D I	2 2	RESULT
01-OCT-1996 (REL. 34, CREATED) 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE) 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE) PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH). PTH.	LT 2 PTHY_CANFA STANDARD; PRT; 115 AA. D53212.	66 SYSEI 70       1 SYSEI 5	Query Match 100.0%; Score 28; DB 1; Length 93; Best Local Similarity 100.0%; Pred. No. 1.27e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	SEQUENCE 93 AA; 10160 MW; C604F894 CRC32;		EMBL; U01159; G398536; PIR; F32238; QQEC25.	M20787; -; NOT_A	-1- FUNCTION: UNKNOWN.	FROST L.S., IPPEN-IHLER K., SKURRAY R.A.;	94359430.	SEOUENCE FROM N.A.	[2]	J.H., IPPEN-IHLER K	89123020.		SEQUENCE FROM N.A.	ENTEROBACTERIACEAE.			ESCHERICHIA COLI.	TRBJ PROTEIN.	(REL. 34, LAST ANNOTATIO	(REL. 31,	1990 (REL.	LT 1 D18353. STANDARD; PRT; 93 AA.

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Search completed: Thu Jul 30 10:08:06 1998 Job time: 7 secs.
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RC TISSUE-PARATHYROID;

RX MEDLINE; 95369696.

RA MEDLINE; 95369696.

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RA ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K
                                                                                                                                                                                                                                                                                                                   uery Match 100.0%;
Best Local Similarity 100.0%;
Matches 5; Conservative
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1 SVSEI 5
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EUKARYOTA; METAAOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; CARNIVORA.
[1]
                                                                                                                                                                                                                                                                                             Score 28; DB 1; Length 115;
Pred. No. 1.27e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                  0;
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28 100.0 113 9 051810 28 100.0 113 9 051810 28 100.0 113 9 051810 28 100.0 126 9 P95985 28 100.0 128 2 015631 28 100.0 228 10 P97891 28 100.0 228 10 062344 28 100.0 228 10 062344 28 100.0 228 10 062343 28 100.0 338 9 044791 28 100.0 338 9 047506 3 28 100.0 378 9 031328 3 28 100.0 378 9 031828 3 28 100.0 389 8 023882 4 28 100.0 389 8 023882 5 28 100.0 389 8 023882 6 28 100.0 389 8 023882 7 28 100.0 389 8 023882 7 28 100.0 389 8 023882 8 28 100.0 394 8 043803 8 28 100.0 394 8 043803 9 28 100.0 394 8 043803 9 28 100.0 394 8 043803 9 28 100.0 394 8 023883	Pred. No. is the number of results predicted score greater than or equal to the score of t and is derived by analysis of the total score SUMMARIES  Result Query No. Score Match Length DB ID Descrip	Database: sptremb15 1:sp_fungi 2:sp_human 3:sp_inve 5:sp_mhc 6:sp_organelle 7:sp_ph 9:sp_bacteria 10:sp_rodent 11:s 13:sp_unclassified  Statistics: Mean 16.468; Variance 10.714; s	Score: 28 : 1 SVSEI 5 : a SVSE	Release 3.1A John F. Collins, Biocompu Copyright (c) 1993-1998 University of Distribution rights by Oxford protein - protein database search, u Thu Jul 30 10:08:23 1998; Mass 59.0 Dutput not generated.  >US-08-817-547A-6  >US-08-817-547A.pep Lon: (1-5) from US08817547A.pep	
CCAL 9.0 KD PR 1.95e (CAL 12.6 KD P 1.95e (CAL 12.6	ed by chance to have a  If the result being printed,  Fore distribution.  Pred. No.	<pre>invertebrate 4:sp_mammal p_phage 8:sp_plant il:sp_virus 12:sp_vertebrate ; scale 1.537</pre>		uting Research Unit. f Edinburgh, U.K. Molecular Ltd using Smith-Waterman algorithm Par time 3.56 Seconds 081 Million cell updates/sec	

44 5	4 4 3	4 6	39 40	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21
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E 2 (CUX-2). TICAL 215.3	KIAA0293 (FRAGMENT). SIMILAR TO KERATIN AND	CUX/CDP (FRAGMENT).	NB-2.	HYPOTHETICAL HELICASE	105	R BY C. ELEG		MCPA PROTEIN.	٠	STRAIN) P83/1	TYPE II SECRETION SYST	DNAK.	PETHY, ZPT4-2.	TRANSCRIPTION FACTOR Z	COSMID F32E10.	SODIUM- AND CHLORIDE-D	1-AMINOCYCLOPROPANE-1-	1-AMINOCYCLOPROPANE 1-	ALPHA-III TUBULIN.	ALPHA TUBULIN.	ALPHA-TUBULIN II.
			ىر د	<u>ب</u>	ч	٢	<u>-</u>	1.9		1.95e+02	٠		1.9		1.9	_	<u>-</u>	1.9		1.95e+0	1.9

# ALIGNMENTS

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RESULT 2

O16290;
AC O16290;
DT O1-CAN-1998 (TREMBLREL O5, CREATED)
DT O1-JAN-1998 (TREMBLREL O5, LAST SEQUENCE UPDATE)
DT O1-JAN-1998 (TREMBLREL O5, LAST ANNOTATION UPDATE)
DT O1-JAN-1998 (TREMBLREL O5, LAST ANNOTATION UPDATE)
DE F32D1.8 PROTEIN.
GN F32D1.8 CAEMORHABDITIS ELEGANS.
OC CAEMORHABDITIS ELEGANS.
OC CUKARYOTA; METAZOA; ACCOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
RN [1]
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE; 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 1
1 O30721;
AC O30721;
DT O31721;
DT O1-JAN-1998 (TREMBLREL. 05, CREATED)
DT O1-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT O1-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DT HYPOTHETICAL 90 KD PROTEIN (FRAKMENT).
OS HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).
OC PROKARYOTA; GRACILICUTES; SCOTOBACTERLA;
OC AEROBIC, MOTILE, HELICAL AND/OR VIBRIOID.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CCUG 17874;
RA MASIGNANI V., ARICO' B.;
RA MASIGNANI V., ARICO' B.;
EMBL; AFO16039; G2367603; -.
KW HYPOTHETICAL PROTEIN.
FT NON_TER 82
SEQUENCE 82 AA; 9025 MW; 25304A67 CRC32;
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Best Local Similarity 100.0%;
Matches 5; Conservative
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STRAIN-CCUG 17874;
MASIGNANU V., ARICO' B.;
SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF016039; G2367603; -.
HYPOTHETICAL PROTEIN.
NON_TER 82 82
SEQUENCE 82 AA; 9025 MW; 25304A67 CRC32;
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1 SVSEI 5
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RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTMORE B., O'CALLAGHAN M.,
RA THIERRY-MIEG J., THOMAS K., VANDIN M., VAGHAN K., WATERSTON R.,
RA HATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RL NATURE 368:32-38(1994).
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA SEQUEN
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Result
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       protein - protein database search, using Smith-Waterman algorithm
     1000.00
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Match
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1:part1 2:0
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8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
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Modified hPTH(7-34)NH
Human parathyroid hor
Parathormone N-termin
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Cyclised human parath
[Ala26]-hPTH(1-36)-NH
[D-Val35]-hPTH(1-36)-NH
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45	44	43	42	41	40	39	3 8	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	
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#### ALIGNMENTS

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RESULTANT REPORT OF THE PROPERTY OF THE PROPER
                                                                                                                                                                                                                                                           New parathyroid hormone analogues - useful for treatment and in vitro diagnosis of PTH-dependent tumours, immune disorders, or steoporosis and hyperparathyroidism.

Claim 1; Column 10; 6pp; English.

The peptide is modified at Lys13 (of the parent PTH) in the epsilon amino acid gp. by N.N-diisobutyl or 3-phenylpropancyl. The PTH analogue binds with high affinity to the peptide hormone receptor without activating the 2nd messenger mol. The modification of the Lys residue stabilises the bioactive conformation of PTH to enhance the activity. The peptide may be used in in vitro bioassays to measure naturally occurring PTH and to diagnose the etiology of or to treat osteoporosis or hypercalcaemia. It may also be used to treat immune diseases such as fumours. It may also be used to the component of the substances, such as inflammation. It is prepd. by solid
Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 10; Conservative
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14-JUL-1992 (first entry)
Modified hPTH(7-34)NH2.
Parathyroid hormone; analogue; osteoporosis; hyperthyroidism;
tumours; hypercalcaemia; renal failure; human.
                                                                                                                                                      treat immune diseases phase synthesis.
See also R22058-75.
Sequence 28 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MERI ) MERCK & CO INC. Rosenblatt M, Roubini E, WPI; 92-096233/12.
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25-APR-1990; US-514394.
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/label= NH2
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/note= "OTHER
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Indels

0

Gaps

0

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RESULT
ID R7
AC R7
AC R7
DT 04
DE H:
KW O:
KW O:
KW M:
KW D:
KW M:
KW D:
KW D:
DD 0
DD 0
DF 2
                                                                                                                                                                                                                              pp 04-MAY-1995.

PF 25-OCT-1993; US-142551.

(AFFY-) AFFYMAX TECHNOLOGIES NV.

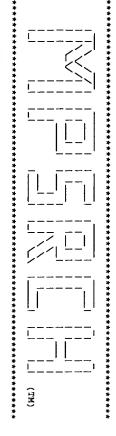
Oldenburg KR, Selick HE;

DR WPI; 95-17880/23.

PT New active analogues of parathyroid hormone - with increased extivity, stability in serum etc., esp. for treating osteoporosis, also related DNA and vectors

PS Disclosure; Page 1: 109pp; English.

CC This sequence represents residues 1-34 of human parathyroid hormone (RPTH). This sequence was used in the production of analogues of the CC truncated form of prH. These analogues have increased activity and CC longer serum half life than native PTH due to eg. substitution of Met CC residues with Leu residues and replacing the carboxy Phe with Tyr. The CC carboxy terminal may also be modified by the addition of a homoserine CC residue or analogue, or by the addition of residues 35-84 of wild type osteoporosis or hypercalcaemia, hyperparathroidism or other metabolic CC have increased iontophoretic transfermal transport compared to wild type Sequence 34 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
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Best Local Similarity 100.0%;
Matches 10; Conservative
rch completed: Thu Jul 30 10:12:36 1998 time : 22 secs.
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R74521;
04-DEC-1995 (first entry)
Human parathyroid hormone (1-34).
Analogue; truncated human parathyroid hormone; PTH; hPTH; substitution; osteoporosis; hypercalcaemia; hyperparathroidism; metabolic bone disease; human; veterinary medicine; iontophoretic transdermal transport; recombinant E.coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
W09511988-A.
                                                                                                 9 hnlgkhlnsm 18
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|||||||||
1 HNLGKHLNSM 10
                                                                               HNLGKHLNSM 10
                                                                                                                                           Score 73; DB 14; Length 34; Pred. No. 1.59e+00; O; Mismatches 0; Indels
                                                                                                                                             0;
                                                                                                                                             Gaps
                                                                                                                                         0
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Jul 30 10:11:22 1998; MasPar time 3.20 Seconds 114.268 Million cell updates/sec

Tabular output not generated.

Title: >US-08-817-547A-7
Description: (1-10) from US08817547A.pep
Perfect Score: 73

Sequence: 1 HNLGKHLNSM 10

Scoring table: PAM 150 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: pir56

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nr13d

Statistics: Mean 22.338; Variance 29.941; scale 0.746

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	89	7	σ	ر.	4	ω	2	1	NO.
47	47	48	48	48	48	49	50	55	59	59	62	69	69	69	73	73	73	73	73	73	73	73	Score
64.4	•		•	•	65.8					•	•	94.5	•	•	•	100.0	•				•	100.0	% Query Match
619	187	437	437	172	172	421	513	34	115	105	115	115	115	37	115	37	36	35	34	34	34	34	Length
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S54636	S25395	S48853	S52014	E69671	A35145	E69467	S21976	1HTH	A05091	I51851	PTPG	PTBO	JC4202	1ZWC	DHTHU	1HPH	1ZWB	1ZWD	1ZWF	1ZWG	1ZWE	12WA	Ħ
	H+-transporting ATP s	H+-transporting ATP s	O	transcriptional repre	-	hypothetical protein	probable RNA-directed	4	hormone	parathyroid hormone -	hormone	parathyroid hormone p	parathyroid hormone -	hormone		parathyroid hormone f	parathyroid hormone (		parathyroid hormone 4	parathyroid hormone 4	parathyroid hormone (	athyr	Description
	2.40e+01	1.56e+01	1.56e+01	1.56e+01	1.56e+01	•	٠.	.54e-	.57e		.17e-		.96€	.96e-		7.13e-05	7.13e-05		7.13e-05	7.13e-05	7.13e-05	7.13e-05	Pred. No.

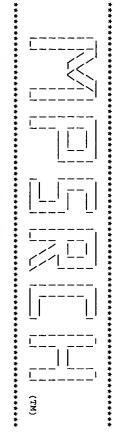
45	44	43	42	41	40	39	38	37	36	S G	34	33	32	31	30	29	28	27	26	25	24
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S59330	VCPVF2	S12053	E65008	A41252	A64646	A47371	F69189	S32373	S63669	S25949	S76244	I52968	A42843	S20608	A40968	A53835	S22310	S22311	A32905	G	1.1
Na+/H+-exchanging pro	structural protein OR	protein-tyrosine-phos	hypothetical protein	4	site-specific recombi	transcription initiat	magnesium chelatase s	DNA-binding protein T	UDPglucoseglycoprot	'n	2				shock pro		HMG-Y-related protein	œ.	plakoglobin, desmosom	plakoglobin - African	plakoglobin – mouse (
				•	•	3.67e+01		3.67e+01								3.67e+01	3.67e+01	3.67e+01	2.40e+01	2.40e+01	2.40e+01

#submission submitted to #cross references pDB:12WE REFERENCE TN001721 #authors Marx, U.C. #book in Strukture pp.0, Bayr	ORGANISM REFERENCE #authors	RESULT 2 ENTRY TITLE ALTERNATE_NAMES PDB_TITLE	Db 9 HNLGKHLNSM	Query Match 100.0%; Best Local Similarity 100.0%; Matches 10; Conservative	FEATURE 6-9 19-30 SUMMARY	ν ×	#cross-references PDB:12WA REFERENCE TN001717 #authors Marx, U.C.	ORGANISM REFERENCE #authors #submission	RESULT 1 ENTRY TITLE ALTERNATE_NAMES PDB_TITLE
the n Ver euth	res ame Homo sapiens #common_name man .; Marx, U.C.	12WE #type complete parathyroid hormone (residues 4-37) - human HPTH(4-37) structure of human parathyroid hormone fragment 4-37, NMR 10	NSM 10	100.0%; Score 73; DB 5; Length 34; Larity 100.0%; Pred. No. 7.13e-05; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	<pre>#region helix (right hand alpha)\ #region helix (right hand alpha) #length 34 #molecular-weight 4118 #checksum 5629</pre>	in Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth: University of Bayreuth (Thesis), 1996 Resolution: not applicable Determination: NMR hormone		structures #formal_name Homo sapiens #common_name man A67856 Roesch, P.; Marx, U.C. submitted to the Brookhaven Protein Data Bank, June 1996	12WA #type complete parathyroid hormone (residues 1-34) - human HPTH(1-34) structure of human parathyroid hormone fragment 1-34, NMR 10

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COMMENT Determination: NMR
KEYWORDS bormone
FEATURE 15-25 #region helix (right hand alpha)
SUMMARY Match 10.0%; Score 73; DB 5; Length 34;
Dest Local Similarity 100.0%; Pred. No. 7.13e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 6 HNIGKHLNSM 15
Qy 1 HNIGKHLNSM 10

Search completed: Thu Jul 30 10:11:56 1998
JOD time: 34 secs.
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MPsrch\_pp on: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:10:15 1998; MasPar time 2.14 Seconds 117.135 Million cell updates/sec

Tabular output not generated.

>US-08-817-547A-7 (1-10) from US08817547A.pep

Title:
Description:
Perfect Score: Sequence: 1 HNLGKHLNSM 10

Scoring table: PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 23.362; Variance 25.262; scale 0.925

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

110 110 110 110 1110 1110 1110 1110 11	Sult No.
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100.0 94.5 94.5 94.5 94.5 94.5 94.5 95.8 84.9 96.5 85.8 86.5 86.5 86.5 86.5 86.5 86.5 8	Query Match
115 115 115 115 115 115 115 115 115 116 117 621 738 743 743 744 117 417 417 417 417 417 417 417 417	Length
	BB
PTHY_HUMAN PTHY_BOVIN PTHY_BOVIN PTHY_FIG PTHY_FIG PTHY_FIG PTHY_FIG PTHY_RAT PAIA_BACSU DHB2_MOUSE PLAK_MOUSE PLAK_MOUSE PLAK_WOUSE PLAK_SOYBN HMGA_SOYBN HMGA_SOYBN SC72_YEAST HS47_HUMAN HS47_HUMAN HS47_HUMAN HS47_BOME CGG1_DROME YFUJ_ECOLI HS47_CHICK PTPE_HUMAN	ID
PARATHYROID HORMONE PR PARATHYROID HORMONE PR PARATHYROID HORMONE PR PARATHYROID HORMONE PR PARATHYROID HORMONE PR PARATHYROID HORMONE PR PROTEASE SYNTHASE AND ESTRADIOL 17 BETA CHA 26S PROTEASOME REGULAT ATP SYNTHASE DELTA CHA JUNCTION PLAKOGLOBIN ( JUNCTION PLAKOGLOBIN ( JUNCTION PLAKOGLOBIN ( JUNCTION PLAKOGLOBIN ( JUNCTION PLAKOGLOBIN ( HMG-Y RELATED PROTEIN HMG-Y RELATED PROTEIN TRANSLOCATION PROTEE 47 KD HEAT SHOCK PROTE 47 KD HEAT SHOCK PROTE COLLAGEN-BLINDING PROTE TRANSCRIPTION INITIATI HYPOTHETICAL 24.6 KD PROTEIN-TYROSINE PHOSP	Description
1.53e-06 1.99e-05 1.99e-05 1.50e-03 3.78e+00 3.78e+00 6.28e+00 6.28e+00 6.28e+00 6.28e+00 1.03e+01 1.03e+01 1.03e+01 1.03e+01 1.03e+01 1.03e+01 1.03e+01 1.03e+01 1.03e+01 1.03e+01 1.03e+01 1.03e+01 1.03e+01 1.03e+01 1.03e+01 1.03e+01 1.03e+01 1.03e+01 1.03e+01 1.03e+01 1.03e+01 1.03e+01 1.03e+01 1.03e+01 1.03e+01 1.03e+01 1.03e+01 1.03e+01	Pred. No.

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43	43	43	43	43	43	44	44	44	44	44	44	44	44	44	44	44	44	44	44	45	45
58.9	58.9	58.9	58.9	58.9	58.9	60.3	60.3	60.3	60.3	60.3	60.3	60.3	60.3	60.3	60.3	60.3	60.3	60.3	60.3	61.6	61.6
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SP14_YEAST	YPT7 CAREL	BICD_DROME	VP4_ROTHU	RADA_METJA	LDH_METJA	POLR_ASGVP	BIMC_EMENI	YG2K_YEAST	YQD3_CAEEL	YFC3_YEAST	Y187_MYCGE	HSF1_HUMAN	HSF1_MOUSE	VC17_VACCC	KSF1_ECOLI	HEMZ_BACSU	YHBV_ECOLI	APA1_PIG	PMGY_MYCLE	NAH_YEAST	NS2_SIDEV
	HYPOTHETICAL 111.7 KD	CYTOSKELETON-LIKE BICA	OUTER CAPSID PROTEIN V	RADA PROTEIN.	L-LACTATE DEHYDROGENAS	GENOME POLYPROTEIN (CN	KINESIN-LIKE PROTEIN B	HYPOTHETICAL 106.5 KD	HYPOTHETICAL 96.7 KD P	HYPOTHETICAL 91.4 KD P	HYPOTHETICAL ABC TRANS	HEAT SHOCK FACTOR PROT	HEAT SHOCK FACTOR PROT	PROTEIN C17/B23.	KPSF PROTEIN.	FERROCHELATASE (EC 4.9	HYPOTHETICAL 33.2 KD P	APOLIPOPROTEIN A-I PRE	ï	PROBABLE NA(+)/H(+) AN	PROBABLE STRUCTURAL PR
4.37e+01	4.37e+01	4.37e+01	4.37e+01	4.37e+01	4.37e+01	2.73e+01	2.73e+01	2.73e+01	2.73e+01	2.73e+01	2.73e+01	2.73e+01	2.73e+01	2.73e+01	2.73e+01	2.73e+01	2.73e+01	2.73e+01	2.73e+01	1.69e+01	1.69e+01

RN	בי	RL	RL	R.A	RA	RP	RN	RĽ	RA	RA	RX	RP	RN	RL	RA	RA	RХ	RP	RN	RĽ.	RA	RX	₽₽	RN	RL	RA	RA	RX	RP	RN	RL	RA	RX	RP :	Z (	88	3	) (2)	2 5	) t	3 5	3 5	A	5	RESULT
[7]		9-14, EXCERPTA MEDICA FOUNDATI		i., por	KEUTMANN H.T., NIALL H.D., JACOBS J.W., BARLING P.M., HENDY G.N.,	-100.	[6]	BIOCHEMISTRY 17:5723-5729(1978).		KEUTMANN H.T., SAUER M.M., HENDY G.N., O'RIORDAN J.L.H.,	855.	SEQUENCE OF 61-83 AND 84-115.		SCI. U.S.A. 7	.L.H., AURBACH G.D.,	R.T., JACOBS	74111656.	UENCE		249:155-157(1974).	JACOBS J.W., KEMPER B., NIALL H.D., HABENER J.F., POTTS J.T. JR.;	MEDLINE; 74174967.	SEQUENCE OF 26-37.		U.S.A. 80:2127	.N., POTTS J.T. JR., RICH A., KRONENBERG H.M.;	T.J., MCCEVITT B.E., FREEMAN		SEQUENCE FROM N.A.		NATL. ACAD. SCI. U.S.A. 78:7365-7369(1981).	N., KRONENBERG H.M., P	MEDLINE: 82150870.	UENCE		PRIMATES.	RYOTA: MI	HOMO SADTENS (HIMAN)	DAG CARACIDINOLD HOMOND FORCONOUN (FONDIBIRIN) (FID).	CARDING DESCRIPCION (DARATHYRIN)	REL	л <u>,</u>	/ BET 01	PTHY HUMAN STANDARD; FRT; IIS AA.	

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Best Local S
Matches 1
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EMBL; J00301; G190704; -.

EMBL; V00597; G37144; -.

EMBL; V00597; G37144; -.

EMBL; A29146; E186700; -.

PIR; A01536; PPHU

PIR; A19339; A19339.

PDB; 11PH; 10-OUL-95.

PDB; 11PH; 10-OUL-95.

PDB; 12WA; 12-MAR-97.

PDB; 12WB; 16-JUN-97.

PDB; 12WG; 16-JUN-97.
                                           CONFLICT
SEQUENCE
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MEDLINE: 73227467.

ANDREATTA R.H., HARTMANN A., JOEHL
RINIKER B., RITTEL W., SIEBER P.;
HELV. CHIM. ACTA 56:470-473(1973).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 95318084.
MARX U.C., AUSTERMANN
STICHT H., WALTER S.,
ROESCH P.;
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BARDEN J.A., CUTHBE
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MEDLINE; 91299748.
KLAUS W., DIECKMANN T., WE
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TREGEAR G.W., VAN RIETSCHOTEN J., GREEN E., NIALL H.E KEUTWANN H.T., PARSONS J.A., O'RIORDAN J.L.H., POTTS HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 355:415-421(1974).
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MEDLINE; 75146516.

KEUTMANN H-T., NIALL H.D., O'RIORDAN J.L.H.,
BIOCHEMISTRY 14:1842-1847(1975).
                                                                                                                                      PROSITE
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Similarity 100.0%;
10; Conservative
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115
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HEM. 215:315-321(1993).
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SCHMID F.-X.,
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N -> D (IN R)
W; 243E87C7 CI
Score 73; DB 1; I
Pred. No. 1.53e-06;
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FORSSMANN W.-G.,
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EMBL; M25082; G1636
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21-JUL-1986
01-NOV-1997
        PIR; A01
PIR; A24
PROSITE;
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                                                                                           POTTS J.T. JR., TREGEAR G.W., KEUTMANN H.T., NIALL H.D DEFTOS L.J., DAWSON B.F., HOGAN M.L., AURBACH G.D.; PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).
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                                                                                                                                                                    SEQUENCE OF 32-115.
MEDLINE; 71063634.
BREWER H.B. JR., RONAN
PROC. NATL. ACAD. SCI.
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NIALL H.D., KEUTMANN H.T.,
AURBACH G.D., POTTS J.T. J
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HAMILTON J.W., NIALL H.D.,
COHN D.V.;
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MEDLINE; 80056617.
KRONENBERG H.M., MCDEVITT
POTTS J.T. JR., RICH A.;
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WEAVER C.A.,
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E18249; ALT_SEQ.
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G163647; -.
G163645; -.
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S.A. 78:4073-4077(1981).
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FT SIGNAL 1 25
FT PROPEP 26 31
FT CHAIN 32 115 PARATHYROID HORMONE.
FT COMPLICT 106 106 V -> G (IN REF. 4).
SQ SEQUENCE 115 AA; 12980 MW; 673EA5F2 CRC32;

Ouery Match 94.5%; Score 69; DB 1; Length 115;
Best Local Similarity 90.0%; Pred. No. 1.99e-05;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 40 HNLGKHLSSM 49
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Qy 1 HNLGKHLSSM 10

Search completed: Thu Jul 30 10:10:23 1998

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UHBW1 PROTEIN.  NITRIC-OXIDE SYNTHASE  ROS1 PROTOONCOGENE (PR	AMIDASE. CARCINOEMBRYONIC ANTIG	TRANSCR	KPSF GENE. 47 KDA HEAT SHOCK PROT	ENVELOPE GLYCOPROTEIN, LACTATE DEHYDROGENASE.	L308_F1_36.	HYPOTHETICAL 22.0 KD P	APOLIPOPROTEIN A-I (FR	COSMID F31D5.	н	YOKA PROTEIN.	FROM BASES 2458322 TO	HUNCHBACK GAP (FRAGMEN	SITE-SPECIFIC RECOMBIN	HYPOTHETICAL 9.6 KD PR	KIAA0302 (FRAGMENT).	MAGNESIUM CHELATASE SU
3.25e+01 5.25e+01 5.25e+01	3.25e+01 3.25e+01	 N N			3.25e+01		3.25e+01	2.00e+01	2.00e+01	2.00e+01	2.00e+01	2.00e+01	2.00e+01	2.00e+01	1.21e+01	1.21e+01

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RESULT
AC Q66
AC Q66
D7 01
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CC ECC
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Best Local Similarity 80.0%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

TISSUE=THYROID, AND PARATHYROID;
SCHMELZER H.J., GROSS G., MAYER H.;
SCHMELZER ETECHNOL. 21:228-229(1984).
EMBL; M54875; G601933; -.

NON_TER 1 1
SEQUENCE 105 AA; 11746 MW; 6AC3163
                                                                                                                                                                                                                                                                 O63778

PRELIMINARY; PRT; 367 AA.

Q63778;
Q63778;
Q1-NOV-1996 (TREMBLREL. 01, CREATED)
Q1-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
Q1-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
HYPOTHETICAL 43.7 KD PROTEIN.
RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
SEQUENCE FROM N.A.
TISSUE-LIVER;
MEDLINE; 8764324.
D'AMBROSIO E., WAITZKIN S.D., WITNEY F.R., SALEMME A., FURANO A.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    063473 PRELIMINARY; PRT; 105 AA.
063473; OFFICE OF CREATED; OFFICE OFFIC
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30 HNLGKHLASV 39
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1 HNLGKHLNSM 10
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Pred. No. 1.01e-02;
1; Mismatches 1; Indels
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RL MOI. CELL. BIOL. 6;411-424(1986).

DR EMBL; MINJOO; G804611; .

SO SEQUENCE 367 AA; 43685 MW; 3D4A69E5 CRC32;

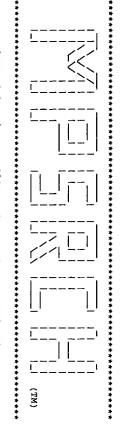
OURTY MATCh
Best Local Similarity 66:78; Fred. No. 1.54e+00;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

DD 74 KLGKHLEHM 82

CY 2 NIGKHLSH 10

Search completed: Thu Jul 30 10:11:05 1998

Job time : 24 secs.
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:14:54 1998; MasPar time 2.63 Seconds 52.587 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Title: >US-08-817-547A-8 (1-9) from US08817547A.pep 64 1 NLGKHLNSM 9

Sequence:

Scoring table: PAM 150 Gap 15

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 15.754; Variance 55.237; scale 0.285

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

110 110 110 1110 1110 1110 1110 1110 1	Result
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	1 -
2 W17968 2 W17968 2 W17969 2 W17969 2 W17959 2 W17959 8 R41557 8 R41557 2 W17951 2 W17955 2 W17955 9 R58279 9 R58279 9 R58279 9 R58279 9 R58279 9 R58279	Ħ
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Query Match
Best Local Similarity 100.0%;

Score 64; DB 22; Pred. No. 3.96e+00;

Length 34;

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stimulat bone fra Claim 11 The pres hormone of the a is alpha at posit analogue medicine conjunct calciton N.B. The correspo as state Sequence	Homo sa synthet Key modifia modifia modifia modifia modifia 13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JUL-13-JU	ULT W1795; W1795; W1795; 29-JUI Human Osteon	44444400000000000000000000000000000000
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glish. specifi specifi com frag om frag at pos cid ha type ha type ha type the rowth costeope rptive rptive prH 1-:	ifie ide	ALIGNMEN 34 AA. 3nalogue ; human;	R58295 R58253 R58253 R58244 R581248 R58125 R58125 R58125 R58269 R58269 R98058 P30015 W21946 W21946 W21946 R42074 R42074 R42074 R42074 R42074 R42074 R42074 R42074 R42074 R421175 R211175 R211175 R211175 R211175 R211175
imple of a human parathy 1-34 in which at least 13, 16, 17, 19 and in this example the Ser in substituted by Aib. To are useful in human or and bone fracture, optopy (bisphosphonates and bear in the specifications) and the specifications are useful the modifications are useful in human or and bone fracture, optopy (bisphosphonates and bone fracture).	ormone 1-34 peptid	ib3]hPT	[D-Val35]-hPTH(1-36)- [A-aminobenzoic acid1 3.96e+00 [Asn1]-hPTH(1-36)-NH2 3.96e+00 [Ala0]-hPTH(1-36)-NH2 3.96e+00 [Ala22]-hPTH(1-38)-OH 3.96e+00 [Gly22]-hPTH(1-38)-OH 3.96e+00 [ILeu19]-hPTH(1-38)-OH 3.96e+00 [Leu19]-hPTH(1-38)-OH 3.96e+00 [Lunan parathyroid hor 3

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Search completed: Thu Jul 30 10:15:09 1998 Job time: 15 secs.
                                                                                                                                                                                                                                                                                                         PD 30-70A-1997.

PP 30-7UL-1996; U11292.

PR 13-UUL-1996; U1292.

PR 13-UUL-1995; US-001105.

PR 06-SEP-1995; US-023305.

PR 29-MAR-1996; US-626186.

PA (BIOM-) BIOMEASURE INC.

PI Dong ZX;

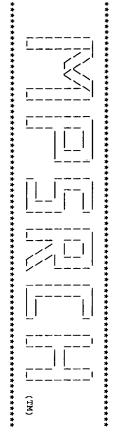
DR WPI; 97-118819/11.

PT New variants of human parathyroid hormone 1-34 peptide - which PI bone fracture : 33pp; English.

CC The present sequence is a specific example of a human parathyroid CC of the amino acid residues at positions 3, 12, 16, 17, 19 and 34 cc at position 19 of the wild-type has been substituted by Aib. The hPTH cc analogues stimulate bone growth and so are useful in human or veterinary cc conjunction with anti-resorptive therapy (bisphosphonates and CC unicitonin).

CC N.B. The present sequence does not appear in the specification. It cas stated in the claim.

Sequence 34 AA;
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                                                                                                                                                                                                                      uery match 100.0%;
best Local Similarity 100.0%;
Matches 9; Conservative
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W17954;
29-JUL-1997 (first entry)
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                                                                                                                                                                                                             Score 64; DB 22; Length 34; Pred. No. 3.96e+00; O; Mismatches 0; Indels
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Jul 30 10:14:18 1998; MasPar time 3.15 Seconds 104.377 Million cell updates/sec

abular output not generated.

Title: Description: Perfect Score: Sequence: >US-08-817-547A-8 (1-9) from US08817547A.pep 64 1 NLGKHLNSM 9

Scoring table: PAM 150 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pirl 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 21.753; Variance 27.858; scale 0.781

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

2221014 23221014 244321114 254321114 254321114	NO.
00000000000000000000000000000000000000	Score
100.0 100.0 100.0 100.0 100.0 100.0 100.0 93.8 93.8 93.8 82.8 82.8 82.8 78.1 78.1 78.1 77.1 75.0 75.0 75.0 71.9 71.9	Query
34 34 34 34 35 36 36 37 37 31 115 115 115 115 115 115 115 115 115	Length
000000000000000000000000000000000000000	80
12WA 12WE 12WE 12WE 12WF 12WD 12WB 11HPH 11HPH 11HPU 12WC 12WC 12WC 12WC 12WC 151851 151851 852014 852014 852014 853016 853016 854636 13111 822311 8523311 8523311	₽
parathyroid hormone ( parathyroid hormone ( parathyroid hormone 4 parathyroid hormone 4 parathyroid hormone ( probable RNA-directed ( atp6 protein ( probable membrane pro ( cyclic parathyroid hormone) MGG-Y-related protein MGG-Y-related protein SEC63 protein complex	Description
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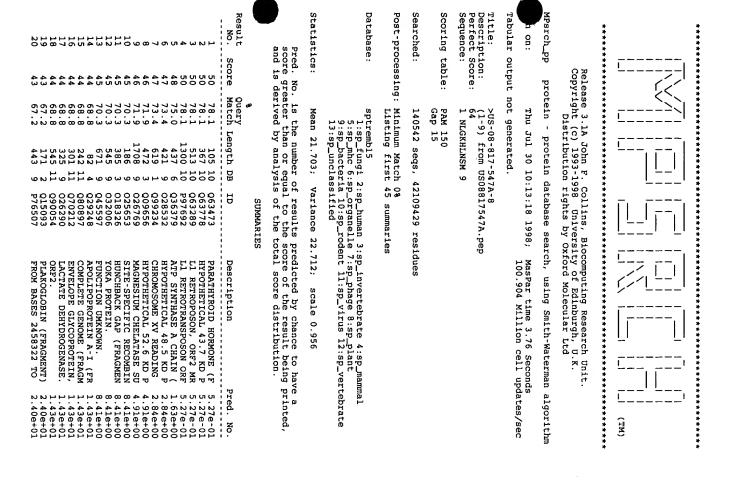
RESULT 2 12WI ENTRY TITLE ALTERNATE_NAMES HPT! PDB_TITLE str ORGANISM #foo REFERENCE #authors Reperences REFERENCE = 100 REFERENCE # 100 REFERENCE ROBE # 100 REFERENCE ROBE # 100 REFERENCE ROBE # 100 REFERENCE ROBE # 100 REFERENCE THOUGHT	Query Match Best Local Simila Matches 9; C Db 10 NLGKHLNSM           Qy 1 NLGKHLNSM	0 0	REFERENCE #authors #book #book COMMENT Resol	OKGANISM #10 REFERENCE A671 #authors Roes #submission submission s	RESULT 1 ENTRY TITLE ALTERNATE_NAMES PDB_TITLE
parathyroid hormone (residues 4-37) - human HPTH(4-37) structure of human parathyroid hormone fragment 4-37, NMR 10 structures #formal_name Homo sapiens #common_name man A67860 Roesch, P.; Marx, U.C. submitted to the Brookhaven Protein Data Bank, June 1996 nces PDB:12WE TN001721 Marx, U.C. in Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth: University of Bayreuth (Thesis), 1996	1 100.0%; Score 64; DB 5; Length 34; Similarity 100.0%; Pred. No. 2.46e-03; 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0; SKHLNSM 18	hormone  #region helix (right hand alpha)\ #region helix (right hand alpha) #length 34 #molecular-weight 4118 #checksum 5629	TN001717  Marx, U.C.  in Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth : University of Bayreuth (Thesis), 1996  Resolution: not applicable Determination: NMR	#IOIMAL_name Homo sapiens #Common_name man A67856 Roesch, P.; Marx, U.C. submitted to the Brookhaven Protein Data Bank, June 1996 nces_PDB:1ZWA	type complete hormone (residues 1-34) - ) human parathyroid hormone

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COMMENT Determination: NNR
RESOlution: NNR
RESOlution: NNR
Determination: NNR
Lind bettermination: NNR
FERMINES
FEATURE
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FROM bormone
Freqion helix (right hand alpha)
15-25
SUMMARY

Query Match
Best Local Similarity 100.0%; Score 64; DB 5; Length 34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 7 NLGKHLNSH 15
Db 11111111
Oy 1 NLGKHLNSH 9

Search completed: Thu Jul 30 10:14:37 1998

Job time: 19 secs.
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43 67.2 554 3 023651 ZK863.3.  43 67.2 646 10 263779 CORPORTICAL 76.2 KD P 43 67.2 719 3 017828 CORPS.2.  43 67.2 745 10 P70565 PLAKOGLOBIN.  43 67.2 745 10 P70565 PLAKOGLOBIN.  43 67.2 745 2 015151 FAKOGLOBIN.  43 67.2 979 3 021962 SIMILAR TO GLYCINE DEH 43 67.2 1854 10 Q63131 RAT LUNG-DERIVED C.O.  43 67.2 2294 2 015265 RAT LUNG-DERIVED C.O.  43 67.2 2338 10 Q63132 RAT HEART-DERIVED C.O.  43 67.2 2338 10 Q64736 ROS1 PROTOONCOGENE (C.O.  43 67.2 2340 10 Q64736 ROS1 PROTOONCOGENE (C.O.  43 67.2 2440 10 Q64736 ROS1 PROTOONCOGENE (C.O.  43 67.2 2440 10 Q64512 PROTEIN TYROSINE PHOSP 43 67.2 2460 10 Q64512 PROTEIN TYROSINE PHOSP 43 67.2 2466 2 Q15264 PROTEIN TYROSINE PHOSP 43 67.2 2466 2 Q15263 PROTEIN TYROSINE PHOSP 43 67.2 2466 2 Q15263 PROTEIN TYROSINE PHOSP 43 67.2 2466 2 Q15263 PROTEIN TYROSINE PHOSP 43 67.2 2485 2 Q15263 PROTEIN TYROSINE PHOSP 43 67.2 2486 2 Q15263 PROTEIN TYROSINE PHOSP 42 65.6 2589 11 Q66776 POLYPROTEIN (FRAGMENT) 42 65.6 2589 11 Q66776 POLYPROTEIN 42 65.6 3896 11 P87514 PESTIVIRUS POLYPROTEIN	45	44	43	42	41	40	39	38	37	36	ω 5	34	ω	32	31	30	29	28	27	26	25	24	23	22
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Best Local :
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Q63778;
Q63778;
O1-NOV-1996 (TREMBLREL. 01, CRE
01-NOV-1996 (TREMBLREL. 01, LAS
01-NOV-1996 (TREMBLREL. 01, LAS
HYPOTHETICAL 43.7 KD PROTEIN.
RATTUS (NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VI
EUTHERIA; RODENTIA.
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TISSUE-THYROID, AND PARATHYROID;
SCHWELZER H.J., GROSS G., MAYER H.;
SCHWELZER H.J., GROSS G., MAYER H.;
ADV. GENE TECHNOL. 21:228-229(1984).
EMBL, M54875; G60193; -.
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NON_TER
105 AA; 11746 MW; 6AC3163
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01-NOV-1996
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SEQUENCE FROM N.A.
TISSUE-LIVER;
MEDLINE; 87064324.
D'AMBROSIO E., WAITZKIN
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PARATHYROID
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|||||| |:
1 NLGKHLNSM 9
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5 (TREMBLREL. 01, LAST
8 (TREMBLREL. 05, LAST
D HORMONE (FRAGMENT).
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Pred. No. 5.
    WITNEY F.R.,
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                                                                                                                                                                                                                                                                         VERTEBRATA;
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5.27e-01;
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    SALEMME A.,
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    FURANO A.V.;
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RL MOL. CELL. BIOL. 6:411-424(1986).

DR EMBL; MI3100; G804041]: .

KW HYPOTHENTCAL PROTEIN.

SO SEQUENCE 367 AA; 43685 MW; 3D4A69E5 CRC32;

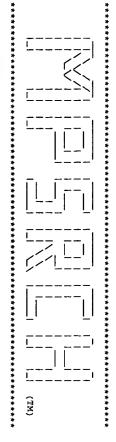
QUESTY MATCH 78.1%; SCOORE 50; DB 10; Length 367;
Best Local Similarity 66.7%; Pred. Mo. 5.27e-01; Length 367;
MATCHES 6; CONSERVATIVE 2; Mismatches 1; Indels 0; Gaps 0;

DD 74 KLGKHLEHM 82

QY 1 NLGKHLENSM 9

Search completed: Thu Jul 30 10:14:00 1998

JOB time : 42 secs.
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

n on: Thu Jul 30 10:12:53 1998; MasPar time 2.12 Seconds 106.569 Million cell updates/sec

Tabular output not generated.

Title:
Description:
Perfect Score:
Sequence: >US-08-817-547A-8 (1-9) from US08817547A.pep 64 1 NLGKHLNSM 9

Scoring table: PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 22.743; Variance 23.428; scale 0.971

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

45	44	43	42	41	40	39	38	37	36	<b>3</b> 5	34	ω ω	32	31	30	29	28	27	26	25	24
41	41	41	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	43	43
64.1	64.1	64.1	•	٠	65.6	•	•	•	•	•	•	•	•	•	•	65.6	•	65.6	ŗ	67.2	67.2
372	270	249	2059	1444	1184	1097	781	601	529	527	505	503	501	359	325	247	246	138	108	782	743
۲	Ь	ب	Н	ب	<b>ب</b> ــر	Н	μ	М	ш	٠4	ш	Н	Н	Н	Ь	Н	μ	۳,	_	_	H
KPL1_HUMAN	VA32_VARV	PMGY_MYCTU	TEGU_HSV7J	RRPL_RDV	BIMC_EMENI	IMB3_HUMAN	YSPL_CAEEL	YAN4_SCHPO	HSF1_HUMAN	YD05_YEAST	SMI1_YEAST	HSF1_MOUSE	YBQ6_YEAST	KIPA_BPT7	PFTB_CAEEL	PMGY_MYCLE	SR1A_PHYPO	YYAN_BACSU	SLIB_HUMAN	BICD_DROME	PLAK_HUMAN
SERINE/THREONINE PROTE	PROTEIN A32.	PHOSPHOGLYCERATE MUTAS	LARGE TEGUMENT PROTEIN	RNA-DIRECTED RNA POLYM	KINESIN-LIKE PROTEIN B	IMPORTIN BETA-3 SUBUNI	HYPOTHETICAL 91.0 KD P	HYPOTHETICAL 69.4 KD P	HEAT SHOCK FACTOR PROT	HYPOTHETICAL 60.9 KD P	SMI1 PROTEIN (KILLER T	HEAT SHOCK FACTOR PROT	HYPOTHETICAL 57.8 KD P	PROTEIN KINASE (EC 2.7	PROBABLE PROTEIN FARNE	PHOSPHOGLYCERATE MUTAS	SPHERULIN 1A PRECURSOR	HYPOTHETICAL TRANSCRIP	SOMATOLIBERIN PRECURSO	CYTOSKELETON-LIKE BICA	JUNCTION PLAKOGLOBIN (
5.90e+01	5.90e+01	5.90e+01	3.63e+01	3.63e+01	3.63e+01	3.63e+01	3.63e+01	3.63e+01		3.63e+01	2.21e+01	2.21e+01									

		R.	RA	R.	RP	RN	RL	RA	RA	RX	RP	RN	RĽ	RA	RA	æ	ŖΡ	RN	RL	RA	RX	RP	RN	RL	RA	RA	æ	R₽	RN	RĽ	RA	RX	RP	RN	റ്റ	8	SO	GN	DE	ΡŢ	DŦ	Di	δt	RESULT
[7]	J.A., EDS., PP.9-14, EXCERPTA MEDICA FOUNDATION		N.J.L.H., POTTS J.T. JR.:	Ξ,	SECUENCE OF 75-100.	[6]	BIOCHEMISTRY 17:5723-5729(1978).	••	H.T., SA	MEDLINE; 79082855.	SEQUENCE OF 61-83 AND 84-115.	[5]	ACAD. SCI. U.S.A. 71:384-388(1974)	L.H., AURBACH G.D., POTTS J.T. JR.;			UENCE		NATURE 249:155-157(1974).	JACOBS J.W., KEMPER B., NIALL H.D., HABENER J.F., POTTS J.T. JR.;		SEQUENCE OF 26-37.		C. NATL. ACAD.	G.N., POTTS J.T. JR., RI	EVITT B.E., FREEMAN		SEQUENCE FROM N.A.		ACAD. SCI.	שי	82150870.	SEQUENCE FROM N.A.	[1]	EUTHERIA; PRIMATES.	M			PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).	(REL. 35, LAST ANNOTATION UPDA	(REL. 05,	21-JUL-1986 (REL. 01, CREATED)		DTHY HIMAN STANDARD: DRT: 115 AA

N

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DR DR FTT FTT FTT SQ
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Best Local S
Matches
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RX MEDLINE; 91009811.

RA ARNOLD A., HORST S.A., GARDELLA T.J., BABA H., LEVINE M.A.,

RA ARNOLD A., HORST S.A., GARDELLA T.J., BABA H., LEVINE M.A.,

RA KRONENBERG H.M.;

R. J. CLIN. INVEST. 86:1084-1087(1990).

CC. 1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN

CC. 1- DISEASE: DEFECTS IN PTH ARE A CAUSE OF FAMILIAL ISOLATED

MEDICAL PROPARATURY ROLDISM (FIH).

CC. HYPOPARATURY ROLDIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
SEQUENCE
                                                                                                                                                  VARIANT
                                                                                                                                                                        CHAIN
                                                                                                                                                                                       PROPEP
                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MARX U.C., AUSTERWANN S., BAYER P.,
STICHT H., WALTER S., SCHMID F.-X.,
ROESCH P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 93345518
BARDEN J.A., CUTHI
EUR. J. BIOCHEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRUCTURE BY NMR OF 32-68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRUCTURE BY NMR OF 32-65.
MEDLINE; 91299748.
KLAUS W., DIECKMANN T., WRAY V.,
BIOCHEMISTRY 30:6936-6942(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRUCTURE BY NMR OF 32-65.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 75059220.

TREGEAR G.W., VAN RIETSCHOTEN J., GREEN E., NIALL H.D., KEUTMANN H.T., PARSONS J.A., O'RIORDAN J.L.H., POTTS J.T. HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 355:415-421(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REVISIONS.
MEDLINE; 75146516.
KEUTMANN H.T., NIALL H.D., O'RIO!
BIOCHEMISTRY 14:1842-1847(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYNTHESIS OF 32-65. MEDLINE; 73227467.
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           Similarity 100.0%;
Similarity 100.0%;
9; Conservative
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115
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                                                                                         AA;
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HEM. 215:315-321(1993).
                                                                                                                                                                                                               PARATHYROID; 1.
DISEASE MUTATION;
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12861
                                                                                       Œ,
         Score 64; DB 1; I
Pred. No. 1.05e-04;
0; Mismatches 0
                                                                             PARATHYROID HORMONE.
C -> R (IN FIH; LEADS TO INEE PROCESSING OF THE PRECURSOR).
N -> D (IN REF. 5).
243E87C7 CRC32;
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                                                                                                                                                                                                           3D-STRUCTURE.
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JAENICKE
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     Indels
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Gaps
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RESULT AC POLY AC POLY
X MEDLINE; 71091588;

A POTTS J.T. JR., TREGEAR G.W., KEUTMANN H.T., NIALL H.D., S A POTTS J.T. JR., DANSON B.F., HOGAN M.L., AURBACH G.D.;

A DEFTOS L.J., DANSON B.F., HOGAN M.L., AURBACH G.D.;

C PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).

C PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).

C POUCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE EMBL; V00106; G85; -.

R EMBL; V00106; G85; -.

R EMBL; J00024; G163641; -.

R EMBL; J00024; E18249; ALT_SEQ.

R EMBL; J00024; E18249; ALT_SEQ.

R EMBL; J00024; E18250; ALT_INIT.

R EMBL; M01938; G163647; -.

R EMBL; M01938; G163645; -.

R EMBL; M25082; G163645; -.

R EMBL; M25082; G163645; -.

R PIR; A24949; 
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MEDLINE; 71076162.

NIALL H.D., KEUTMANN H.T., S
AURBACH G.D., POTTS J.T. JR.
HOPPE-SEYLER'S Z. PHYSIOL. (
77)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 710
BREWER H.B.
PROC. NATL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYNTHESIS OF 32-65.
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MEDLINE; 74142666.
HAMILTON J.W., NIALL H.D.,
COHN D.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE; 84262483.
MEAVER C.A., GORDON D.F.,
GENE 28:319-329(1984).
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BOS TAURUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE; 83105964.
WEAVER C.A., GORDON D.F., KEMPER B.;
MOL. CELL. ENDOCRINOL. 28:411-424(1982).
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21-JUL-1986
01-NOV-1997
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P01268;
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; 71063634.
" B. JR., RONAN R
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METAZOA; CHORDATA; VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37785.
, GORDON D.F., , SCI. U.S
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(REL. 01, LAST SEQUENCE UPDATE)
(REL. 35, LAST ANNOTATION UPDATE)
HORMONE PRECURSOR (PARATHYRIN) (PTH).
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OL. CHEM.
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.S.A. 78:4073-4077(1981).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HOGAN M.L., DAWSON
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                                                                                                                                                                                                                                                                                                                                                                                NIALL H.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D.A.,
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FT SIGNAL 1 25
FT CHAIL 32 115
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FT CONFLICT 106 106
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FT CONFLICT 106 106
FT CHAIL 107
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Search completed: Thu Jul 30 10:12:59 1998 Job time: 6 secs.



Tabular output not generated.

Description: Perfect Score: Title: >US-08-817-547A-9 (1-8) from US08817547A.pep 59 1 LGKHLNSM 8

Scoring table: РАМ 150 Gap 15 Sequence:

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match Listing first 0% 45 summaries

Database:

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 15.458; Variance 50.932; scale 0.303

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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esult No.	ב	N	ω	4	ψ	o	7	œ	9	10	11	12	13	14	15	16	17	18	19
Score	59	59	59	59	59	59	59	59	59	59	59	59	59	59	59	59	59	59	59
Query	100.0		٠	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Length	34	34	34	34	34	34	34	34	34	34	34	34	34	34	36	36	36	36	36
gg	22	22	22	22	7	22	22	4	œ	œ	19	22	22	22	9	9	9	v	ဖ
ID	W20000	W17949	W17955	W17950	R34355	W17969	W17951	R22293	R41557	R41550	R98951	W17948	W17947	W17957	R58263	R58268	R58229	R58297	R58295
Description	Cyclised human parath	Human parathyroid hor	Human parathyroid hor	Human PTH analogue [C	Human parathyroid hor	Human parathyroid hor	Human parathyroid hor	Human parathyroid hor	[Gln25,26,27]hPTH (1-	[D-Ala3]hPTH (1-34).	Target peptide (PTH(1		Human parathyroid hor	Human parathyroid hor	[D-Ile5]-hPTH(1-36)-N	[Cha8]-hPTH(1-36)-NH2	[Ala30]-hPTH(1-36)-NH	[Pro35]-hPTH(1-36)-NH	[ D-Va ] 25 ] - hpm2 / 1 - 26 / -
Pred. No.	7.14e+00	7.14e+00	7.14e+00	7.14e+00	7.14e+00	7.14e+00	7.14e+00	7.14e+00	7.14e+00	7.14e+00	7.14e+00								

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11 lgkhlnsm 18

59 100.0 36 9 R58233 [Ap-His32]-hPTH(1-36)-NH2 59 100.0 36 9 R58244 [Ala0]-hPTH(1-36)-NH2 59 100.0 37 9 R58244 [Ala0]-hPTH(1-36)-NH2 59 100.0 38 9 R58148 [Ala22]-hPTH(1-38)-OH 59 100.0 38 9 R58145 [Gly22]-hPTH(1-38)-OH 59 100.0 38 9 R58134 [Ile19]-hPTH(1-38)-OH 59 100.0 38 9 R58075 [Ile2]-hPTH(1-38)-OH 59 100.0 38 9 R58075 [Ile2]-hPTH(1-38)-OH 59 100.0 38 19 R98958 Target peptide (PTH(1-59)-100.0 38 19 R98958 [Ile3]-hPTH(1-38)-PTH(1-59)-100.0 44 26 R2533-hPTH(1-59)-100.0 47 25 W21946 Fusion protien comprise for the comprise for	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
36 9 R58233 [D-H±32]-hPTH(1-36) 37 9 R58244 [Ala0]-hPTH(1-36) 38 9 R58148 [Ala2]-hPTH(1-36) 38 9 R58148 [Ala2]-hPTH(1-36) 38 9 R58145 [Gly22]-hPTH(1-38) 38 9 R58145 [Gly22]-hPTH(1-38) 38 9 R58134 [Ile19]-hPTH(1-38) 38 9 R58137 [Ile19]-hPTH(1-38) 38 9 R58157 [Ile19]-hPTH(1-38) 38 19 R98958 Target peptide (PT) 38 9 R58167 [Ile31, Arg 33]-hPTH 42 6 P30015 Human parathyroid 47 25 W2146 Fusion protien con 47 25 W2146 Fusion protien con 48 4 R21180 Human parathyroid 49 4 R21181 Human parathyroid 40 4 R211220 Human parathyroid 40 4 R21220 Human parathyroid 41 4 R21220 Human parathyroid 42 6 W2420 Human parathyroid 43 8 R42068 Stability-enhancec 44 R21222 Human parathyroid 45 W29420 Human parathyroid 46 4 R21223 Human parathyroid 47 R3233 Human parathyroid 48 4 R21233 Human parathyroid 48 R42034 Human parathyroid 49 R42234 Human parathyroid	59	59	59	59	59	59	59	59	59	59	59	59	59	59	59	59	59	59	59	59	59	59	59	59	59	59
6 9 R58233 [D-H±32]-hPTH(1-36)- 7 9 R58244 [Ala0]-hPTH(1-36)- 7 9 R58244 [Ala0]-hPTH(1-36)- 8 9 R58148 [Ala0]-hPTH(1-38)- 8 9 R58145 [Gly22]-hPTH(1-38)- 8 9 R58145 [Gly22]-hPTH(1-38)- 8 9 R58134 [Ile19]-hPTH(1-38)- 8 9 R58134 [Ile19]-hPTH(1-38)- 8 19 R58078 [Arget peptide (PT)- 8 9 R58167 [Ile31, Arg33]-hPTH- 4 26 P30015 Human parathyroid 4 R21120 Human parathyroid 4 R21220 Human parathyroid 5 R42074 Human parathyroid 6 R42068 Stability-enhanced 6 R42074 Human parathyroid 6 R421223 Human parathyroid 6 R21323 Human parathyroid 6 R23331 Human parathyroid 6 R23331 Human parathyroid 6 R23331 Human parathyroid 7 R3460 Human parathyroid 8 R42120 Human parathyroid 9 R	•	٠	•	٠	•	٠	٠	٠	٠	٠	•	•	•	•	٠	٠	٠				•		•	•	•	•
9 R58233 [D-H1332]-hpTH(1-36) 9 R58244 [Ala0]-hpTH(1-36) 9 R58244 [Ala0]-hpTH(1-36) 9 R58148 [Ala0]-hpTH(1-38) 9 R58145 [G1y22]-hpTH(1-38) 9 R58134 [Ile19]-hpTH(1-38) 9 R58134 [Ile19]-hpTH(1-38) 9 R58075 [Ser33]-hpTH(1-38) 9 R58075 [Ile19]-hpTH(1-38) 9 R58075 [Ile19]-hpTH(1-38) 9 R58075 [Ile19]-hpTH(1-38) 9 R58075 [Ile19]-hpTH(1-38) 9 R58167 [Ile19]-hpTH(1-38) 9 R58134 [Ile19]-hpTH(1-38) 9 R58134 [Ile19]-hpTH(1-38) 9 R58134 [Ile19]-hpTH(1-36) 1 R21181 [Ile19]-hpTH(1-38) 1 R21180 [Ile19]-hpTH(1-38) 1 R21181 [Ile19]-hpTH(1-36) 1 R21181 [Ile19]-hpTH(1-38) 1 R38167 [Ile19]-hpTH(1-38) 1 R	84	84	84	84	84	84	84	84	84	84	84	84	84	84	47	44	38	38	38	38	38	38	38	37	36	36
[D-His32]-hpTH(1-36)- 8224 [Ala0]-hpTH(1-36)- 8244 [Ala0]-hpTH(1-36)- 8244 [Ala0]-hpTH(1-38)- 8244 [Ala0]-hpTH(1-38)- 8244 [Ala0]-hpTH(1-38)- 8248 [Ala22]-hpTH(1-38)- 8248 Parathyroid hormon- 8134 [Ile1]-hpTH(1-38)- 8075 [Ile3]-hpTH(1-38)- 8075 [Ile3]-hpTH(1-38)- 8075 [Ile3]-hpTH(1-38)- 8075 [Ile3]-hpTH(1-38)- 8075 [Ile3]-hpTH(1-38)- 8167 [Ile3]-hpTH(1-38)- 8167 [Ile3]-hpTH(1-3)-hpTH- 90015 [Ile3]-hpTH(1-3)-hpTH- 9016 [Ile3]-hpTH(1-3)-hpTH- 9016 [Ile3]-hpTH(1-3)-hpTH- 9016 [Ile3]-hpTH(1-3)-hpTH- 9016 [Ile3]-hpTH(1-38)-hpTH- 9016 [Ile3]-hpTH(1-36)-hpTH- 9016 [Ile3]-hpTH(1-36)-hpTH- 9016 [Ile3]-hpTH(1-36)-hpTH- 9016 [Ile3]-hpTH(1-36)-hpTH- 9016 [Ile3]-hpTH(1-36)-hpTH- 9016 [Ile3]-hpTH(1-36)-hpTH- 9016 [Ile3]-hpTH(1-38)-hpTH- 9016 [Il	4	4	4	4	4	25	œ	œ	7	4	4	4	4	27	25	26	ø	19	ø	9	ហ	9	9	ø	φ	Q
s32]-hPTH(1-36)- j-hPTH(1-36)- j-hPTH(1-38)- 2]-hPTH(1-38)- 2]-hPTH(1-38)- 3]-hPTH(1-38)- j-hPTH(1-38)- j-hPTH(1-38)- j-hPTH(1-38)- j-hPTH(1-38)- j-hPTH(1-38)- j-hPTH(1-38)- j-hPTH(1-38)- j-hPTH(1-38)- j-hPTH(1-38)- p-rathyroid parathyroid	120	123	323	122	122	42	9	206	446	119	122	118	118	568	194	8	816	895	807	813	024	814	814	824	825	823
	parathyroid	parathyroid	parathyroid	parathyroid	parathyroid	parathyroid	tability-enhanced	tability-enhanced	parathyroid	parathyroid	parathyroid	parathyroid	parathyroid	parathyroid	protien com	parathyroid	, Arg33] -hPTH(1	peptide (PTH(	er33]-hPTH(1-38)-	}-hPTH(1-38)-	yroid ho	1у22]-һРТН(1-38)-	a22]-hPTH(1-38)-	0]-hPTH(1-36)-	n1]-hPTH(1-36)-	-H1s32]-hPTH(1-36

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IRESULT
ACCOMMENTATION
ACCOMMENTATIO
                                                                                                                                         New cyclic analogues of parathyroid hormone - having disulphide or anide bond between residues 13 and 17 and/or between residues 26 and 30, useful for treating osteoporosis and bone fractures claim 6; Page -; 23pp; English.

W20000 is a cyclised peptide derived from the N-terminal sequence of human parathyroid hormone (PTH). The peptide is able to bind to PTH receptors and stimulate adenylate cyclase activity. Cyclised PTH peptides stimulate bone growth and thus are useful in the treatment of osteoporosis and bone fractures. Optionally they may be administered concurrently with antiresorptive therapy (e.g. bisphosphonate and calicitonin).

N.B. sequence of amino acids 1-34 of human PTH.
Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W20000 standard; peptide; 34 AA.
W20000;
28-AUG-1997 (first entry)
28-AUG-1997 (first entry)
Cyclised human parathyroid hormone (1-34) amide.
Parathyroid hormone; PTH; amino terminus; cyclic
adenylate cyclase activity; bone growth; osteopo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note=
misc_difference 30
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06-JUN-1996; U09674.
07-JUN-1995; US-488105.
(BETH-) BETH ISRAEL HOSPITAL ASSOC.
Chorev M, Rosenblatt M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo
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   Score 59; DB 22;
Pred. No. 7.14e+00;
0; Mismatches C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; cyclic; analogue; osteoporosis; fracture;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to residue 26'
           0;
                                                                          Length 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         residue
           Indels
       0;
       Gaps
       0
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Search completed: Thu Jul 30 10:17:29 1998 Job time : 17 secs.
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                                                                                               B
                                                                                                                                                                PI Dong ZX;

DR WPI: 97-118819/11.

PT New Variants of human parathyroid hormone 1-34 peptide - which stimulate bone growth and are used for treatment of osteoporosis and PT stimulate bone growth and are used for treatment of osteoporosis and PT bone fracture

PT bone fracture

PT bone fracture

CC claim 7; Page -; 33pp; English.

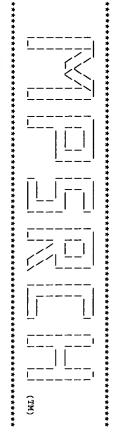
CC The present sequence is a specific example of a human parathyroid control of the amino acid residues at positions 7, 11, 23, 24, 27, 28 and 31 control of the amino acid residues at positions 7, 11, 23, 24, 27, 28 and 31 control of the amino 24 and 28, and the val residue at position 31 of the position 24 and 28, and the val residue at position 31 of the control of the are useful in human or veterinary medicine for the tenament of osteoporosis and bone fracture, optionally in conjunction N.B. The present sequence does not appear in the specification. It as stated in the claim.

Sequence 34 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
ID W1
AC W1
AC W1
DT 25
DE H(
KW OC
KW OC
KW DC
S S;
FH K(
FT m/
                                                                                                                  Query Match
Best Local Similarity 100.0%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09702834-A1.
30-JAN-1997.
03-JUL-1995; U11292.
13-JUL-1995; US-001105.
06-SEP-1995; US-003305.
29-MAR-1996; US-626186.
(BIOM-) BIOMEASURE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W17949 standard; peptide; 34 AA.
W17949;
W17949;
29-JUL-1997 (first entry)
Human parathyroid hormone analogue [Cha24,28,31]hPTH(1-34)NH2.
Osteoporosis; agonist; PTH; human; anti-resorptive therapy;
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified_site
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/note= "Cha"
34
/note= "In amide form"
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/note- "Cha"
31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Cyclohexylalanine (Cha)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label- OTHER
                                                                                                             Score 59; DB 22; Le
Pred. No. 7.14e+00;
0; Mismatches 0;
                                                                                                                                          Length 34;
                                                                                                               Indels
                                                                                                             0,
                                                                                                            Gaps
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FT SIGNAL 1 25
FT PROPEP 26 31
FT CHAIN 32 115 PARATHYROID HORMONE.
FT CONFLICT 106 106 V -> G (IN REF. 4).
SQ SEQUENCE 115 AA; 12980 MW; 673EA5F2 CRC32;
Query Match 92.2%; Score 47; DB 1; Length 115;
Best Local Similarity 85.7%; Pred. No. 1.19e-01;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 43 GKHLSSM 49
| | | | | | | | |
Oy 1 GKHLNSM 7

Search completed: Thu Jul 30 10:17:55 1998
Job time: 8 secs.
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MPsrch\_pp n on: protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Thu Jul 30 10:15:51 1998; MasPar time 3.14 Seconds 93.097 Million cell updates/sec

Description:
Perfect Score:
Sequence: >US-08-817-547A-9 (1-8) from US08817547A.pep 59

Title:

Scoring table: 1 LGKHLNSM 8

PAM 150 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 21.301; Variance 26.286; scale 0.810

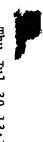
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

1 2 3 3 3 4 4 4 4 4 7 7 7 7 112 112 113 114 115 116 117 117 117 118 119 119 119 119 119 119 119 119 119	sult No.
<b>₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩</b>	Score
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parathyroid hormone ( parathyroid hormone 4 parathyroid hormone 4 parathyroid hormone 4 parathyroid hormone 6 parathyroid hormone 6 parathyroid hormone 6 parathyroid hormone 6 parathyroid hormone 9 parathyroid normone 9 parathyroid mormone 9 parathyroid hormone 9 parathyroid hormone 9 parathyroid hormone 9 parathyroid hormone 9 DNA recombinase homol DNA recombinase homol DNA-binding protein T	Description
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45	44	43	42	41	40	39	38	37	36	35	34	u u	32	3 1-1	30	29	28	27	26	25	24
42	42	42	42	42	42	43	43	43	<u>4</u> ω	43	44	44	44	44	44	44	44	44	44	44	45
71.2	71.2	71.2	71.2	71.2	71.2	72.9	72.9	72.9	72.9	72.9	74.6	74.6		74.6			74.6	74.6	74.6	74.6	76.3
762	363	247	187	138	108	1708	744	738	621	313	2105	936	700	671	619	325	265	264	231	208	2068
Ν	N	N	N	N	Н	N	N	N	N	N	μ.	ν	N	ᆫ	N	N	N	N	N	N	N
E64597	н69393	S72904	S25395	S66004	RHHUS	F69189	A32905	S35093	S35092	B64361	A44059	S64384	S12053	C69621	S54636	E69118	A46018	S31394	JQ0704	D65041	A47371
DNA mismatch repair p	iron-sulfur cluster b	phosphoglycerate muta	H+-transporting ATP s	transcriptional regul	somatoliberin precurs	magnesium chelatase s	plakoglobín, desmosom	plakoglobin – African	plakoglobin – mouse (	L-lactate dehydrogena	RNA-directed RNA poly	probable membrane pro	protein-tyrosine-phos	fructose-bisphosphata	probable membrane pro	lactate dehydrogenase	apolipoprotein AI - p	apolipoprotein A-I -	apolipoprotein A-I -	hypothetical protein	transcription initiat
6.84e+01	6.84e+01	6.84e+01	6.84e+01	6.84e+01	6.84e+01	4.38e+01	4.38e+01	4.38e+01	4.38e+01	4.38e+01	2.78e+01		2.78e+01	2.78e+01	2.78e+01	2.78e+01	2.78e+01	2.78e+01	2.78e+01	2.78e+01	1.75e+01

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COMMENT Resolution: Not applicable
COMMENT Determination: NNR
KENYORDS
LSTATURE
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(ME)

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Jul 30 10:15:27 1998; MasPar time 2.12 Seconds 94.808 Million cell updates/sec

Tabular output not generated.

Title: >US-08-817-547A-9
Description: (1-8) from US08817547A.pep
Perfect Score: 59

Sequence: 1 LGKHLNSM 8

Scoring table: PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 22.280; Variance 22.155; scale 1.006

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

No.	Score 59	<b>ωωοι</b> († (δ)		1 1 1 B	PTHY_HUMAN PTHY_BOVIN	HORMONE	Pred. No. 9.29e-04 1.20e-02
ωN	555		115 115		PTHY_BOVIN	HORMONE	1.20e-02 1.20e-02
4	48	$\vdash$	115	_	PTHY_PIG	HORMONE	8.11e-01
u	46	78.0	152	_	HMGB_SOYBN	HMG-Y RELATED PROTEIN	2.51e+00
σ	46		176	$\vdash$	HMGA_SOYBN	HMG-Y RELATED PROTEIN	
7	46	78.0	192	سو	SC72_YEAST	TRANSLOCATION PROTEIN	2.51e+00
8	45	76.3	115	$\vdash$	PTHY_RAT	PARATHYROID HORMONE PR	4.37e+00
9	45	76.3	985	<b>-</b>	NAH_YEAST	PROBABLE NA(+)/H(+) AN	4.37e+00
10	45	76.3	2068	<b></b>	CCG1_DROME	TRANSCRIPTION INITIATI	4.37e+00
11	44	74.6	208	Ľ	YFJJ_ECOLI	HYPOTHETICAL 24.6 KD P	7.51e+00
12	44	74.6	265	$\vdash$	APA1_PIG	APOLIPOPROTEIN A-I PRE	7.51e+00
13	44	74.6	700	Н	PTPE_HUMAN	PROTEIN-TYROSINE PHOSP	7.51e+00
14	44	74.6	936	H	YG2K_YEAST	HYPOTHETICAL 106.5 KD	7.51e+00
15	44	74.6	2105	μ	POLR_ASGVP	GENOME POLYPROTEIN (CN	7.51e+00
16	43	72.9	313	۳	LDH_METJA	L-LACTATE DEHYDROGENAS	1.28e+01
17	43	72.9	621	ш	PLAK_MOUSE	JUNCTION PLAKOGLOBIN (	1.28e+01
18	43	72.9	738	ш	PLAK_XENLA	JUNCTION PLAKOGLOBIN (	1.28e+01
19	43	72.9	743	щ	PLAK_HUMAN	JUNCTION PLAKOGLOBIN (	٠
20	42		108	ш	SLIB_HUMAN	SOMATOLIBERIN PRECURSO	2.16e+01
21	42	71.2	138	Н	YYAN_BACSU	HYPOTHETICAL TRANSCRIP	
22	42		187	ш	ATPD_ODOSI	ATP SYNTHASE DELTA CHA	2.16e+01
ر س	;	1,			DACK AACLE	DHOCKBROOK TOCKBROOK	3 160+01

SEQUENCE OF 75-100.

KEUTHANN H.T., NIALL H.D., JACOBS J.W., BARLING P.M., HENDY G.

O'RIORDAN J.L.H., POTTS J.T. JR.;

(1N) CALCIUM-REGULATING HORMONES, TALMADGE R.V., OWEN M.,

PARSONS J.A., EDS., PP.9-14, EXCERPTA MEDICA FOUNDATION, AMSTERDATION, 1975).

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YA73_SCHPO YA6_SCHPO	ST13_SCHPO	BDH_HUMAN BDH_RAT KITH_HSV11	ZFH2_DROME DYHC_CAEEL	RRPL_RDV	GUTR_BACSU	YAN4_SCHPO	YGZB YEAST	HSF1_MOUSE	KPL1_HUMAN	PMGY_MYCTU	BICD_DROME	YSPL_CAEEL	YBQ6_YEAST
HYPOTHETICAL 80.4 KD P HYPOTHETICAL 92.1 KD P HYPOTHETICAL 140.8 KD	60.9	D-BETA-HYDROXYBUTYRATE D-BETA-HYDROXYBUTYRATE THYMIDINE KINASE (EC 2	ZINC-FINGER PROTEIN 2 DYNEIN HEAVY CHAIN, CY	RNA-DIRECTED RNA POLYM	TRANSCRIPTION ACTIVATO	Ğ	THETICAL 64.9	HEAT SHOCK FACTOR PROT	SERINE/THREONINE PROTE	PHOSPHOGLYCERATE MUTAS	CYTOSKELETON-LIKE BICA	HYPOTHETICAL 91.0 KD P	HYPOTHETICAL 57.8 KD P
		5.93e+01 5.93e+01 5.93e+01			3.60e+01			3.60e+01	٠		2.16e+01	2.16e+01	2.16e+01

## ALIGNMENTS

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	PTHY_HUMAN STANDARD; PRT; 115 AA.	
	1986	
	(REL. 05,	
	THYROID	
	CADTONIC	
	HOMO SAFIENS (HOMAN). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	
	EUTHERIA; PRIMATES.	
	CENTENCE EDOM N 2	
	BERG H.M., F	
-	U.S.A. 78:7365-7369(19	
	[2] SEQUENCE FROM N.A.	
	MEDLINE; 83169834.	
•	B.E., FREEMAN M.W., FENNI	
	PROC. NATL. ACAD. SCI. U.S.A. 80:212/-2131(1983). [3]	
Ť	SEQUENCE OF 26-37.	
•	MEDLINE; 74174967.	
	JACOBS J.W., KEMPER B., NIALL H.D., HABENER J.F., POTTS J.T. JR.;	
-	NATURE 249:155-157(1974).	
	SEQUENCE OF 32-68.	
•	MEDLINE; 74111656.	
-	NIALL H.D., SAUER R.T., JACOBS J.W., KEUTMANN H.T., SEGRE G.V.,	
-	O'RIORDAN J.L.H., AURBACH G.D., POTTS J.T. JR.;	
-	PROC. NATL. ACAD. SCI. U.S.A. 71:384-388(1974).	
	[5] SHOTTENCE OF 61-83 AND 84-115	
•	MEDLINE: 79082855.	
	KEUTMANN H.T., SAUER M.M., HENDY G.N., O'RIORDAN J.L.H.,	
_	POTTS J.T. JR.;	
	BIOCHEMISTRY 17:5723-5729(1978).	
_	SHOTTENON OF 75-100	

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42

LGKHLNSM

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Query Match
         Matches
                                                      SEQUENCE
                                                               CONFLICT
                                                                                                                                                                                                                                                              -I- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS
BONE AND PREVENTING THEIR RENAL EXCRETION.
-I- DISEASE: DEFECTS IN PTH ARE A CAUSE OF FAMILIAL ISOLATED
HYPOPARATHYROLDISM (FIH).
EMBL; J00301; G199704; -.
EMBL; V00597; G37144; -.
EMBL; A29146; E186700; -.
PIR; A19339; A19339.
PIR; A19339; A19339.
                                                                                     VARIANT
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KRONENBERG H.M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 93345518.
BARDEN J.A., CUTHBERTSON R.M.;
EUR. J. BIOCHEM. 215:315-321(1993).
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MEDLINE; 91299748.
KLAUS W., DIECKMANN T., WR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANDREATTA R.H., HARTMANN A., JOEHL A., RINIKER B., RITTEL W., SIEBER P., HELV. CHIM. ACTA 56:470-473(1973).
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TREGEAR G.W., VAN RIETSCHOTEN J., GREEN E., NIALL H. KEUTMANN H.T., PARSONS J.A., O'RIORDAN J.L.H., POTT! HOPPE-SEXLER'S Z. PHYSIOL. CHEM. 355:415-421(1974).
                    Local
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MEDLINE: 73227467.
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MEDLINE; 75146516.

MEDLINE; 75146516.

MEDUTMANN H.T., NIALL H.D., O'RIORDAN J.L.H., POTTS J.T. JR.;

BIOCHEMISTRY 14:1842-1847(1975).
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1ZWB;
1ZWC;
1ZWD;
1ZWE;
      h 100.0%;
Similarity 100.0%;
8; Conservative
                                                                                 SIGNAL; DISEASE MUTATION; 3D-STRUCTURE.

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26 31
32 115 PARATHYROID HORMONE
18 18 C -> R (IN FIH; LEA
                                                                                                                                    PS00335; PARATHYROID;
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12-MAR-97.
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115
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12-MAR-97.
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    Score 59; DB 1;
Pred. No. 9.29e-04
0; Mismatches
                                         PARATHYROID HORMONE.
C -> R (IN FH; LEADS TO INEFFICIENT PROCESSING OF THE PRECURSOR).
N -> D (IN REF. 5).
243E87C7 CRC32;
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JAENICKE
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FORSSMANN W.-G.,
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S J.T.
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RESOLUTION OF THE STATE OF THE 
                                               PROC. MALE PARTES CALCALL.

-!- FUNCTION: PTH ELEVATES CALCALL.

BONE AND PREVENTING THEIR RENAL EX

EMBL; V00106; 685; -...

EMBL; J00023; G163641; -...

EMBL; J00024; G163643; -...

EMBL; J00024; E18249; ALT_SEQ.

EMBL; J00024; E18250; ALT_INIT.

R EMBL; M01938; G163647; -...

R EMBL; M01938; G163647; -...

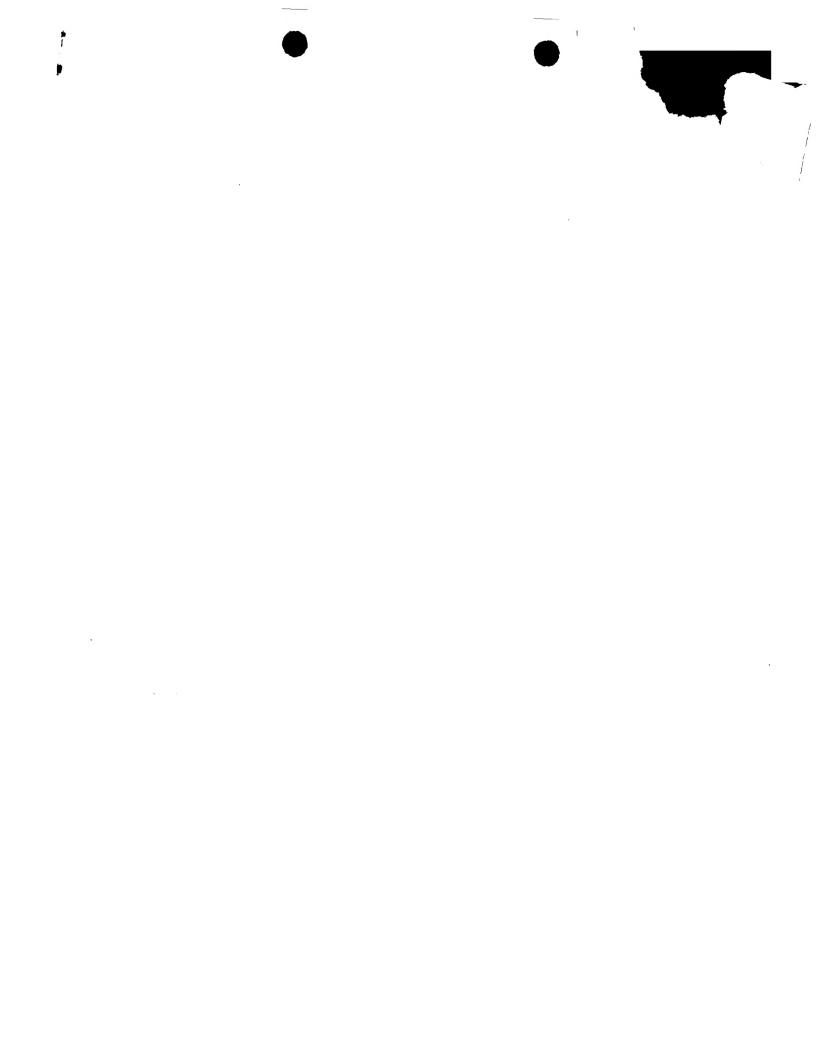
R EMBL; M01938; G163647; -...
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BREWER H.B.
PROC. NATL.
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NIALL H.D., KEUTMANN H.T., SI
AURBACH G.D., POTTS J.T. JR.
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MEDLINE; 84262483.
WEAVER C.A., GORDON D.F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 26-115.
MEDLINE; 74142666.
HAMILTON J.W., NIALL H.D.,
COHN D.V.;
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EUKARYOTA; ,
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MEDLINE; 71076162.
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WEAVER C.A., GORDON D.
MOL. CELL. ENDOCRINOL.
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WEAVER C.
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POTTS J.T. JR., RICH A.,
PROC. NATL. ACAD. SCI. U.S.A. 76
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21-JUL-1986
01-NOV-1997
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        ; A01534; PTBO.
; A24949; A24949.
SITE; PS00335; PA
                                                                                                                                                                                                                            J.T. JR., TREGEAR G.W., KEUTMANN H.T., NIALL H.D. S.L.J., DAWSON B.F., HOGAN M.L., AURBACH G.D.; NATL. ACAD. SCI. U.S.A. 68:63-67(1971). G.D.; UNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING
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METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
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, GORDON D.F., K
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          PARATHYROID;
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:411-424(1982).
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S.A. 78:4073-4077(1981).
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H G.D.;
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SIGNAL.

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FT SIGNAL
FT CHAIN
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FT CONFILCT
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SOURCE 115
AA; 12990 MA; 0738AFS CRC32;
OMETY MATCH
SOURCE 115
BAST Local Similarity 91.2%; Score 55; DB 1; Length 115;
MATCHES 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 42 LOKHISM 49
OY 1 LOKHINSM 8

Search completed: Thu Jul 30 10:15:34 1998
Job time: 7 secs.
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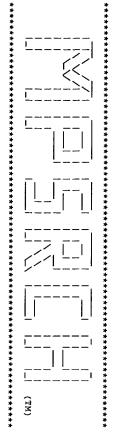
1 49 83 3 49 83 47 79 5 46 76 6 45 76 7 45 76 8 44 74 110 44 74 112 44 74 113 43 72 116 43 72 20 42 71	Pred. No. is t score greater and is derived and is derived and score Match No. Score Match	Database: s	Release Copyric prote utput no on: core: core:	
.1 367 10 Q 1.1 1300 10 P 1300 10 P 1437 6 Q 10 Q	the number of result: than or equal to the by analysis of the SUMMAR	sptremb15 1:sp_fung1 2:sp_human 1:sp_fung1 2:sp_organe1 5:sp_bacteria 10:sp_r 13:sp_unclassified Mean 21.247; Variance	1A John F. Collins (c) 1993-1998 Uniteribution rights - protein database Jul 30 10:16:32 1 Jenerated.  3-08-817-547A-9 8) from US08817547 GKHLNSM 8 4 150 5 15 150 150 150 151 150 151 150 150 151 150 150	
HYPOTHETICAL 43.7 KD P L1 RETROPOSON, ORF2 MR L1 RETROPOSON ORF 4 ATP SYNTHASE A CHAIN ( HYPOTHETICAL 52.6 KD P PARATHYROID HORMONE (F VOKA PROTEIN A-I (F APOLIPOPROTEIN A-I (FR APOLIPOPROTEIN G ENVELOPE GLYCOPROTEIN, LACTATE DEHYDROGENASE. CHROMOSOME XV READING FUNCTION UMKNOWN, PLAKOGLOBIN (FRAGMENT) 1 ZK863.3 1 CORFS.2. PLAKOGLOBIN.	redicted by chance to have core of the result being pr tal score distribution.  Description  Pr	nan 3:sp_invertebrate 4:sp_mammal nelle 7:sp_phage 8:sp_plant p_rodent 11:sp_virus 12:sp_vertebrate ne 21.504; scale 0.988	computing Research Un ty of Edinburgh, U.K. ford Molecular Ltd ch, using Smith-Water MasPar time 3.68 Sec 91.451 Million cell	
	a inted,	brate	lgorith es/sec	(HH)

42 71.2 228 1 P89049 42 71.2 278 9 Q55106 42 71.2 290 9 Q03086 REPLICATION PROTEIN A 42 71.2 362 9 Q05512 BACILLUS SP. MANNAN EN 42 71.2 363 9 Q29112 IRON SULFUR CLUSTER BI 42 71.2 421 9 Q28532 HYPOTHETICAL 48.5 KD P 42 71.2 439 8 Q41770 ALPHA-AMYLASE. 42 71.2 518 12 Q13035 PROSAPOSIN. 42 71.2 646 10 Q63779 HYPOTHETICAL 76.2 KD P 42 71.2 762 9 Q25338 DNA MISMATCH REPRIR PR 42 71.2 825 8 Q25224 T3266.14 PROTEIN 42 71.2 1067 11 Q65447 SIMILAR TO GLYCINE DEH 42 71.2 1067 11 P89047 POLYEROTEIN PR 42 71.2 1067 11 P89047 POLYEROTEIN TYROSINE PHOSP 42 71.2 224 2 Q15262 PROTEIN TYROSINE PHOSP 42 71.2 2466 2 Q16826 PROTEIN TYROSINE PHOSP 42 71.2 2466 3 Q16826 PROTEIN TYROSINE PHOSP 42 71.2 2466 3 Q16826 PROTEIN TYROSINE PHOSP 42 71.2 2466 3 Q16826 PROTEIN TYROSINE PHOSP 42 71.2 2466 10 Q16826 PROTEIN TYROSINE PHOSP 42
22 278 9 055106 REPLICATION PROTEIN 2 278 9 055106 REPLICATION PROTEIN 2 290 9 003086 REPLICATION PROTEIN 2 362 9 005512 BACILLUS SP. MANNAN 2 363 9 029112 IRON-SULFUR CLUSTER 2 421 9 028532 HYPOTHETICAL 48.5 KI 2 421 9 028532 HYPOTHETICAL 76.2 KI 2 421 9 025338 DANA MISMATCH REPAIR 2 1071 12 03035 PROSAPOSIN. 2 518 12 013035 PROSAPOSIN. 2 518 12 013035 PROSAPOSIN. 2 646 10 063779 HYPOTHETICAL 76.2 KI 2 762 9 025338 DANA MISMATCH REPAIR 2 1071 11 P89047 STRUCTURAL POLYEROTEIN. 2 1067 11 P89047 POLYEROTEIN TYROSINE PHC 2 1067 11 P89047 PROTEIN TYROSINE PHC 2 2450 10 062135 PROTEIN TYROSINE PHC 2 2460 2 015264 PROTEIN TYROSINE PHC 2 2460 2 016826 PROTEIN TYROSINE PHC 2 2466 2 016826 PROTEIN TYROSINE PHC 2 2460 2 015263 PROTEIN TYROSINE PHC 2 2460 2 016826 PROTEIN TYROSINE PHC 2 2460 2 016826 PROTEIN TYROSINE PHC 2 2460 2 012923 PROTEIN TYROSINE PHC 2 2460 2 012924 PROTEIN TYROSINE PHC 2 2460 2 012924 PROTEIN TYROSINE PHC 2 2460 2 012924 PROTEIN TYROSINE PHC 2 2
11 P8949  9 055136  9 005512  9 005512  10 005512  10 005512  10 005512  10 005512  10 005512  10 005512  10 005512  10 005512  10 005512  10 005512  10 005512  10 005512  10 005512  10 005513  10 005512  10 005512  10 005513  10 005513  10 005513  10 005513  10 005513  10 005513  10 005513  10 005513  10 005513  10 005513  10 005513  10 005513  10 005514  11 0055144  12 005524  13 021962  14 0056144  15 0056144  16 0056144  17 0056144  10 005614
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HOWOLOGUE TO PROTEIN REPLICATION PROTEIN REPLICATION PROTEIN REPLICATION PROTEIN RACILLUS SP. MANNAN IRON-SULFUR CLUSTER HYPOTHETICAL 48.5 KI ALPHA-AMYLASE. PROSAPOSIN. PROSAPOSIN. HYPOTHETICAL 76.2 KI DNA, MISMATCH REPAIR T3266.14 PROTEIN SIMILAR TO GLYCINE I SIMILAR TO GLYCINE I SIMILAR TO GLYCINE PHOTEIN TYROSINE PHOPOTEIN TYROSINE
LOGGE TO PROTEIN ICATION PROTEIN ILLUS SP. MANNAN -SULFUR CLUSTER THETICAL 48.5 KI A-AMYLASE. APOSIN. APOSIN. 6.14 PROTEIN. 6.14 PROTEIN. 6.14 PROTEIN. ILAR TO GLYCINE I CTURAL POLYPROTE PROTEIN (FRAGNE PHO EIN TYROSINE PHO EIN

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AC 066
A
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D Q63289;
AC Q63289;
DT 01-NOV-1996 (TREMBLREL 01, CREATED)
DT 01-NOV-1996 (TREMBLREL 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL 01, LAST ANNOTATION UPDATE)
DT 01-NOV-1996 (TREMBLREL 01, LAST ANNOTATION UPDATE)
DT 01-NOV-1996 (TREMBLREL 01, CAST ANNOTATION UPDATE)
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1 063778;
AC 063778;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 43.7 KD PROTEIN.
DS RATTUS NORVEGICUS (RAT).
DS EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
NC EUTHERIA; RODENTIA.
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Best Local Similarity 75.0%;
Matches 6; Conservative
SEQUENCE FROM N.A. TISSUE-LIVER; MEDLINE; 92375092. ILVES H., KAHRE O., S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE-LIVER;
MEDLINE: 87064324.
D'AMBROSIO E., WAITZKIN S.D., WITNEY F.R.,
MCL. CELL. BIOL. 6:411-424(1986).
EMBL; M13100; 6804811; -.
HYPOTHETICAL PROTEIN.
SEQUENCE 367 AA; 43685 MW; 3D4A69E5 CRC
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1 LGKHLNSM 8
                SPEEK M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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MPsrch\_pp on :: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:20:02 1998;

MasPar time 2.67 Seconds 40.289 Million cell upda updates/sec

abular output not generated.

Description: Perfect Scor Title: Score: >US-08-817-547A-10 (1-7) from US08817547A.pep

Sequence: 51 1 GKHLNSM 7

Scoring table: PAM 150 Gap 15

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 14.516; Variance 40.392; scale 0.359

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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118 117 118 118 118 118 118 118 118 118	esult No.
25 25 25 25 25 25 25 25 25 25 25 25 25 2	Score
	. : G.7
	Length
00000 001100 00000 00000000000000000000	BB
W17955 W17955 W17955 W17955 W17955 W17955 W17962 W17962 W17943 W1794 W17943 W1794 W17943 W179	
Sequence of parathyroid hor Human parathyroid hor Target peptide (PTH(1 Human parathyroid hor Propargyl-[Al]-hPTH(1 [Morpholine-2-carboxy [Nval]-hPTH(1-36)-NH2 [Phe8]-hPTH(1-36)-NH2 [Cha8]-hPTH(1-36)-NH2 [Ala30]-hPTH(1-36)-NH2 [Ala30]-NH2 [Ala30]-NH2 [Ala30]-NH2 [Ala30]-NH2 [Ala30]-NH2 [Ala3]	
1.10e+01 1.10e+01 1.10e+01 1.10e+01 1.10e+01 1.10e+01 1.10e+01 1.10e+01 1.10e+01 1.10e+01 1.10e+01 1.10e+01 1.10e+01 1.10e+01 1.10e+01 1.10e+01 1.10e+01	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	
51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	
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R4969	R2121	R2121	R232	R2119	R2324	4 R23229	W2942	R212	R212	R344	R235	4 R23226	R2122	R211		W2568	W2194	6 P30015	R5812	R9895	R5807	R580	R5814	9 R58141	9 R58244	
Sequence of variant o						Human parathyroid hor	Human parathyroid hor	Human parathyroid hor	parathyroid	Human parathyroid hor	Human parathyroid hor	Human parathyroid hor	parathyro	Human parathyroid hor	parathyro	~	Fusion protien compri	Ē	.9]-hPTH(1-	et peptide (	(1-38)	3]-hPTH(1-	2]-hPTH(1-38)	[Leu21]-hPTH(1-38)-OH	[Ala0]-hPTH(1-36)-NH2	
<u>-</u>	<u>-</u>	1	1	_	_	1	_	_	_	1.10e+01	_	1.10e+01	_	-	<u>-</u>	_ر		Н	_ 	_		<u>, , , , , , , , , , , , , , , , , , , </u>	<u>,</u>	٠	1.10e+01	

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RESULT
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AC WI
DT 20
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                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%;
                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                    parathyroid hormone peptide analogues - used for treating osteoporosis, hypercalcaemia, hyperparathyroidism and hormone dependent tumours, and in vitro for bio:assays Claim 3; column 8; 5pp; English.

The PTH analogues of the invention are used for inhibiting the naturally-occurring hormone in vivo and in vitro. They have high binding affinity for their resp. cell surface receptors while not stimulating prodn. of second messenger molecules. They may be used in vitro in a bioassay for PTH and in vivo for therapy and diagnosis. They are prepd. in dosage forms for oral, parenteral, rectal, intransal or topical admin.
W17939 standard; peptide; 34 AA.
W17939;
29-JUL-1997 (first entry)
Human parathyroid hormone analogue [Cha7,11]hPTH(1-34)NH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
US4771124-A.
13-SEP-1988.
26-MAY-1987: US-054359.
26-MAY-1987: US-054359.
(MERI ) MERCK & CO INC.
Rosenblatt M, Caporale LH, Nutt RF, Levy JJ, Chorev M;
WPI; 88-278169/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-MAR-1992 (first entry)
Sequence of parathyroid hormone (PTH) analogue [L-Phe23]hPTH(7-34)NH2.
Parathyroid hormone analogue; osteoporosis therapy; hypercalcaemia;
hyperparathyroidism; hormone dependent tumour; bloassay; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P82185 standard; Protein; 27 AA. P82185; 06-MAR-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  treatment.
                                                                                                                     1 GKHLNSM 7
                                                                                                                                          6 gkhlnsm 12
                                                                                                                                                                                     Conservative
                                                                                                                                                                                                     Score 51; DB 3;
Pred. No. 1.10e+01
                                                                                                                                                                                       0;
                                                                                                                                                                                         Mismatches
                                                                                                                                                                                       0,
                                                                                                                                                                                                                       Length
                                                                                                                                                                                       Indels
                                                                                                                                                                                                                       27;
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Claim 5; Page -; 33pp; English.

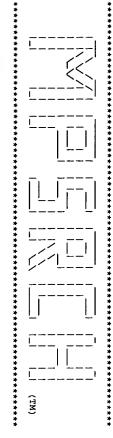
Claim 5; Page -; 33pp; English.

The present sequence is a specific example of a human parathyroid formone (hPTH) analogue from fragment 1-34 in which at least one of the amino acid residues at positions 7, 11, 23, 24, 27, 28 and 31 crossition and the Leu at positions 11 in the wild-type have been constituted by Cha. The hPTH analogues stimulate bone growth and so crossition and bone fracture, optionally in conjunction with a crossorptive therapy (bisphosphonates and calcitonin).

Claim 1: resorptive therapy (bisphosphonates and calcitonin).

Claim 2: Analogue fracture, optionally in conjunction with a corresponds to the known hPTH 1-34 fragment with the modifications constated in the claim.
                                                                                                                             Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JAN-1997.
03-JUL-1996; U11292.
13-JUL-1995; US-001105.
06-SEP-1995; US-003305.
29-MAR-1995; US-26186.
(BIOM-) BIOMEASURE INC.
Dong ZX;
WPI; 97-118819/11.
New variants of human parathyroid hormone 1-34 peptide - which stimulate bone growth and are used for treatment of osteoporosis and bone from from the province of the province o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Osteoporosis; agonist; PTH; human; anti-resorptive therapy; bone fracture. Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9702834-A1.
30-JAN-1997.
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12 gkhlnsm 18
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1 GKHLNSM 7
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/note= "Cha"
34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "In amide form"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Cyclohexylalanine (Cha)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'label- OTHER
                                                                                                                                 Score 51; DB 22; Length 34; Pred. No. 1.10e+01; 0; Mismatches 0; Indels
                                                                                                                                                                                                   Length 34;
                                                                                                                                        0;
                                                                                                                                        Gaps
                                                                                                                                        0;
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arch completed: Thu Jul 30 10:20:20 1998 b time : 18 secs.



MPsrch\_pp on : protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:19:17 1998; MasPar time 3.25 Seconds 78.689 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Title: >US-08-817-547A-10 (1-7) from US08817547A.pep 51 1 GKHLNSM 7

Sequence:

Scoring table: PAM 150 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 19.845; Variance 21.817; scale 0.910

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

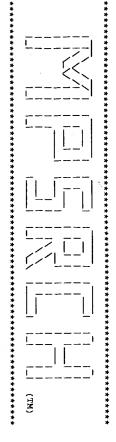
Query

23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	œ	7	σ	ហ	4	ω	2	_	No.
39	40	40	40	41	41	41	41	42	42	42	44	47	47	47	51	51	51	51	51	51	51	51	Score
76.5	78.4	78.4	78.4	80.4	80.4	80.4	80.4	82.4	82.4	82.4	86.3	92.2		92.2	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	Match
176	690	545	115	3005	558	513	421	501	363	362	2105		115	37	115	37	36	35	34	34	34	34	Length
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pituitary adenylate c	triacylglycerol lipas	orf2 protein - Junoni	parathyroid hormone p	homeotic protein zfh-	probable membrane pro	probable RNA-directed	conserved hypothetica	glucan 1,3-beta-gluco	iron-sulfur cluster b	mannan endo-1,4-beta-	RNA-directed RNA poly	parathyroid hormone p	parathyroid hormone -	parathyroid hormone (	parathyroid hormone p	parathyroid hormone f	parathyroid hormone (	parathyroid hormone (	parathyroid hormone 4	parathyroid hormone 4	parathyroid hormone (	parathyroid hormone (	Description
	3.45e+01	3.45e+01	3.45e+01	2.08e+01	2.08e+01	2.08e+01	N	1.24e+01	1.24e+01	1.24e+01	4.31e+00	œ	8.32e-01	8.32e-01	8.41e-02	8.41e-02	8.41e-02	8.41e-02	8.41e-02	٠	8.41e-02	8.41e-02	Pred. No.

4.4	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24
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72.5	72.5	٠	•			74.5	•						•	•					76.5	
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Aspartate transcarbam signal transducer amp		Aspartate transcarbam	phosphoglycerate muta	hypothetical protein	protein kinase (EC 2.	DNA recombinase homol	RepA protein - Escher		hypothetical protein	HMG-Y-related protein	HMG-Y-related protein	probable membrane pro	cycK protein homolog	D-lactate dehydrogena	H+-transporting ATP s	atp6 protein - common	outer membrane protei	SMR1 protein - Podosp	COI intron 13 protein	polysaccharide deacet
1.49e+02	1.49e+0	1.49e+02	1.49e+0;	1.49e+02	9.24e+01	9.24e+01	9.24e+01	9.24e+01	9.24e+01		9.24e+01	5.67e+01	5.67e+01	5.67e+01	5.67e+01	5.67e+01	5.67e+0:	5.67e+0:	5.67e+0	5.67e+0

ORGANISM #formal_name REFERENCE A67860 #authors Roesch, P.; #submission submitted to #cross-references PDB:12WE REFERENCE TN001721 #authors Marx, U.C. #authors in Strukture pp.0, Bayr	RESULT 2 ENTRY TITLE ALTERNATE_NAMES PDB_TITLE	Db 12 GKHLNSM          Qy 1 GKHLNSM	Query Match Best Local Similarity Matches 7; Conse	6-9 19-30 SUMMARY	rs	REFERENCE A67856 #authors Roesch, P.; #submission submitted to #cross-references PDB:1ZWA REFERENCE TN001717	RESULT 1 ENTRY TITLE TITLE ALTERNATE_NAMES PDB_TITLE ORGANISM
#formal_name Homo sapiens #common_name man A67860 Roessch, P.; Marx, U.C. submitted to the Brookhaven Protein Data Bank, June 1996 sees PDB:12WE TN001721 Marx, U.C. in Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth: University of Bayreuth (Thesis), 1996	ype ( jormoj	4 18 4 7	100.0%; Score 51; DB 5; Length 34; llarity 100.0%; Pred. No. 8.41e-02; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	<pre>#region helix (right hand alpha)\ #region helix (right hand alpha) #length 34 #molecular-weight 4118 #checksum 5629</pre>	Marx, U.C. In Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth : University of Bayreuth (Thesis), 1996 Resolution: not applicable Determination: NMR - hormone	Marx, U.C. the Brookhave	12WA #type complete parathyroid hormone (residues 1-34) - human HPTH(1-34) structure of human parathyroid hormone fragment 1-34, NMR 10 structures #formal_name Homo sapiens #common_name man

	Search comp Job time :	δ B	COMMENT COMMENT KEYWORDS FEATURE 15-25 SUMMARY Query M Best Lo
	Search completed: Thu Jul 30 10:19:45 1998 Job time : 28 secs.	;	Resolution: not applicable Determination: NMR hormone  #region helix (right hand alpha) #length 34 #molecular-weight 4128 #checksum 5508 Match 100.0%; Score 51; DB 5; Length 34; scal Similarity 100.0%; Pred. No. 8.41e-02; s 7; Conservative 0; Mismatches 0; Indels 0; Gans



MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. n on: Thu Jul 30 10:17:47 1998; MasPar time 2.06 Seconds 85.162 Million cell updates/sec

Description: Perfect Score: Title: >US-08-817-547A-10 (1-7) from US08817547A.pep 51 1 GKHLNSM 7

Sequence:

Scoring table: PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 20.740; Variance 18.384; scale 1.128

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

45	44	43	42	41	40	39	38	37	36	35	34	ယ ယ	32	31	30 0	29	28	27	26	25	24
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SPCO_HUMAN	CCG1_DROME	NAH_YEAST	DING_BACSU	MAOX_HAEIN	MBA2_ECOLI	PTPE_HUMAN	YYI3_CAEEL	SYT_ECOLI	LIM_HALRO	AMPG_ECOLI	YDD2_SCHPO	DFP_ECOLI	THBG_HUMAN	Y432_MYCPN	Y039_MYCPN	P2C1_YEAST	PMGM_RAT	YFJJ_ECOLI	FRIL_RABIT	HBA3_PLEWA	LEU2_AZOVI
SPECTRIN BETA CHAIN, B	TRANSCRIPTION INITIATI	PROBABLE NA(+)/H(+) AN	PROBABLE ATP-DEPENDENT	PUTATIVE MALATE OXIDOR	MOBILIZATION PROTEIN A	PROTEIN-TYROSINE PHOSP	PROBABLE G PROTEIN-COU	THREONYL-TRNA SYNTHETA	HOMEOBOX PROTEIN LIM (	AMPG PROTEIN.	HYPOTHETICAL 55.4 KD P	DNA/PANTOTHENATE METAB	THYROXINE-BINDING GLOB	HYPOTHETICAL PROTEIN M	HYPOTHETICAL PROTEIN M	PROTEIN PHOSPHATASE 2C	PHOSPHOGLYCERATE MUTAS	HYPOTHETICAL 24.6 KD P	FERRITIN LIGHT CHAIN.	HEMOGLOBIN ALPHA CHAIN	3-ISOPROPYLMALATE DEHY
5.38e+01	5.38e+01	5.38e+01		5.38e+01			٠	٠	٠	5.38e+01	5.38e+01	٠		5.38e+01			5.38e+01	5.38e+01	5.38e+01	5.38e+01	3.09e+01

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O'RICKUAN J.H., FOITS J.T. UR.; (IN) CALCIUM-REGULATING HORMONES, TALMADGE R.V., OWEN M., PARSONS J.A., EDS., PP.9-14, EXCERPTA MEDICA FOUNDATION, AMSTERDAM, (1975). [7]		POTTS J.T. JR.; BIOCHEMISTRY 17:5723-5729(1978).	NN	SEQUENCE OF 61-83 AND 84-115.		ATTREACH G D	111656.	[4]	249:155-157(1974).	KEMPER B. NTALL H.D. HABENER J.F.	SEQUENCE OF 26-37.	PROC. NATH. ACAD. SCI. U.S.A. 80:212/-2131(1983). [3]	G.N., POTTS J.T. JR., RI	T.J., MCCEVITT B.E., FREEMAN	SEQUENCE FROM N.A. MEDLINE: 83169834.		NATL. ACAD. SCI. U.S.A. 78:7365-7369(1981).	BERG H.M., POTTS J.J	SEQUENCE FROM N.A.	[1]	ME	HOMO SAPIENS (HUMAN).	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).	(REL. 35, LAST ANNOTATION UPDAT	(REL. 05, LAST	1986 (REL.	PTHY_HUMAN STANDARD; PRT; 115 AA.	JLT 1

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RA ARNOLD A., HORST S.A., GARDELLA T.J., BABA H., LEVINE M.A.,
RA KRONENBERG H.M.;

RI J. CLIN. INVEST. 86:1084-1087(1990).

CC -:- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN

CC BONE AND PREVENTING THEIR RENAL EXCRETION.

CC -I- DISEASE: DEFECTS IN PTH ARE A CAUSE OF FAMILIAL ISOLATED

HYPOPARATEVROLDISM (FIH).

REMEL; J00301; G190704; -.

PREMEL; J00301; G190704; -.

REMEL; J00301; G190704; -.

REMEL; A00597; G37144; -.

EMBL; A01536; PTHU.

PIR; A01536; PTHU.

PIR; A01539; A19339.

PDB; 11TH; 15-OCT-97.

PDB; 11TH; 15-OCT-97.

PDB; 12WB; 12-MAR-97.

PDB; 12WB; 12-MAR-97.

PDB; 12WB; 12-MAR-97.

PDB; 12WB; 11-MAR-97.

PDB; 12WB; 16-JUN-97.

PDB; 12WB; 16-JUN-97.

PDB; 12WB; 16-JUN-97.
 Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 7; Conservative
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MEDLINE; 95318084.
MARX U.C., AUSTERMANN S., B
STICHT H., WALTER S., SCHMI
ROESCH P.;
                                                CONFLICT
SEQUENCE
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MEDLINE; 93345518.
BARDEN J.A., CUTHBERTSON |
EUR. J. BIOCHEM. 215:315-
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KLAUS W., DIECKMANN T., WRAY V.,
BIOCHEMISTRY 30:6936-6942(1991).
                                                                                 VARIANT
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MEDLINE; 91009811.
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MEDLINE; 7327467.

ANDREATTA R.H., HARTMANN A., JOEHL
RINIKER B., RITTEL W., SIEBER P.;
RINIKER B., ROTA 56:470-473(1973).
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MEDLINE: 75059220.

TREGEAR G.W., VAN RIETSCHOTEN J., GREEN E., NIALL H
KEUTMANN H.T., PARSONS J.A., O'RIORDAN J.L.H., POTT
HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 355:415-421(1974).
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MEDLINE; 75146516.

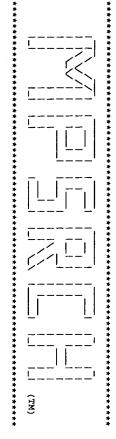
KEUTMANN H.T., NIALL H.D., O'RIORDAN J.L.H., POTTS J.T.
BIOCHEMISTRY 14:1842-1847(1975).
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HEM. 215:315-321(1993).
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DISEASE MUTATION;
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31
115
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                                           PARATHYROID HORMONE.
C -> R (IN FIH; LEADS
PROCESSING OF THE PRI
N -> D (IN REF. 5).
W; 243E87C7 CRC32;
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EMBL; J00023; G163641; --
EMBL; J00024; G163643; --
EMBL; J00024; E18249; ALT_SEQ.
EMBL; J00024; E18250; ALT_INIT.
EMBL; K01938; G163647; --
EMBL; M25082; G163645; --
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POTTS J.T. JR., TREGEAR G.W., KEUTMANN H.T., NIALL H.D. DEFTOS L.J., DAWSON B.F., HOGAN M.L., AURBACH G.D.; PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).

-i- function: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING
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21-JUL-1986
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                  PIR; A24;
PROSITE;
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MEDLINE; 71076162.
NIALL H.D., KEUTMANN H.T.,
AURBACH G.D., POTTS J.T. J.
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MEDLINE; 74142666.
HAMILTON J.W., NIALL H.D.,
COHN D.V.;
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MEDLINE; 84262483.
WEAVER C.A., GORDON D.
GENE 28:319-329(1984).
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WEAVER C.A., GORDON D.:
MOL. CELL. ENDOCRINOL.
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MEDLINE; 71063634.
BREWER H.B. JR., RONAN
PROC. NATL. ACAD. SCI.
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JR., RICH A.;
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METAZOA; CHORDATA;
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HORMONE PRECURSOR (PARATHYRIN) (PTH)
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                    PARATHYROID;
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OL. 28:411-424(1982).
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3.A. 78:4073-4077(1981).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NATHANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEMPER
                                                                                                                                                                                                                                                                                            H.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J.,
                                                                                                                                                                                                                                     THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTTS
                                                                                                                                                                                                                                                                                            SAUER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SHARP
                                                                                                                                                                                                                                     SALTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J.T.
                                                                                                                                                                                                                                   H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JR.,
```



Psrch\_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. on: Thu Jul 30 10:18:13 1998; MasPar time 3.99 Seconds 73.877 Million cell updates/sec

Description: Perfect Score: >US-08-817-547A-10 (1-7) from US08817547A.pep

Title:

Sequence: 1 GKHLNSM 7

Scoring table: PAM 150 Gap 15

Searched: 140542 segs, 42109429 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb15
1:sp\_fung1 2:sp\_human 3:sp\_invertebrate 4:sp\_mammal
5:sp\_mhc 6:sp\_organelle 7:sp\_phage 8:sp\_plant
9:sp\_bacteria 10:sp\_rodent 11:sp\_virus 12:sp\_vertebrate
13:sp\_unclassified

Statistics: Mean 19.774; Variance 18.165; scale 1.089

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

41 80.4 1300 41 80.4 3703 41 80.4 3726 40 78.4 545 39 76.5 243 39 76.5 263 39 76.5 263 39 76.5 318 39 76.5 437 39 76.5 643 39 76.5 643	Result No. 1 2 3 4 4 7	Score 43 42 41 41	V20   64444	1 '	DB 3 9 9 9 10 110 110 110 110 110 110 110 11	ID 017828 005512 029112 029112 038347 038347 0363778 034378	Description  COBF6. 2.  BACILLUS SP. MANNAN  IRON-SULFUR CLUSTER  ORF75.  HYPOTHETICAL 43.7 KI  YRVN PROTEIN.  L1 RETROPOSON, ORF2
41 80.4 367 41 80.4 513 41 80.4 1072 41 80.4 1370 41 80.4 3703 41 80.4 3703 41 76.5 263 39 76.5 263 39 76.5 263 39 76.5 437 39 76.5 437 39 76.5 643	ωa	42 41	82.4 80.4	363 75	7 9	029112 Q38347	
41 80.4 513 41 80.4 1300 41 80.4 3703 41 80.4 3703 41 80.4 3703 40 78.4 545 39 76.5 143 39 76.5 243 39 76.5 263 39 76.5 263 39 76.5 318 39 76.5 318 39 76.5 643 39 76.5 3429	თ თ	41 41	80.4 80.4	367 421	9	Q63778 034528	
41 80.4 3706 41 80.4 3726 41 80.4 3726 40 78.4 545 39 76.5 39 39 76.5 242 39 76.5 263 39 76.5 318 39 76.5 318 39 76.5 437 39 76.5 643 39 76.5 643	8	41 41	80.4 80.4	513 1072	20	Q63289 015101	
41 80.4 3726 40 78.4 3726 40 78.5 39 39 76.5 143 39 76.5 242 39 76.5 263 39 76.5 318 39 76.5 318 39 76.5 318 39 76.5 437 39 76.5 437		41	80.4	1300	010	P97692	
40 78.4 545 39 76.5 143 39 76.5 242 39 76.5 263 39 76.5 263 39 76.5 313 39 76.5 433 39 76.5 643 39 76.5 3429	116	4.1 4.1		3726	10	061329	
39 76.5 143 39 76.5 242 39 76.5 263 39 76.5 318 39 76.5 318 39 76.5 643 39 76.5 643	12	40	78.4		11	Q90054	
39 76.5 242 39 76.5 263 39 76.5 318 39 76.5 437 39 76.5 643 39 76.5 3429	13 14	3 3 9 9	76.5 76.5		7	Q66546 003935	
39 76.5 318 39 76.5 437 39 76.5 643 39 76.5 3429	15	۳ و ه	76.5	242	ρω	018238	
39 76.5 437 39 76.5 643 39 76.5 3429	17	39	76.5	318	6	Q02684	
39 76.5	18 19	ა ა 9 9	76.5 76.5	437 643	ω თ	Q36379 O22010	
	20	39	76.5	3429	w	Q24593	

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21
37	37	37	37	37	37	37	37	37	37	37	37	37	38	3 8	38	38	3 8	38	38	38	38	38	38	38
72.5	72.5	72.5	72.5	72.5	72.5	72.5	72.5	72.5	72.5	72.5	72.5	72.5	74.5	74.5	74.5	74.5	74.5	74.5	74.5		74.5	٠	74.5	74.5
1371	940												1372											
N	1	11	11	11	2	۲	ω	ø	ø	ဖ	5	9	ω	w	ω	9	ω	9	ω	œ	9	w	9	9
015067	Q07048	037319	007041	010621	013035	Q08558	023434	007821	006737	028516	Q63473	Q53074	P91526	Q10908	Q25826	P95539	P92006	032006	Q09656	Q41770	Q45125	Q21593	Q03086	Q58155
KIAA0361 (FRAGMENT).	RNA POLYMERASE (FRAGME	NUCLEOSIDE TRIPHOSPHAT	G3R PROTEIN.	CHITINASE.	PROSAPOSIN.	CHROMOSOME XV READING	HYPOTHETICAL PROTEIN.	SULFIDE-DEHYDROGENASE	PUTATIVE - POSSIBLE PH	HYPOTHETICAL 22.0 KD P	PARATHYROID HORMONE (F	UVRB (FRAGMENT).	SIMILARITY TO MULTIPLE	HYPOTHETICAL 140.5 KD		CATALASE (EC 1.11.1.6)	M04G12.3.	YOKA PROTEIN.	HYPOTHETICAL 52.6 KD P	ALPHA-AMYLASE.	MOBILIZATION PROTEIN.	HYPOTHETICAL 36.4 KD P	REPLICATION PROTEIN A	HYPOTHETICAL 21.1 KD P
6.49e+01	6.49e+01	6.49e+01	6.49e+01	6.49e+01	6.49e+01	6.49e+01	6.49e+01	6.49e+01	6.49e+01		6.49e+01	6.49e+01		3.69e+01	3.69e+01	3.69e+01	3.69e+01	3.69e+01	3.69e+01	3.69e+01	3.69e+01	3.69e+01	3.69e+01	3.69e+01

D D D	RESULT ID O	ОУ	Ma Be Qu	SQ	DR	R R	RA A	R.A	RA	R R	RA	₽.	R X	RP	RN	P.	7 5	RN	8	OS E	Ü	ğ	DT	ĕΒ	RESULT
01-JUL-1997 01-JUL-1997	O05512	637 SKHLDSM :   :   1 GKHLNSM	Query Match Best Local Simi Matches 5;	SEQUENCE 7		WATSON A., W	THIERRY-MIEG	PARSONS J.,	LIGHTNING J.	JONES M., KERSHAW J.,	CRAXTON M.,	BONFIELD J.	MEDLINE; 94150718. WILSON R., AINSCOUGH			SUBMITTED (M	n E		EUKARYOTA; M	CAENORHABDITIS ELEGANS	01-NOV-1996	01-NOV-1996	01-NOV-1996	Q17828 Q17828;	ILT 1
(TREMBLREL. 04,	PRELIMINARY;	643	1 84.3%; Similarity 71.4%; 5; Conservative	719 AA; 81009 M	Z73103; E242596;	A., WEINSTOCK L., WI 368:32-38(1994).	THIERRY-MIEG J., THOMAS K.,	J., PERCY C., RIFKE	LLOYD C., MCM	즈본	DEAR S., DU Z.,		94150718. AINSCOUGH R., AN	FROM N.A.		(MAY-1996) TO EMB	FROM N.A.		EUKARYOTA; METAZOA; ACOELOMATES;	IS ELEGANS.	(TREMBLREL. 01,		(TREMBLREL. 01,	PRELIMINARY;	
CREATED) LAST SEQUENCE	PRT;		Score 43; Pred. No. 2; Mism	MW; E206BB38		WILKINSON-SPROAT J.,	VAUDIN M.	N L., ROOF	URRAY A.	HAWKINS T., HILLIER KIRSTEN J., LAISTER	DURBIN R.	NELL M.	R. ANDERSON K. BAYNES			EMBL/GENBANK/DDBJ					LAST ANNO		CREATED)	PRT;	
ENCE UPDATE)	362 AA.		.43; DB 3; Length 719; No. 1.84e+00; Mismatches 0; Indels 0; Gaps 0;	38 CRC32;		ROAT J., WOHLDMAN P.;	G J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,	RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,	LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,	HILLIER L., JIER M., JOHNSTON L., LAISTER N., LATREILLE P.,	Z., DURBIN R., FAVELLO A., FULTON L.,	COOPER	BAYNES C., BERKS M.,			DDBJ DATA BANKS.			NEMATODA; SECERNENTEA; RHABDITIDA.		ANNOTATION UPDATE)			719 AA.	

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Search completed: Thu Jul 30 10:18:58 1998 Job time: 45 secs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RAMEDIA N., MOSZER I., ALBERTINI A.M., ALLONI G.,
RA BORRISS R., BERSTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,
RA BORRISS R., BRUSCIEL C.V., CALDWELL B., CAPUANO V., CARTER N.M.,
RA BOUILLET S., BRUSCIEL C.V., CALDWELL B., CAPUANO V., CARTER N.M.,
RA CHOI S.K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J. DANLEL R.A.,
RA DENIZOT F., DEVINE K.M., DUSTERHOFT A., EHRLICH S.D., EMMERSON P.T.,
RA CHIZ C., FUJITA M., FUJITA Y., FUMA S., GALLEZI A., GALLERO N.,
RA CHIZ C., FUJITA M., FUJITA Y., FUMA S., GALLEZI A., GALLERO N.,
RA CHIZ C., FUJITA M., FUJITA Y., FUMA S., GALLEZI A., GALLERO N.,
RA CHIZ S.Y., GLASER P., GOFERU N., GOLOGHIY F.J., GRANDI G.,
RA GHIM S.Y., GLASER P., GOFERU N., GOLOGHIY F.J., GRANDI G.,
RA GHIM S.Y., CLASER P., GOFERU N., GOLOGHIY F.J., GRANDI G.,
RA GHIM S.Y., CLASER P., GONINGSTEIN G., KROCH S., KUMANO M.,
RA JORIS B., KARMATA D., KASAHARA Y., KLAER-BLANCHARD M., KLEIN C.,
RA KURITA K., LAPIDUS A., LARDINOIS S., LAUBER J., LAZAREVIC V.,
RA KURITA K., LAPIDUS A., LARDINOIS S., LAUBER J., LAZAREVIC V.,
RA NOONE D., O'REILLY M., OGAMA K., OGIMARA A., OUDEGA B., PARK S.H.,
RA PARGO V., POHL T.M., PORTEELLE D., PORWOLLIK S., PRESCOTT A.M.,
RA RIEGER M., RIVOLTA C., ROCHA E., ROCHA E., ROSEM M., SENGOLLE S.,
RA SATO T., SCANLAN E., SCHLEILE B., RAPOPORT G., REY M., REYNOLDS S.,
RA SATO T., SEKOMSKA A., SEROR S.J., SERROR P., SELIN B.S., SOLDO B.,
RA AKEUCHI M., TAMAKOSHI A., TANAKA T., TERPSTRA P., TOGNONI A.,
RA TAKEUCHI M., TAMAKOSHI A., TANAKA T., TERPSTRA P., TOGNONI A.,
RA WINTERS P., WIDLER E., WEDLER E., WEDLER F., WASSAROTTI A.,
NAPURE 390:249-256(1997).

1016
11 M., TANAKOSHI A., TANAKO T., TERPSTRA P., TOGNONI A.,
NAPURE 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches
                                                                                                                                                                                                                          SEQUENCE FROM N.A.

STRAIN=168;

KUNGT F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;

KUNGT F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;

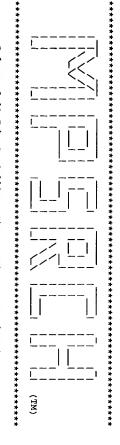
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

EMBL; D88802; D1020491; -.

EMBL; 299107; E1182567; -.

SEQUENCE 362 AA; 40834 MW; 616962F9 CRC32;
                                                                                                                           162 GKRLNAM 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBMITTED (APR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SADAIE Y., YATA K., FUJITA M., SAGAI H., ITAYA M., KASAHARA Y.,
OGASAWARA N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-168;
SADAIE Y., YATA K., FUJITA M., SAGAI H., ITAYA M., KASAHARA Y.,
OGASAWARA N.;
                                                                                   1 GKHLNSM
                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBMITTED (APR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE) BACILLUS SP. MANNAN ENDO-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROKARYOTA; FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BACILLUS SUBTILIS
                                                                                                                                                                       5;
                                                                                      7
                                                                                                                                                                  Conservative
                                                                                                                                                                                       82.48;
                                                                                                                                                         Score 42; DB 9; Length 362;
Pred. No. 3.42e+00;
2; Mismatches 0; Indels
                                                                                                                                                         0;
                                                                                                                                                         Gaps
                                                                                                                                                    0;
```

Ş В SORRERE



Psrch\_pp 8:: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:22:22 1998;

Tabular output not generated MasPar time 2.66 Seconds 34.605 Million cell upda cell updates/sec

Title: Description: Perfect Scor Score: (1-6) from US08817547A.pep 44 1 KHLNSM 6 >US-08-817-547A-11

Sequence:

Scoring table: PAM 150 Gap 15

124785 seqs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 13.509; Variance 37.219; scale 0.363

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

15 44 100.0 16 44 100.0 17 44 100.0	44	44		44	44	44	44	44	44	_	100		100		100	2 44 100.0		Result Query No. Score Match
.0 36	36		36				34	34	34	34	34	34	34	34	34 :	34	34 :	Length 1
9	9	9	9	9	9	22	22	22	9	19	œ	22	22	22	22	22	22	DB
R58230	R58268	R58267	R58243	R58026	R58262	W17947	W17944	W17943	R58016	R98951	R41557	W17951	W17969	W17954	W17955	W17939	W17968	ID
[D-Val31]-hPTH(1-36)-	[Cha8]-hPTH(1-36)-NH2	1.	Propargyl-[A1]-hPTH(1	N-alpha-methyl[Ala1]	[Ala1]-hPTH(1-36)-NH2			14	-Isopropy	Target peptide (PTH(1	_	Human parathyroid hor	Human parathyroid hor	_	Human parathyroid hor	Human parathyroid hor	Human parathyroid hor	Description
4.47e+01	4.47e+01	4.47e+01	4.47e+01	4.47e+01	4.47e+01	4.47e+01	4.47e+01	4.47e+01	4.47e+01	4.47e+01	4.47e+01	4.47e+01	4.47e+01	4.47e+01	4.47e+01	4.47e+01	4.47e+01	Pred. No.

Query Match

100.0%;

Score 44; В 22;

Length

34

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
44	44	44	44	44	44	44	44	44	44	44	44	44	44	44	44	44	44	44	44	44	44	44	44	44	44
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
84	84	84	84	84	84	84	84				84														
4	4	4	4	4	4	4	4	4	25	4	4	4	4	4	4	27	σ	σ	25						
R21153	R23231	R23227	R21218	R21254	R23236	R21160	R21161	R21253	W29420	0	R23523	R23235	R23526	R23232	R21210	W25687	R30854	R30859	W21946	P30015	R98958	R58132	R58128	R58147	R58141
Human para	Human para	Human para	Human para	Human para	Human para	Human pare	-		-		Human para	Human para		Human para	Human para	Human para	hPTH mutein	HI	Fusion pro		Target pe	[Pro19]-hI	[Met19]-hI	٠.	[Leu21]-h
		parathyroid :		parathyroid :			parathyroid			parathyroid				parathyroid		yroid	≊	$\overline{}$	g	oid	e F	-38)	1-38)	8	hPTH(1-38)
hor	hor	hor	hor	hor	hor	hor	hor	hor	hor	hor	hor	hor	hor	hor	hor	hor	Q ω	mute	pri	hor	TH(1	H0-	HO-	HO-	<u>-</u>
	4.47e+01								4.47e+01							4.47e+01	٠	4.47e+01	٠	4.47e+01	4.47e+01	4.47e+01			4.47e+01

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HERSULATION OF STREET OF S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JAN-1997, U11292.
03-JUL-1996; U11292.
13-JUL-1995; US-003105.
06-SEP-1995; US-003305.
29-MAR-1996; US-626186.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JUL-1997 (first entry)
Human parathyroid hormone analogue [Nle31]hPTH(1-34)NH2.
Osteoporosis; agonist; PTH; human; anti-resorptive therapy;
bone fracture.
                                                                                                                                                                    The present sequence is a specific example of a human parathyroid hormone (hpTH) analogue from fragment 1-34 in which at least the amino acid residue at position 1 is alpha, beta-diaminopropionic acid, the amino acid residue at position 27 is homoarginine, or the amino aci residue at position 27 is homoarginine, or the amino aci residue at position 31 is norleucine. In this example the Val residue at position 31 in the wild-type has been substituted by Mie. The hpTH analogues stimulate bone growth and so are useful in human or veterinary medicine for treatment of osteoporosis and bone fracture, optionally in conjunction with anti-resorptive therapy (bisphosphonates
                             and calcitonin).

N.B. The present sequence does not appear in the corresponds to the known hPTH 1-34 fragment with as stated in the claim.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20; Page -; 33pp; English. The present sequence is a specif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 97-118819/11.
New variants of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9702834-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W17968 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bone fracture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           stimulate bone growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     {\tt Synthetic.}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sapiens.
in the claim.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note=
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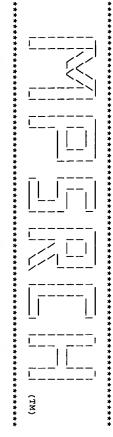
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RESULT
ID WI
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Claim 5, Page -; 33pp; English.

Claim 5, Page -; 33pp; English.

The present sequence is a specific example of a human parathyroid of the present sequence is a specific example of a human parathyroid of the present sequence is a specific example of an inchination of the foundations of 11, 23, 24, 27, 28 and 31 of the foundation of the positions of the position of the foundation of the foun
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Best Local Similarity 100.0%;
Matches 6; Conservative
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03-JUL-1996; U11292.
13-JUL-1995; US-001105.
06-SEP-1995; US-003305.
29-MAR-1996; US-626186.
(BIOM-) BIOMEASURE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4y-JUL-1997 (first entry)
Human parathyroid hormone analogue [Cha7,11]hPTH(1-34)NH2.
Osteoporosis; agonist; PTH; human; anti-resorptive therapy;
bone fracture.
Homo sapiens.
Synthation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dong 2X; wpT; 97-118819/11.

New variants of human parathyroid hormone 1-34 peptide - which stimulate bone growth and are used for treatment of osteoporosis
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W17939 standard; peptide; 34
W17939;
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1 KHLNSM 6
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11
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/note= "Cha"
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Pred. No. 4.47e+01;
0; Mismatches 0;
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Sabular output not generated. 900: Thu Jul 30 10:21:36 1998; MasPar time 3.04 Seconds 72.203 Million cell updates/sec

Title:
Description:
Perfect Score:
Sequence: >US-08-817-547A-11 (1-6) from US08817547A.pep 44 1 KHLNSM 6

Scoring table: PAM 150 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 18.883; Variance 20.866; scale 0.905

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1ZWE 1ZWE 1ZWE 1ZWD 1ZWD 1HPH 1HPH PTHU A44059 S33642 1ZWC PTB0 D69981 S61193 E699907 E699839 C69839	Ħ
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S31164	H64045	JC1404	S04071	S64056	S51823	G69615	S12053	NPVZAM	NPVZCP	C36858	S37391	140989	140991	140990	A64147	A65165	S73429	OWBSAC	2AT2C	2AT2B	2AT2A
4	msbA protein - Haemop	CDEI-box DNA-binding	hemoglobin alpha chai	probable membrane pro	myosin heavy chain AT	ATP-dependent DNA hel	protein-tyrosine-phos	nucleoside-triphospha	nucleoside-triphospha	G3R protein – variola	ampG protein - Escher	signal transducer amp	signal transducer amp	signal transducer amp	hypothetical protein	protein dfp - Escheri	glycerol-3-phospate d	aspartate carbamoyltr	Aspartate transcarbam	Aspartate transcarbam	Aspartate transcarbam
1.32e+02	1.32e+02	1.32e+02	1.32e+02	1.32e+02	8.09e+01		8.09e+01	8.09e+01	8.09e+01	8.09e+01	8.09e+01	8.09e+01	8.09e+01								

ALTERNATE_NAMES HPTH(4-37)  PDB_TITLE structure of structure of structures  ORGANISM #formal_name REFERENCE A67800 #authors Rossch, P; #submission submitted to #oross-references PDB:12WE REFERENCE TN001721 #authors Marx, U.C. #authors in Strukture pp.0, Bayr	KHLNSM 2	Db 13 KHLNSM	Query Match Best Local Similarity Matches 6; Conse	6-9 19-30 SUMMARY	S	REFERENCE #authors #book	#authors Roesch, P.; #submission submitted to #cross-references PDB:12WA	ORGANISM	RESULT 1 ENTRY TITLE ALTERNATE_NAMES PDB_TITLE
structure of human parathyroid hormone fragment 4-37, NMR 10 structures structures #formal_name Homo sapiens #common_name man A67860 Roesch, P.; Marx, U.C. submitted to the Brookhaven Protein Data Bank, June 1996 ces PDB:1ZWE TN001721 Marx, U.C. in Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth: University of Bayreuth (Thesis), 1996	6  12WE #type complete parathyroid hormone (residues 4-37) - human	18	100.0%; Score 44; DB 5; Length 34; larity 100.0%; Pred. No. 2.07e+00; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	<pre>#region helix (right hand alpha)\ #region helix (right hand alpha) #length 34 #molecular-weight 4118 #checksum 5629</pre>	pp.0, Bayreuth : University of Bayreuth (Thesis), 1996 Resolution: not applicable Determination: NMR hormone	n Verschiedener Parathormonfragmente in	AV/070 Roesch, P.; Marx, U.C. submitted to the Brookhaven Protein Data Bank, June 1996 Ices PDB:12WA	ctures l_name	12WA #type complete garathyroid hormone (residues 1-34) - human HPTH(1-34) structure of human parathyroid hormone fragment 1-34, NMR 10

COMMENT COMMENT COMMENT Determination: NMR

REYNORDS hormone

FEATURE 15-25 #region helix (right hand alpha)

SUMMARY #length 34 #molecular-weight 4128 #checksum 5508

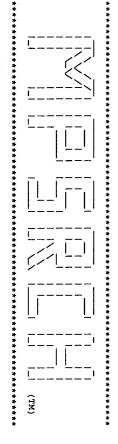
Ouery Match
Best Local Similarity 100.0%; Score 44; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.07e+00;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 10 KHLNSN 15

Dy 1 KHLNSN 6

Search completed: Thu Jul 30 10:22:04 1998

Job time : 28 secs.



Psrch\_pp 9 :: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:20:37 1998; MasPar time 2.04 Seconds 73.747 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-817-547A-11 (1-6) from US08817547A.pep 44 1 KHLNSM 6

Scoring table: PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing:

Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 19.767; Variance 17.440; scale 1.133

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

23	22	21	20	19	18	17	16	15	14	13	12	11	10	ø	œ	7	o	u	4	ω	N	_	Sult No.
36	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	39	40	40	40	41	44	44	Score
81.8	84.1	84.1	84.1	84.1	84.1	84.1	84.1	84.1	84.1	84.1	84.1	84.1	84.1	84.1	84.1	88.6	90.9	90.9	90.9	93.2	100.0	100.0	Query Match
101	931	700	692	648	648	491	478	438	430	384	304	252	252	247	208	662	373	115	115	3005	2105	115	Length
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YGF2_YEAST	DING_BACSU	PTPE_HUMAN	YYI3_CAEEL	NTP1_CBEPV	NTP1_AMEPV	AMPG_ECOLI	YDD2_SCHPO	Y281_HAEIN	DFP_ECOLI	Y039_MYCPN	PYRB_BACSU	PMGM_HUMAN	PMGM_RAT	PMGY_MYCLE	YFJJ_ECOLI	PMT7_YEAST	LEF3_NPVOP	PTHY_CANFA	PTHY_BOVIN	ZFH2_DROME	POLR_ASGVP	PTHY_HUMAN	Ħ
HYPOTHETICAL 12.1 KD P	PROBABLE ATP-DEPENDENT	PROTEIN-TYROSINE PHOSP	PROBABLE G PROTEIN-COU	NUCLEOSIDE TRIPHOSPHAT	NUCLEOSIDE TRIPHOSPHAT	AMPG PROTEIN.	HYPOTHETICAL 55.4 KD P	HYPOTHETICAL METABOLIT	DNA/PANTOTHENATE METAB	HYPOTHETICAL PROTEIN M	ASPARTATE CARBAMOYLTRA	PHOSPHOGLYCERATE MUTAS	PHOSPHOGLYCERATE MUTAS	PHOSPHOGLYCERATE MUTAS	HYPOTHETICAL 24.6 KD P	DOLICHYL-PHOSPHATE-MAN	LATE EXPRESSION FACTOR	PARATHYROID HORMONE PR	PARATHYROID HORMONE PR	ZINC-FINGER PROTEIN 2	GENOME POLYPROTEIN (CN	PARATHYROID HORMONE PR	Description
4.45e+01	2.51e+01	2.51e+01	2.51e+01	2.51e+01		2.51e+01	2.51e+01	2.51e+01	2.51e+01	2.51e+01	2.51e+01	2.51e+01	2.51e+01		2.51e+01	7.68e+00	4.17e+00	4.17e+00	4.17e+00	2.23e+00	3.21e-01	3.21e-01	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24
35	35	35	35	35	35	35	35	35	35	36	36	36	36	36	36	36	36	36	36	36	36
79.5	79.5	79.5	79.5	79.5	79.5	79.5	79.5	79.5	79.5	81.8	81.8	81.8	81.8	81.8	81.8	81.8	81.8	81.8	81.8		81.8
4568	3411	782	696	398	396	362	355	138	113	2133	1128	922	859	765	763	722	695	587	500	249	142
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DYHC_CAEEL	POLG_YEFV2	BICD_DROME	YHFK_ECOLI	CHSY_ORYSA	CHSY_PINSY	SERC_BACCI	DVR1_BRARE	YYAN_BACSU	YKR3_CAEEL	FA8_PIG	BEM3_YEAST	CLPA_PEA	YQD3_CAEEL	APP2_RAT	APP2_HUMAN	YG42_YEAST	APP2_MOUSE	MSBA_HAEIN	ANP1_YEAST	PMGY_MYCTU	HBA3_PLEWA
DYNEIN HEAVY CHAIN, CY	GENOME POLYPROTEIN (CO		HYPOTHETICAL 79.5 KD P	CHALCONE SYNTHASE (EC	CHALCONE SYNTHASE (EC	PHOSPHOSERINE AMINOTRA	DVR-1 PROTEIN PRECURSO	HYPOTHETICAL TRANSCRIP	HYPOTHETICAL 11.3 KD P	COAGULATION FACTOR VII	BEM3 PROTEIN.	ATP-DEPENDENT CLP PROT	HYPOTHETICAL 96.7 KD P	AMYLOID-LIKE PROTEIN 2	AMYLOID-LIKE PROTEIN 2	HYPOTHETICAL 78.8 KD P	AMYLOID-LIKE PROTEIN 2	PROBABLE TRANSPORT ATP	AMINONITROPHENYL PROPA	PHOSPHOGLYCERATE MUTAS	HEMOGLOBIN ALPHA CHAIN
7.77e+01	7.77e+01	7.77e+01	7.77e+01	7.77e+01	7.77e+01	7.77e+01	7.77e+01	7.77e+01		4.45e+01	4.45e+01	4.45e+01	4.45e+01	4.45e+01	4.45e+01	4.45e+01	4.45e+01	4.45e+01	4.45e+01	4.45e+01	4.45e+01

RR RA RE	RA R	RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	R R R R R R C C C	RESU ID AC DT DT DT DT
	SEQUENCE OF 32- MEDLINE; 741116 NIALL H.D., SAU O'RIORDAN J.L.; PROC. NATL. ACI [5] SEQUENCE OF 61- MEDLINE; 790826 KEUTMANN H.T., POTTS J.T. JR.; BIOCHEMISTRY 17 [6]		HOMO SAPLENS (HUMAN).  EUKARKOTA; METAKOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  EUTHERIA; PRIMATES.  [1]  SEQUENCE FROM N.A.  MEDLINE; 82150870.  HENDY G.N., KROMENBERG H.M., POTTS J.T. JR., RICH A.;  PROC. NATL. ACAD. SCI. U.S.A. 78:7365-7369(1981).  [2]	SULT 1 PTHY_HUMAN P01270; 21-JUL-1986 ( 21-AUG-1987 ( 01-NOV-1997 ( 01-NOV-1997 PARATHYROID H PTH.

REVISIONS, MEDILNE; 75146516. KEUTMANN H.T., NIALL H.D., O'RIO BIOCHEMISTRY 14:1842-1847(1975).

O'RIORDAN J.L.H., POTTS J.T.

JR.;

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SO STITE
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Best Local Similarity 100.0%;
Matches 6; Conservative
                                                                              CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARNOLD A., HORST S.A., GARDELLA T.J., BABA H., LEVINE M.A.,
KRONENBERG H.M.;
J. CLIN. INVEST. 86:1084-1087(1990).
I. CHURTION: PHE ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS
BONE AND PREVENTING THEIR RENAL EXCRETION.
II DISEASE: DEFECTS IN PTH ARE A CAUSE OF FAMILIAL ISOLATED
HYPOPARATHYROLISM (FIH).
                                                                                                                                                        PROPEP
                                                                                                                                                                                                                                                                                                               EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRUCTURE BY NMR OF 32-68.
MEDLINE; 95318084.
MARX U.C., AUSTERMANN S.,
STICHT H., WALTER S., SCHM
ROESCH P.;
                                                                                                                                        VARIANT
                                                                                                                                                                                                  SIGNAL
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EUR. J. BIOCHEM. 215:315-321(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRUCTURE BY NMR OF 32-65
MEDLINE; 93345518.
BARDEN J.A., CUTHBERTSON 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRUCTURE BY NMR OF 32-65.
MEDLINE: 91299748.
KLAUS W., DIECKMANN T., WRAY V.,
PIOCHEMISTRY 30:6936-6942(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANDREATTA R.H., HARTMANN A., JOEHL A., RINIKER B., RITTEL W., SIEBER P.; HELV. CHIM. ACTA 56:470-473(1973).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 91009811.
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TREGEAR G.W., VAN RIETSCHOTEN J., GREEN E., NIALL H.D. KEUTMANN H.T., PARSONS J.A., O'RIORDAN J.L.H., POTTS J. HOPPE-SEYLER'S 2. PHYSIOL. CHEM. 355:415-421(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYNTHESIS OF 32-65. MEDLINE; 73227467.
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A19339; A19339.

A19339; A19339.

A194339; A19339.

A194339; A19339.

A194339; A19339.

A194339; A194339.

A194344; A19434.

A19434; A19434.

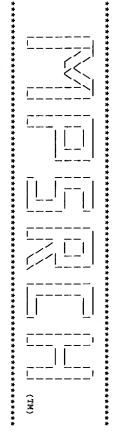
A1944.

A1944
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12-MAR-97.
12-MAR-97.
12-MAR-97.
16-JUN-97.
16-JUN-97.
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15-OCT-97.
12-MAR-97.
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115
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DISEASE MUTATION;
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                                                                            MW;
Score 44; DB 1; I
Pred. No. 3.21e-01;
0; Mismatches 0
                                                                    PARATHYROID HORMONE.
C -> R (IN EH; LEADS TO INEF PROCESSING OF THE PRECURSOR).
N -> D (IN REF. 5).
; 243E87C7 CRC32;
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JAENICKE
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FORSSMANN W.-G.,
Indels
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Best Local Similarity 100.0%;
Matches 6; Conservative
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                                                                                          1794 KHLNSM 1799
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YOSHIKAWA N., SASAKI E., KATO M
VIROLOGY 191:98-105(1992).
-I- PTM: THE N-TERMINAL OF THE (
-I- THE COAT PROTEIN IS LOCATED
THIS POLYPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; D14995; G285608; -. PIR; A44059; A44059. RNA-DIRECTED RNA POLYMERASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 93033164.
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1364
2105
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Pred. No. 3.21e-01
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                ATP (POTENTIAL).
POLYMERASE ACTIVE
W; B3EE0C2C CRC32
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O IN THE CARBOXY-TERMINAL REGION
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                                                                                                                                                                                                                                                                                                                                                                                CRC32;
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Of
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Search completed: Thu Job time: 7 secs. Jul 30 10:20:44 1998



MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

n on: Thu Jul 30 10:21:01 1998; MasPar time 3.61 Seconds 69.980 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-817-547A-11 (1-6) from US08817547A.pep 44 1 KHLNSM 6

Scoring table: PAM 150 Gap 15

Searched: 140542 seqs, 42109429 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb15
1:sp\_fungi 2:sp\_human 3:sp\_invertebrate 4:sp\_mammal
5:sp\_mhc 6:sp\_organelle 7:sp\_phage 8:sp\_plant
9:sp\_bacteria 10:sp\_rodent 11:sp\_virus 12:sp\_vertebrate
13:sp\_unclassified

Statistics: Mean 18.888; Variance 17.056; scale 1.107

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

20	19	18	17	16	15	14	13	12	11	10	9	<b>&amp;</b>	7	0	5	4	ω	N	ᆫ	Result
37	37	37	37	37	37	37	37	37	37	38	38	38	38	38	40	41	41	41	42	Score
84.1	84.1	84.1	84.1	84.1	84.1	84.1	84.1	84.1	84.1	86.4	86.4	86.4	86.4	86.4	90.9	93.2	93.2	93.2	95.5	Query Match
554	518	491	439	271	258	196	193	193	133	711	686	545	367	315	421	3726	3703	1072	719	Length
ω	12	œ	œ	<u>س</u>	6	9	9	9	4	9	ω	9	9	ω	9	10	N	N	ω	BB
023651	013035	Q96275	Q41770	Q08558	Q35690	006737	Q53772	028516	Q29256	P95539	P92006	032006	Q45125	Q21593	034528	Q61329	Q15911	015101	Q17828	Ħ
ZK863.3.	PROSAPOSIN.	MCM2-RELATED PROTEIN (	ALPHA-AMYLASE.	CHROMOSOME XV READING	COX1 INTRON 1 ORF.	PUTATIVE - POSSIBLE PH	TRANSPOSON TN5405 AND	HYPOTHETICAL 22.0 KD P	UNKNOWN PROTEIN (FRAGM	CATALASE (EC 1.11.1.6)	M04G12.3.	YOKA PROTEIN.	MOBILIZATION PROTEIN.	HYPOTHETICAL 36.4 KD P	YRVN PROTEIN.	AT MOTIF BINDING FACTO	ZINC FINGER HOMEODOMAI	ZINC FINGER HOMEODOMAI	C08F8.2.	Description
2.91e+01	2.91e+01	2.91e+01	2.91e+01	2.91e+01	2.91e+01	2.91e+01	2.91e+01	2.91e+01	2.91e+01	1.60e+01	1.60e+01	1.60e+01	1.60e+01	1.60e+01	4.68e+00	2.48e+00	2.48e+00	2.48e+00	1.30e+00	Pred. No.

44	43	42	41	40	39	38	37	36	35 5	34	33	32	31	30	29	28	27	26	25	24	23	22	21
ა ა თ თ	35	ა 5	36	36	36	36	36	36	36	36	36	3 6	36	36	36	36	36	37	37	37	37	37	37
79.5 79.5		•	•	•	•	•	•	•		•	•		•		•							84.1	
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Q89278 Q89275	09113		018806	Q6148			Q64348			Q14662									S.		037319	Q89097	007041
POLYPROTEIN. POLYPROTEIN PRECURSOR.	COBRA VENOM FACTOR PRE	HER-6 PROTEIN.	FACTOR VIII.	CDE1-BINDING PROTEIN.	AMYLOID BETA (A4) PREC	C06B3.8.	AMYLOID BETA (A4) PREC	DNA-BINDING PROTEIN (F	ACETOLACTATE SYNTHASE.	BINDING PROTEIN (FRAGM	GTP-BINDING PROTEIN, F	BINDING PROTEIN (FRAGM	$^{\circ}$	ENDONUCLEASE III (NTH)	RYE MRNA FRAGMENT FOR	COLICIN U IMMUNITY PRO	HOST SHUT OFF VIRION P	X GENE.	ZK930.1.	MYOSIN (FRAGMENT).	NUCLEOSIDE TRIPHOSPHAT	GARCIA-1966 RIGHT NEAR	G3R PROTEIN.
9.25e+01 9.25e+01		9.25e+01			5.23e+01		5.23e+01			٠,	N				5.23e+01		٠	٠		٠		2.91e+01	

RESULT ID O AC O DT 0	Оy	Д Ве Ма	SO	75 E	RA A	R R	RA :	₽ ₹	R.R.	RA S	R R	ŖР	RR	R	RP	RN	გ	လ လ	ď	ğ	ΔŢ	AC	ij	RESULT
O15101 PRELIMINARY; PRT; 1072 AA. O15101; O1-JAN-1998 (TREMBLREL. 05, CREATED) O1-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)	638 KHLDSM 643    :   1 KHLNSM 6	Query Match 95.5%; Score 42: DB 3; Length 719; Best Local Similarity 83.3%; Pred. No. 1.30e+00; Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	NCE 719 AA; 810	368:32-38(1994). 773103: F242596: -	MIEC	PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R., SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,	MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,	JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LAIREILLE P.,	DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,	CONNELL M., COPSEY T., CC	BAYNES C BERKS	UENCE	SUBMITTED (MAI-1990) TO EMBL/GENDANN/DDBU DATA BANNS.	'WAY - 1996' TO EVET (CENTAUX /TOPT DAM'S	SEQUENCE FROM N.A.		EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.	CAENORHABDITIS ELEGANS.	01-NOV-1996 (TREMBLREE: 01, LAST ANNOTATION UPDATE)	(TREMBLREL. 01, LAST	(TREMBLREL.		017828 PRELIMINARY; PRT; 719 AA.	JLT 1

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DI JAN-1986 (TREMBLEL. O.S. LAST ANNOTATION UPDATE)
EN ZIMC FINGER HOMEODOMAIN PROTEIN (3' PARTIAL) (FRAGMENT).

OR EUKARYOR: METAZOA: CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

RE SEQUENCE FROM N.A.

RA BANNON N.D., LOFTUS B.J., ZHOU L., LABOMBARD M., FUHRMANN J.,

RA BANNON N.C., KIM U.J., KERLAVGER A.R., VENTER J.C.;

RL SUBMITIED (JUN-1997) TO SEBL/GENBANK/DDBJ DATA BANKS.

REMEL; ACOUZO44; G2347080; -

THONEOSON: DNA-SINDING; NUCLEAR PROTEIN.

THONEOSON: DNA-SINDING; NUCLEAR PROTEIN.

TO SEQUENCE 1072 AD; 115896 MW; 78611913 CRC32;

QUETY MATCH

93.28; SCOTE 41; DB 2; Length 1072;

MATCHS 5; CONSERVATIVE 1; Mismatches 0; Indels 0; Gaps 0;

749 KILNINM 754

1 KHLNSM 6

Search completed: Thu Jul 30 10:21:19 1998

JOD time: 18 secs.
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                    (MI)
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(Psrch\_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output on: not generated. Thu Jul 30 10:24:45 1998; MasPar time 2.51 Seconds 30.581 Million cell updates/sec

Sequence: Perfect Score: Description: >US-08-817-547A-12 (1-5) from US08817547A.pep 37 1 HLNSM 5

Title:

Scoring table: PAM 150 Gap 15

Searched: 124785 segs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq31-2

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 12.437; Variance 34.377; scale 0.362

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

1 3 3 3 4 4 4 7 6 6 7 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result
30 30 30 30 30 30 30 30 30 30 30 30 30 3	Score
	Query Match I
33333333333333333333333333333333333333	Length DB
R22066 P40427 R58189 W17968 W17939 W17954 W17954 W17954 W17959 W17959 W17959 W17959 W17951 R34364 W17943 W1794 W17943 W17	Ħ
Modified [D-Trp_12Tyr parathyroid antagonis [F23, H25, H26, L27, 128, Human parathyroid hor Human parathyroid	Description
1.89e+02	Pred. No.

Query Match 100.0%; Best Local Similarity 100.0%; Matches 5; Conservative

Score 37; DB 4; Ler Pred. No. 1.89e+02; 0; Mismatches 0;

Length 28; Indels

0

Gaps

0

45	44	43	42	41	40	39	38	37	36	မ	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20
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R21236	R21212	R21213	R21154	R21156	W29420	R21211	R21210	R21254	R23524	R21242	W25687	W21946	P30015	_	R98958	R58153	R58124	R58157	ω	R58273	R58278	R58257	R58260	R58211	R58279
Human parathyroid hor		Human parathyroid hor			Ò,	ά	Human parathyroid hor	Human parathyroid hor			Human parathyroid hor	ō	ä	]-hPTH(1-38)	~	-hPTH(1-3	]-hPTH(1-	7] -	]-hPTH(1-3	[D-Leu15]-hPTH(1-36)-	-hPTH(1	lglycin	TH(1-36	116]-hPTH(1-36	H(1-36
÷	÷	.89e+0	÷	.89e+0	.89e+0	÷	÷	1.89e+02	.89e+0	<u>.</u>	<u>.</u>	.89e+0	.89e+0	<u>.</u>	<u>.</u>	<u>.</u>	٠	<u>.</u>	œ			. 89	'n	. 89	'n

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when parathyroid hormone analogues - useful for treatment and in vitro diagnosis of PTH-dependent tumours, immune disorders, osteoporosis and hyperparathyroidism.

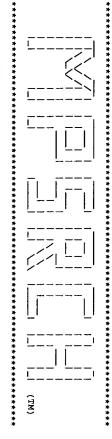
Sclaim 1; Column 10; 6pp; English.

The peptide is modified at Lys13 (of the parent PTH) in the epsilon amino acid gp. by N,N-diisobutyl or 3-phenylpropanoyl. The PTH canalogue binds with high affinity to the peptide hormone receptor without activating the 2nd messenger mol. The modification of the Lys residue stabilises the bioactive conformation of PTH to enhance the activity. The peptide may be used in in vitro bioassays to measure naturally occurring PTH and to diagnose the etology of or to treat osteoporosis or hypercalcaemia. It may also be used to treat hyperthyroidism and diseases caused by abberrent production because the story of the correct by a story of the correct 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R22066; standard; Protein; 28 AA.
R22066;
14-JUL-1992 (first entry)
Modified [D-Trp_12Tyr_34]hPTH(7-34)NH2.
Parathyroid hormone; analogue; osteoporosis; hyperthyroidism; tumours; hypercalcaemia; renal failure; human.
                              phase synthesis.
See also R22058-75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MERI ) MERCK & CO INC.

ROSenblatt M, Roubini E, Chorev M, Nutt RF;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                treat immune diseases such as inflammation. It is prepd. by solid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 92-096233/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-APR-1990; 514394.
25-APR-1990; US-514394.
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   28 AA;
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/label= NH2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= OTHER
/note= "OTHER
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Qy Db

8 hlnsm 12 ||||| 1 HLNSM 5



#Psrch\_pp protein - protein database search, using Smith-Waterman algorithm 0n: Thu Jul 30 10:24:01 1998; MasPar time 3.08 Seconds 59.270 Million cell updates/sec

Title: Tabular output not generated.

Description: Perfect Score: >US-08-817-547A-12 (1-5) from US08817547A.pep 37 1 HLNSM 5

Sequence:

Scoring table: PAM 150 Gap 15

120441 segs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 17.600; Variance 17.971; scale 0.979

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

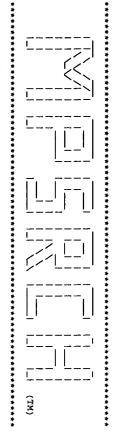
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RESULT 2  ENTRY  FITLE  Parathyroid hormone (residues 4-37) - human  ALTERNATE_NAMES HPTH(4-37)  PDB_TITLE  Structure of human parathyroid hormone fragment .  Structures  ORGANISM  REFERENCE  # formal_name Homo sapiens #common_name man  REFERENCE  # authors  # submission  # pross-references  # PDB:1ZME  REFERENCE  # TN001721  # authors  Marx, U.C.  # authors  # cross-references PDB:1ZME  REFERENCE  # authors  Marx, U.C.  # authors  Marx, U.C.  # submission  Strukturen Verschiedener Parathormonfragmente  pp.0, Bayreuth: University of Bayreuth (Thesi	9	structures #formal_name Homo sapiens #common A67856 rs Roesch, P.; Marx, U.C. ssion submitted to the Brookhaven Prote references PDB:IZWA TN001717 rs Marx, U.C. in Strukturen Verschiedener Parai pp.0, Bayreuth: University of Resolution: not applicable Determination: NMR hormone #region helix (right hand a:	RESULT 1 1ZWA #type complete TITLE parathyroid hormone (residues 1-34) - h ALTERNATE_NAMES HPTH(1-34) PDB_TITLE structure of human parathyroid hormone
4-37) - human hormone fragment 4-37, NMR 10 non_name man otein Data Bank, June 1996 of Bayreuth (Thesis), 1996	5; Length 34; 5+01; 5 0; Indels 0; Gaps 0;	non_name man  otein Data Bank, June 1996  rathormonfragmente in Loesung,  of Bayreuth (Thesis), 1996  alpha)  alpha)  alpha)  alpha)  alpha)  becksum 5629	1-34) - human hormone fragment 1-34, NMR 10

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COMMENT Determination: not applicable COMMENT Determination: NMR

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Psrch\_pp protein - protein database search, using Smith-Waterman algorithm

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Description: Perfect Score: Title: >US-08-817-547A-12 (1-5) from US08817547A.pep 37 1 HLNSM 5

Sequence:

Scoring table: PAM 150 Gap 15

Searched: 69111 segs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 18.404; Variance 15.219; scale 1.209

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

sult No:	Score	Query Match	Length	BG	ID	Description	Pred. No
ь.	37	100.0	115	ь ;	PTHY_HUMAN	PARATHYROID HORMONE PR	5.14e+00
N	37	100.0	208	٢		L 24.6 KD	<u>.</u>
ω	37	100.0	384	$\vdash$	Y039_MYCPN	HYPOTHETICAL PROTEIN M	5.14e+00
4	37	100.0	692	Н	YYI3_CAEEL	PROBABLE G PROTEIN-COU	5.14e+00
տ	37	100.0	2105	Н	POLR_ASGVP	GENOME POLYPROTEIN (CN	
σ	<b>з</b>	•	389	μ	CHS2_LYCES	CHALCONE SYNTHASE 2 (E	
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9	35	٠	422	Н	SYH_HAEIN	HISTIDYL-TRNA SYNTHETA	1.85e+01
10	35	٠	500	Н	ANP1_YEAST	AMINONITROPHENYL PROPA	1.85e+01
11	35	٠	587	_	DLD1_YEAST	D-LACTATE DEHYDROGENAS	1.85e+01
12	35	94.6	662	μ	PMT7_YEAST	DOLICHYL-PHOSPHATE-MAN	1.85e+01
13	35	•	696	مبر	YHFK_ECOLI	HYPOTHETICAL 79.5 KD P	1.85e+01
14	35		859	سر	YQD3_CAEEL	HYPOTHETICAL 96.7 KD P	1.85e+01
15	35		880	μ	ARG2_YEAST	ARGININE METABOLISM RE	1.85e+01
16	35	•	922	Н	CLPA_PEA	ATP-DEPENDENT CLP PROT	1.85e+01
17	35	•	3411	μ	POLG_YEFV1	GENOME POLYPROTEIN (CO	1.85e+01
18	35		3411	Н	POLG_YEFV2	GENOME POLYPROTEIN (CO	1.85e+01
19	34		154	Ь	YR7E_ECOLI	HYPOTHETICAL 18.0 KD P	3.44e+01
20	34		255	Н	YKB4_CAEEL	HYPOTHETICAL 28.1 KD P	3.44e+01
21	34		339	Н	RMAR_CANGA	MITOCHONDRIAL RIBOSOMA	3.44e+01
22	34	91.9	355	μ	DVR1_BRARE	DVR-1 PROTEIN PRECURSO	3.44e+01
23	34	91.9	396	<b>}</b>	RMAR_YEAST	MITOCHONDRIAL RIBOSOMA	3.44e+01

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YKQ0_CAEEL TOP2_CRIFA	EBN6_EBV	NIA CICIN	VGLB HCMVA	SPO2_MOUSE	RELA_STRCO	YER8_YEAST	HSF1_HUMAN	SKI_AVIES	YGCA_ECOLI	PO3B_XENLA	VANS_ENTEC	PO3A_XENLA	LEF3_NPVOP	YGCA_VIBSS	PTHY_BOVIN	Y080_BPP2	ZFH2_DROME	RYK_MOUSE	YCAJ_ECOLI
DNA TOPOISOMERASE II (	EBNA-6 NUCLEAR PROTEIN	CIA	GLYCOPROTEIN B PRECURS	PRESYNAPTICAL OR O ED D	GTP PYROPHOSPHOKINASE	HYPOTHETICAL 73.0 KD P	HEAT SHOCK FACTOR PROT	TRANSFORMING PROTEIN S	HYPOTHETICAL RNA METHY	TRANSCRIPTION FACTOR P	SENSOR PROTEIN VANS (E	TRANSCRIPTION FACTOR P	LATE EXPRESSION FACTOR	HYPOTHETICAL RNA METHY	PARATHYROID HORMONE PR	HYPOTHETICAL 8.3 KD PR	ZINC-FINGER PROTEIN 2	TYROSINE-PROTEIN KINAS	HYPOTHETICAL 49.6 KD P
6.29e+01 6.29e+01	6.29e+01	6.29e+01	6.29e+01	6.296+01	6.29e+01	6.29e+01	6.29e+01	6.29e+01	6.29e+01	6.29e+01	6.29e+01	6.29e+01	6.29e+01	6.29e+01	6.29e+01	6.29e+01	3.44e+01	3.44e+01	3.44e+01

REVISIONS.
MEDLINE; 75146516.
MEDLINE; 75146516.
KEUTMANN H.T., NIALL H.D., O'RIORDAN J.L.H., POTTS J.T. JR.;
BIOCHEMISTRY 14:1842-1847(1975).

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Query Match
Best Local Similarity 100.0%;
Matches 5; Conservative
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W MEDLINE; 91009811.

A ARNOLD A., HORST S.A., GARDELLA T.J., BABA H., LEVINE M.A.,

A ARNOLD A., HORST S.A., GARDELLA T.J., BABA H., LEVINE M.A.,

A CLIN. INVEST. 86:1084-1087(1990).

C -!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN

C -!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN

C -!- DISEASE: DEFECTS IN PTH ARE A CAUSE OF FAMILIAL ISOLATED

C HYDOPARATHYROIDISM (FIH).

C EMBL; J00301; G190704; -.

DR EMBL; V00597; G37144; -.

DR EMBL; A29146; E186700; -.
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MEDLINE, 95318084.
MARX U.C., AUSTERMANN S., B
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MEDLINE; 91299748.

KLAUS W., DIECKMANN T., WRAY V., SCHOMBURG D., WINGENDER E., MAYER H.;
BIOCHEMISTRY 30:6936-6942(1991).
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MEDLINE: 7327467.
ANDREATTA R.H., HARTMANN A., JOEHL A.,
RINIKER B., RITTEL W., SIEBER P.,
HELV. CHIM. ACTA 56:470-473(1973).
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MEDLINE; 75059220.

TREGEAR G.W., VAN RIETSCHOTEN J., GREEN E., NIALL H.D.,
KEUTMANN H.T., PARSONS J.A., O'RIORDAN J.L.H., POTTS J.T.
HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 355:415-421(1974).
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RA KLENK H.P., CLAYTON R.A., TOMB J., WHITE O., NELSON K.E., KETCHUM K.A.,

RA KLENK H.P., CLAYTON R.A., TOMB J., WHITE O., NELSON K.E., KETCHUM K.A.,

RA DODSON R.J., GGNINN M. HICKEY E.K.,

RA DOUGHERTY B.A., GRAHAM D.E., KYRPIDES N.C., FIEISCHMANN R.D.,

RA CHICKENBUSH J., LEE N.H., SUTTON G.G., GILL S., KIRKNESS E.F.,

RA DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOPTUS B., PETERSON S.,

RA REICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A., ZHOU L., OVERBEEK R.,

RA GOCAYNE J.D., WEIDMAN J.F., MCDONALD L., UTTERBACK T., COTTON M.D.,

RA SPRIGGS T., ARTIACH P., KAINE B.P., SYRES S.M., SADOW P.W.,

OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.;

SUBMITTED (NOV.1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

SUBMITTED (NOV.1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

SEQUENCE 193 AA; 22041 MW; 59F1EDOE CRC32;
                                                                                                                                                                                                   Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S., KIRKNESS E.F.,
DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B., PETERSON S.,
REICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A., ZHOU L., OVERBEEK R.,
GCCAYNE J.D., WELDMAN J.F., MCDONALD L., UTTERBACK T., COTTON M.D.,
ERRIGGS T., ARTIACH P., KAINE B.P., SYKES S.M., SADOW P.W.,
D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A., MASON T.M.,
OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.,
SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                  44 HLNSM 48
                                                                                                        1 HLNSM 5
                                                                                                                                                                                           Score 37; DB 9; Length 193;
Pred. No. 6.33e+00;
0; Mismatches 0; Indels
                                                                                                                                                                                        0;
                                                                                                                                                                                        Gaps
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Release 3.1A John F. Colling, Biocomputing Research Unit.	*
e 3.1A John F. Collins, Biocomputing	*****
A John F. Collins, Biocomputing	****
Collins, Biocomputing	******
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MPsrch\_pp 900 protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:27:11 1998; MasPar time 2.6 52.320 Million 2.64 Seconds

cell updates/sec

Tabular output not generated

Description: Perfect Score: Title: >US-08-817-547A-13 (1-9) from US08817547A.pep 62

Sequence: HNLGKHLNS

Scoring table: PAM 150 Gap 15

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match Listing first 45 summaries

Database:

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 15.334; Variance 52.987; scale 0.289

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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19	18	17	16	15	14	13	12	11	10	9	œ	7	6	G	4	w	2	1	esult No.
62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	Score
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36	35	35	35	35	35	35	34	34	34	34	34	34	34	34	34	34	34	34	Length
ဖ	14	14	14	14	14	14	22	22	22	7	7	22	22	22	22	22	22	9	80
R58182	R74431	R74429	R74401	R74402	R74517	R74516	W17948	W17949	W17943	R34353	R34354	W17970	W17969	W17950	W17955	W17954	W17957	R58181	ID
[Nva8]-hPTH(1-36)-NH2	Parathyroid hormone p	Human parathyroid hor		Human parathyroid hor	Human parathyroid hor	Human parathyroid hor	Human PTH analogue [D	Human parathyroid hor	Human PTH analogue (C	Human parathyroid hor	Human parathyroid hor	Human parathyroid hor	[Thr33, Ala34]-hPTH(1	Description					
4.68e+00	4.68e+00	4.68e+00	4.68e+00	4.68e+00	4.68e+00	4.68e+00	4.68e+00	4.68e+00	4.68e+00	4.68e+00	4.68e+00	Pred. No							

Query Match 100.0%; Best Local Similarity 100.0%;

Score Pred. NO ;

DB 9; Length 34; 4.68e+00;

20 62 100.0 36 9 R58279 [Lys20]-hPTH(1-36)-NH 21 62 100.0 36 9 R58176 [Moxpholine-2-carboxy 22 62 100.0 36 9 R58176 [Moxpholine-2-carboxy 23 62 100.0 36 9 R58248 N-Dimethyl-[Alal]-hPT 24 62 100.0 36 9 R58247 [Hyp]-hFTH(1-36)-NH2 25 62 100.0 36 9 R58246 Acetyl-hPTH(1-36)-NH2 26 62 100.0 36 9 R58246 Acetyl-hPTH(1-36)-NH2 27 62 100.0 36 9 R58164 [Lys(Isopropyl)13]-hP 28 62 100.0 36 9 R58175 [Lys(Isopropyl)13]-hP 29 62 100.0 36 9 R58164 [Lys(Isopropyl)13]-hP 29 62 100.0 36 9 R58164 [Lys(Isopropyl)13]-hP 20 62 100.0 44 26 P30015 [D-Val35]-hPTH(1-38)-OH 21 62 100.0 44 27 W25687 Human parathyroid hor 22 62 100.0 84 4 R21199 Human parathyroid hor 23 62 100.0 84 4 R21199 Human parathyroid hor 24 62 100.0 84 4 R21199 Human parathyroid hor 25 82 100.0 84 4 R21152 Human parathyroid hor 26 100.0 84 4 R21152 Human parathyroid hor 27 62 100.0 84 4 R21153 Human parathyroid hor 28 62 100.0 84 4 R21153 Human parathyroid hor 29 62 100.0 84 4 R21154 Human parathyroid hor 20 62 100.0 84 4 R21251 Human parathyroid hor 20 62 100.0 84 4 R21251 Human parathyroid hor 21 100.0 84 4 R21251 Human parathyroid hor 22 100.0 84 4 R21251 Human parathyroid hor 23 62 100.0 84 4 R21251 Human parathyroid hor 24 62 100.0 84 4 R21251 Human parathyroid hor 25 82 100.0 84 4 R21251 Human parathyroid hor 26 100.0 84 4 R21251 Human parathyroid hor 27 62 100.0 84 4 R21251 Human parathyroid hor 28 62 100.0 84 4 R21251 Human parathyroid hor 29 62 100.0 84 4 R21251 Human parathyroid hor 20 100.0 84 4 R21251 Human parathyroid hor 20 100.0 84 4 R21251 Human parathyroid hor 20 100.0 84 4 R21251 Human parathyroid hor 21 100.0 84 4 R21251 Human parathyroid hor 22 100.0 84 4 R21251 Human parathyroid hor 23 100.0 84 4 R21251 Human parathyroid hor 24 62 100.0 84 4 R21251 Human parathyroid hor 25 100.0 84 4 R21251 Human parathyroid hor 26 100.0 84 4 R21251 Human parathyroid hor 27 62 100.0 84 4 R21251 Human parathyroid hor 28 62 100.0 84 4 R21251 Human parathyroid hor 29 62 100.0 84 4 R21251 Human parathyroid hor
2 100.0 36 9 R58279 [Lys20] 2 100.0 36 9 R58177 [Morph] 2 100.0 36 9 R58177 [Hexah] 2 100.0 36 9 R58248 N-Dime 2 100.0 36 9 R58244 [Hypa] 2 100.0 36 9 R58245 Acety] 2 100.0 36 9 R58245 [Lyscot] 2 100.0 36 9 R58245 [Lyscot] 2 100.0 36 9 R58215 [Lyscot] 2 100.0 44 26 P30015 [Lyscot] 2 100.0 44 27 R58216 [Lyscot] 2 100.0 44 27 R72119 Human 2 100.0 84 4 R21119 Human 2 100.0 84 4 R21115 Human 2 100.0 84 4 R2115 Human 2 100.0 84 4 R2125 Human
.0 36 9 R58279 [Lys20] .0 36 9 R58176 [Mexah] .0 36 9 R58176 [Mexah] .0 36 9 R58176 [Meyah] .0 36 9 R58248 [MyDlime] .0 36 9 R58245 [MyDlime] .0 36 9 R58245 [MyDlime] .0 36 9 R58245 [MySlime] .0 36 9 R5825 [MySlime] .0 36 9 R58295 [MySlime] .0 44 26 P30015 [MySlime] .0 44 26 P3015 Human .0 84 4 R21199 Human .0 84 4 R21153 Human .0 84 4 R21153 Human .0 84 4 R21250 Human .0 84 4 R21251 Human
9 R58279 [Lys20] 9 R58176 [Hexah] 9 R58176 [Heyah] 9 R58248 N-Dime 9 R58248 N-Dime 9 R58246 Lys (Lys (Cys (Cys (Cys (Cys (Cys (Cys (Cys (C
9 R58279 [Mys2) 9 R58177 [Morph) 9 R58176 [Hexat] 9 R58248 N-Dime 9 R58247 [Hyman] 2 R23995 Human 9 R58164 [Lys (Lys (Cys (Lys (Cys (Lys (Cys (Lys (Cys (Lys (Cys (Lys (Cys (Lys (Lys (Cys (Lys (Lys (Lys (Lys (Lys (Lys (Lys (L
[Lys20 [Morp] [Hexah] [Hexah] N-Dime (Hypi) Human
[Lys20]-hPTH(1-36) NH [Morpholline-2-carboxy] [Hexahydropyridazine- N-Dimethyl-[Alal]-hPT [Hyp1]-hPTH(1-36)-NH2 Human paprthyroid hor Acetyl-hPTH(1-36)-NH2 [Lys(Isopropyl)13]-hP [Pyridine-2-carboxyli [D-Val35]-hPTH(1-36)-(Asg)3]-hPTH(1-36)-(

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R58181 standard; peptide; 34 AA.
R58181;
20-SBE-1994 (first entry)
[Thr33, Ala34]-hPTH(1-34)-NH2.
Human parathyroid hormone; hPTH; variant; an calcium; depletion; fixation; resorption; os hypoparathyroidism.
                                                                                                                                                                                                                           12-JUL-1993; 014384.

15-JUL-1992; GB-015009

18-DEC-1992; GB-026859.

23-DEC-1992; GB-026861.

23-DEC-1992; GB-026861.

23-DEC-1992; GB-001691.

28-JAN-1993; GB-001692.

14-APR-1993; GB-007673.

19-APR-1993; GB-008033.
                         New active para-thyroid hormone variants - used for treating or preventing osteopprosis etc.

Example 179; Page 43; 92pp; English.

This peptide is an example of a highly generic formula covering parathyroid hormone variants useful for treating or preventing bone conditions associated with calcium depletion/resorption, in cases where calcium fixation is required (esp. osteopprosis) or to treat
                                                                                                                                                                          (BAUE/)
(SANO)
(SANO)
hypoparathyroidism. Sequence 34 AA;
                                                                                                                     Albert R, Bauer W, B
Gombert F, Gram H, L
Waelchli R, Rainer A;
WPI; 94-018352/03.
                                                                                                                                                                                                                                                                                                                                                   GB2269176-A.
02-FEB-1994.
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                                                                                                                                                                                                                 SANO
                                                                                                                         ) SANCE.
/) BAUER W.
/) SANDOZ PATENT GMBH.
/) SANDOZ-ERFINDUNGEN VERW GES MBH.
3 ) SANDOZ-ERFINDUNGEN VERW GES MBH.
Gram H, Lewis I, Ramage P,
                                                                                                                                                                                                                 SANDOZ LTD.
                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                              /note=
                                                                                                                                                                                                                                                                                                                                                                              "in
                                                                                                                                                                                                                                                                                                                                                                              amide form"
                                                                                                                                                Cardinaux F;
P, Schneider
                                                                                                                                                                                                                                                                                                                                                                                                                                                osteopathy; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              analogue;
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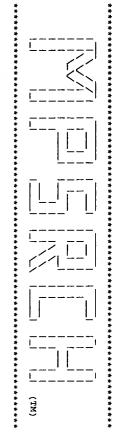
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RESULT
ID W1
AC W1
DT 25
DE H
KW 06
KW 06
KW 06
OS H
OS S
FH K
FT m
FT
Search completed: Thu Jul 30 10:27:26 1998 Job time: 15 secs.
                                                                                                                                                                   pr bone fracture

Statistics of the present sequence is a specific example of a human parathyroid commone (hprH) analogue from fragment 1-34 in which at least one cof the amino acid residues at positions 3, 12, 16, 17, 19 and 34 corresponds to the wild-type has been substituted by Aib. The hprH canalogues stimulate bone growth and so are useful in human or veterinary computation for treatment of osteoporosis and bone fracture, optionally in conjunction with anti-resorptive therapy (bisphosphonates and calcitonin).

CC N.B. The present sequence does not appear in the specification. It corresponds to the known hprH 1-34 fragment with the modifications con stated in the claim.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
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                                                                                                              lest Local s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                       30-JAN-1997.
30-JAN-1997.
30-JAN-1996; U11292.
30-JUL-1995; US-001105.
30-SEP-1995; US-003305.
29-MAR-1996; US-626186.
(BIOM-) BIOMEASURE INC.
Dong ZX;
WPI; 97-118819/11.
New variants of human parathyroid hormone 1-34 peptide - which stimulate bone growth and are used for treatment of osteoporosis and broad fracture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J-JUL-1997 (first entry)
Human parathyroid hormone analogue [Aib3]hPTH(1-34)NH2.
Osteoporosis; agonist; PTH; human; anti-resorptive therapy;
Homo sapiens.
Syntheti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9702834-A1.
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W17957;
w17957;
29-JUL-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                       y Match 100.0%;
Local Similarity 100.0%;
hes 9; Conservative
                                                                       9 hnlgkhlns 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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1 HNLGKHLNS 9
                                                          HNLGKHLNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9;
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                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34
/note= "In amide form"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label=
                                                                                                         Score 62; DB 22;
Pred. No. 4.68e+00;
0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                  Length 34;
                                                                                                        Indels
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                                                                                                        0;
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                                                                                                        Gaps
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                                                                                                        0;
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Psrch\_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Jul 30 10:26:25 1998; MasPar time 3.14 Seconds 104.605 Million cell updates/sec

Tabular output not generated.

Title: >US-08-817-547A-13 (1-9) from US08817547A.pep 62 1 HNLGKHLNS 9

Description: Perfect Score: Sequence:

Scoring table: РАМ 150 Gap 15

Searched: 120441 segs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 21.210; Variance 26.968; scale 0.787

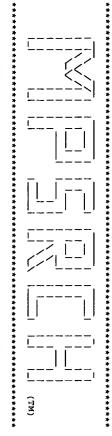
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	21												_	œ	7	თ	ر.	4	-	2	1	sult No. Score
•	47	47	47	48	48															62 1	- 1	
	75.8	75.8		77.4	77.4		88.7						93.5	.00.0	100.0		100.0	100.0	100.0	00.0	100.0	Query Match Le
568	744	738	621	172	172	421	34	115	105	115	115	115	37	115	37	36	S S	34	34	34	34	Length 1
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S76244	A32905	S35093	S35092	E69671	A35145	E69467	1HTH	A05091	I51851	PTBO	PTPG	JC4202	12WC	PTHU	1HPH	12WB	12WD	12WF	12WG	1ZWE	1ZWA	Ħ
μ,	Ω	•	Ö		transcriptional regul	hypothetical protein	thyroid h	Ξ.	parathyroid hormone -	parathyroid hormone p	parathyroid hormone p	parathyroid hormone -	_	_	parathyroid hormone f	_	parathyroid hormone (	parathyroid hormone 4	_	parathyroid hormone (	parathyroid hormone (	Description
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45	44	43	42	41	40	39	ω 8	37	36	35	34	<b>ω</b>	32	31	30	29	28	27	26	25	24
42	42	42	42	43	43	43	43	43	43	43	43	43	44	44	44	44	44	44	44	44	45
67.7	67.7	67.7	67.7	69.4	69.4	69.4	69.4	69.4	69.4	69.4	69.4	69.4	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0	12.6
4930	417	292	193	2340	2338	2317	1854	1021	985	310	310	308	1447	585	386	317	265	264	231	186	ST0
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E69679	S20608	S64361	A53835	I48310	173957	I56752	I73956	S44644	S59330	1FJI	C47045	1AK1	S63669	G64220	D42528	A49915	A46018	S31394	JQ0704	A64646	504636
polyketide synthase p	heat shock protein Hs	hypothetical protein	SEC63 protein complex	kinase-related protei	c-ros-1 tyrosine kina	c-ros-1 tyrosine kina	c-ros-1 unknown prote		Na+/H+-exchanging pro	ferrochelatase (EC 4.	ferrochelatase (EC 4.	ferrochelatase (EC 4.	UDPglucoseglycoprot	ATP-binding protein m	B23R protein - vaccin	GutQ homolog - Escher	apolipoprotein AI - p	apolipoprotein A-I -	apolipoprotein A-I -		probable membrane pro
7.60e+01	7.60e+01	7.60e+01	7.60e+01	4.92e+01	4.92e+01	4.92e+01	4.92e+01	4.92e+01	4.92e+01	4.92e+01	4.92e+01	4.92e+01	3.16e+01	3.16e+01	3.16e+01	3.16e+01	3.16e+01	3.16e+01	3.16e+01	3.16e+01	2.02e+01

TITLE ALTERNATE_NAMES PDB_TITLE ORGANISM REFERENCE # authors # submission # cross-referen REFERENCE # authors # book	Db 9 HNLGKHLNS	Query Match Best Local Similarity Matches 9; Conse	6-9 19-30 SUMMARY	#DOOK  #DOOK  COMMENT Resolu  COMMENT Detern  KEYWORDS  FEATURE	#authors #submission #cross-referen REFERENCE	RESULT 1 ENTRY TITLE ALTERNATE_NAMES PDB_TITLE ORGANISE DEFENDATE
L2WE parathyroid hormone (residues 4-37) - human ERNATE_NAMES HPTH(4-37)  _TITLE structures  ANISM #formal_name Homo sapiens #common_name man ERENCE Roesch, P.; Marx, U.C. #submission submitted to the Brookhaven Protein Data Bank, June 1996 #rcross-references pDB:1ZWE ERENCE TN001721 #authors Marx, U.C. #submission submitted to the Brookhaven Protein Data Bank, June 1996 #rcross-references pDB:1ZWE ERENCE TN001721 #authors in Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth: University of Bayreuth (Thesis), 1996	17 9	100.0%; Score 62; DB 5; Length 34; nilarity 100.0%; Pred. No. 4.02e-03; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	<pre>#region helix (right hand alpha)\ #region helix (right hand alpha) #length 34 #molecular-weight 4118 #checksum 5629</pre>	in Strukturen Verschiedener Parathormonfragmente in Loesung, in Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth : University of Bayreuth (Thesis), 1996 Resolution: not applicable Determination: NMR Determination: NMR	#AUTHORS ROSSON, P.; MAIX, U.C. #authors Rosson, P.; MAIX, U.C. #submission submitted to the Brookhaven Protein Data Bank, June 1996 #cross-references PDB:1ZWA #CREMCE TN001717	1ZWA #type complete parathyroid hormone (residues 1-34) - human HPTH(1-34) structure of human parathyroid hormone fragment 1-34, NMR 10 structures #formal_name Homo saplens #common_name man



Psrch\_pp protein - protein database search, using Smith-Waterman algorithm

on : Thu Jul 30 10:25:15 1998; MasPar time 2.12 Seconds 106.609 Million cell updates/sec

Tabular output not generated.

Title:
Description:
Perfect Score:
Sequence: >US-08-817-547A-13 (1-9) from US08817547A.pep 62 1 HNLGKHLNS 9

Scoring table: PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 22.158; Variance 22.443; scale 0.987

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

sult No.	Score	Query	Length	BB	IJ	Description	Pred. No.
1	62	100.0	115	ь;	PTHY_HUMAN	PARATHYROID HORMONE PR	1.55e-04
2	58		115	μ	PTHY_PIG	HORMONE	
ω	58	w	115	<del>ب</del>	PTHY_CANFA	PARATHYROID HORMONE PR	2.07e-03
4	58	93.5	115	ب	PTHY_BOVIN	PARATHYROID HORMONE PR	
ر ن	57	91.9	115	н	PTHY_RAT	PARATHYROID HORMONE PR	3.90e-03
6	48	77.4	171	4ب	PAIA_BACSU	PROTEASE SYNTHASE AND	
7	47	75.8	621	۳	PLAK_MOUSE	JUNCTION PLAKOGLOBIN (	
œ	47	75.8	738	L	PLAK_XENLA	JUNCTION PLAKOGLOBIN (	1.52e+00
9	47	75.8	743	Н	PLAK_HUMAN	JUNCTION PLAKOGLOBIN (	1.52e+00
10	45	72.6	187	μ	ATPD_ODOSI	ATP SYNTHASE DELTA CHA	4.57e+00
11	45	72.6	381	1	DHB2_MOUSE	ESTRADIOL 17 BETA-DEHY	4.57e+00
12	44	71.0	265	_	APA1_PIG	APOLIPOPROTEIN A-I PRE	7.80e+00
13	44		317	<b>;</b>	KSF1_ECOLI	KPSF PROTEIN.	7.80e+00
14	44	71.0	386	Н	VC17_VACCC	PROTEIN C17/B23.	7.80e+00
15	44	71.0	585	_	Y187_MYCGE	HYPOTHETICAL ABC TRANS	7.80e+00
16	43	69.4	310	-	HEMZ_BACSU	FERROCHELATASE (EC 4.9	1.32e+01
17	43	69.4	985	_	NAH_YEAST	PROBABLE NA(+)/H(+) AN	1.32e+01
18	43	69.4	1021	_	YPT7_CAEEL	HYPOTHETICAL 111.7 KD	1.32e+01
19	42	67.7	180	۳	Y088_METJA	HYPOTHETICAL PROTEIN M	2.21e+01
20	42	67.7	192	μ	SC72_YEAST	TRANSLOCATION PROTEIN	2.21e+01
21	42	67.7	246	ш	SR1A_PHYPO	SPHERULIN 1A PRECURSOR	
22	42	67.7	292	L	YG29_YEAST	HYPOTHETICAL 34.0 KD P	
23	42	67.7	417	r	HS47_HUMAN	47 KD HEAT SHOCK PROTE	

2222222 222222 22222 2222 2322 2322 23	24
**************************************	42
00000000000000000000000000000000000000	67.7
1184 1195 1195 1195 1195 1195 1195 1195 119	417
	_
HS47_MOUSE CBP2_HUWAN SMI1_YEAST MY54_SCHPO BIMC_EMENI UBR1_YEAST YEAF_STANU PFLA_ECOLI VA32_VACCV VA32_VACCV VA32_VACCV VA32_VACCV VA7C_HUWAN HS47_CHTCK SR54_SCHPO TOD5_YEAST YO36_HAEIN PSM_HUMAN	HS47 RAT
HEAT SHOCK GEN-BINDING PROTEIN (KIE PROTEIN (KIE PROTEIN (KIE ROTELSOME RE IN LIKE PROT -RECOGNIZING BLE RIBOSOMA ATE FORMATE- IN A32. IN A32. IN A32. L RECOGNITIO HEAT SHOCK L RECOGNITIO HETICAL ABC ATE-SPECIFIC	47 KD HEAT SHOCK PROTE
	2.21e+01

RN	RL	RL	RL	RA	RA	RP	RN	RL	RA	RA	RX	RP	RN	RĽ.	RA	RA A	RX	RP	RN	RL	RA	RX	ŖP	RN	RL	RA	RA	RX	RP	Z	2	RA.	Z :	RP	<b>d</b> C	3 8	200	Q Q	DE	ΡŢ	ij	Ų,	A	RESULT	
[7]		9-14, EXCERPTA MEDICA FOUR		N J.L.H., POTTS J.T. JR.;		SEQUENCE OF 75-100.	[6]			H.T., SA	790	SEQUENCE OF 61-83 AND 84-115.		PROC. NATL. ACAD. SCI. U.S.A. 71:384-388(1974).	AURBACH G.D., POTTS J.T. JR.;	NIALL H.D., SAUER R.T., JACOBS J.W., KEUTMANN H.T., SEGRE G.V.,	MEDLINE; 74111656.	UENCE		249:155-157(1974).	JACOBS J.W., KEMPER B., NIALL H.D., HABENER J.F., POTTS J.T. JR.;	MEDLINE; 74174967.	SEQUENCE OF 26-37.		U.S.A. 80:2127-2131(1983)	.N., POTTS J.T. JR., RICH A., KRONENBERG H.M	VASICEK T.J., MCCEVITT B.E., FREEMAN M.W., FENNICK B.J.,	MEDLINE; 83169834.	UENCE		NATL. ACAD. SCI. U.S.A. 78:7365-7369(1981).	N. KRONENBERG H.M. P	MEDLINE: 82150870.	SEQUENCE FROM N.A.	111 FOLDOLD, FOLDOLDS.	EUKARIOTA; METAJOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMADIA; EUMHUTETA, DETAJOTO	)·		THYROID HORMON	35, LAST ANNOTATION	(REL. 05,	1986 (REL.	70:	DTHY HIMAN STANDARD: PRT: 115 AA.	

REVISIONS.
MEDLINE; 75146516.
MEDLINE; 75146516.
KEUTMANN H.T., NIALL H.D., O'RIORDAN J.L.H.,
BIOCHEMISTRY 14:1842-1847(1975).

POTTS J.T. JR.;

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AX MEDLIANS; 91009811.

RA ARNOLD A., HORST S.A., GARDELLA T.J., BABA H., LEVINE M.A.,

RA RONDENERG H.M.;

RA KRONENBERG H.M.;

RI J. CLIN. INVEST. 86:1084-1087(1990).

C. -: FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN

C. -: DISEASE DEFECTS IN PTH ARE A CAUSE OF FAMILIAL ISOLATED

C. HYPOPARATHYROIDISM (FIH).

DR EMBL; JOO301; G190704; -.

DR EMBL; V00597; G37144; -.

DR EMBL; V00597; G37144; -.

DR EMBL; A19339; A19339.

PDB; 11FH; 10-JUL-95.

PDB; 11FH; 15-CCT-97.

PDB; 12FW; 12-MAR-97.

DR PDB; 12FW; 16-JUN-97.

DR PDB; 12FW; 16-JUN-97.

DR PDB; 12FW; 16-JUN-97.

DR PDB; 12FW; 16-JUN-97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%;
Matches 9; Conservative
                                                         CONFLICT
SEQUENCE
                                                                                                                     PROPEP
                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYNHESIS OF 32-65.

SYNHESIS OF 32-65.

MEDLINE; 75059220.

TREGEAR G.W., VAN RIETSCHOTEN J., GREEN E., NIALL H.D.,

KEUTMANN H.T., PARSONS J.A., O'RIORDAN J.L.H., POTTS J.T.

HOPPE-SEYLER'S 2. PHYSIOL. CHEM. 355:415-421(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 95318084.

MARX U.C., AUSTERMANN S., BAYER P.,
STICHT H., WALTER S., SCHMID F.-X.,
ROESCH P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 93345518.
BARDEN J.A., CUTHBERTSON R.M.;
BUR. J. BICCHEM. 215:315-321(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRUCTURE BY NMR OF 32-65.
MEDLINE; 91299748.
KLAUS W., DIECKMANN T., WRAY V.,
BIOCHEMISTRY 30:6936-6942(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYNTHESIS OF 32-65.

MEDLINE; 73227467.

ANDREATTA R.H., HARTMANN A., JOEHL A.,

RINIKER B., RITTEL W., SIEBER P.;

HELV. CHIM. ACTA 56:470-473(1973).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT ARG-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRUCTURE BY NMR OF 32-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRUCTURE BY NMR OF 32-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BIOL. CHEM. 270:15194-15202(1995).
                                                                                                                                   PS00335; PARATHYROID; 1.
SIGNAL; DISEASE MUTATION; 3D-STRUCTURE.
                                                     107
115
                                                       AA;
                                                      107
12861
                                                                                         25
31
115
18
                                                     , ww
     Score 62; DB 1; I
Pred. No. 1.55e-04;
0; Mismatches 0
                                               PARATHYROID HORMONE.
C -> R (IN FH; LEADS TO INEFFICIENT PROCESSING OF THE PRECURSOR).
N -> D (IN REF. 5).
243E87C7 CRC32;
   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADERMANN
JAENICKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KAMBER B., MAIER
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   0;
                         Length 115;
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FORSSMANN
  Indels
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 Gaps
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Search completed: Thu Jul Job time : 6 secs.

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RESOLDE

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Best Local S
Matches
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SAUER R.T., NIALL H.D., HOGAN M.L., KEUTMANN H.T., V SAUER R.T., JR.;

POTTS J.T. JR.;

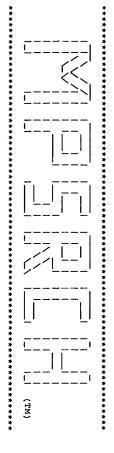
BICCHEMISTRY 13:1994-1999(1974).

-!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING BONE AND PREVENTING THEIR RENAL EXCRETION.

EMBL; X05722; G1839; -.
                                                                                                                                                                                         PROPEP
CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                HORMONE; SIGNAL. SIGNAL 1
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01-JAN-1988
01-FEB-1996
                                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 76018954.
CHU L.L.H., HUANG W.-Y., LITTLEDIKE E.T.,
BIOCHEMISTRY 14:3631-3635(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCHMELZER H.-J., GI
NUCLEIC ACIDS RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE; 87316938.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 32-115.
MEDLINE; 74253317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 26-115.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUTHERIA; ARTIODACTYLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUS SCROFA (PIG).
EUKARYOTA; METAZO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PARATHYROID
                                             40 HNLGKHLSS 48
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     μ
                                                                                                                                                                                                                                                                                                 ; A01535; PTPG.

2; B26806; B26806.

DSITE; PS00335; PA
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  HNLGKHLNS
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                                                                                                                    Similarity
                                                                                                                                                                                    1
26
32
115 AA;
                                                                                        93.5%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (REL. 01, CREATED)
(REL. 06, LAST SEQUENCE UPDATE)
(REL. 33, LAST ANNOTATION UPDATE)
HORMONE PRECURSOR (PARATHYRIN) (PTH).
ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GROSS G., WIDERA G.,
S. 15:6740-6740(1987).
                                                                                                                                                                                    25
31
115
P
12852 MW;
                                                                                                                                                                                                                                                                                                         PARATHYROID;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                 Score 58; DB 1; Le
Pred. No. 2.07e-03;
1; Mismatches 0;
                                                                                                                                                                            PARATHYROID HORMONE.; 98B67F47 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAYER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAMILTON J.W., COHN D.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Η.;
                                                                                                                              Length 115;
                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O'RIORDAN J.L.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                   THE SALTS
                                                                                 0;
                                                                            Gaps
                                                                              0
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srch\_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output Thu Jul 30 10:25:38 1998; MasPar time 3.77 Seconds 100.539 Million cell updates/sec

not generated

Description: Perfect Score: Title: >US-08-817-547A-13 (1-9) from US08817547A.pep 62

Sequence: 1 HNLGKHLNS 9

Scoring table: PAM 150 Gap 15

Searched 140542 seqs, 42109429 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb15
1:sp\_fung1 2:sp\_human 3:sp\_invertebrate 4:sp\_mammal
5:sp\_mhc 6:sp\_organelle 7:sp\_phage 8:sp\_plant
9:sp\_bacteria 10:sp\_rodent 11:sp\_virus 12:sp\_vertebrate
13:sp\_unclassified

Statistics: Mean 21.246; Variance 22.169; scale 0.958

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

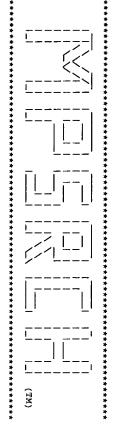
# SUMMARIES

19 20	16 17	13 14	11 12	10	7 8	o u	<b>4</b> (	-24	Result
43	44	44 44 44	4.5 4.4	<b>4</b> 5	45 45	47 47	48 47	57 49	Score
69.4	71.0 71.0	71.0 71.0 71.0	72.6 71.0	72.6 72.6	74.2 72.6	75.8 75.8	75.8		Query Match 1
123 298	327 1447	96 186 301	1817 82	385 619	568 381	745 745	171	105 421	Length
122	<b>9</b> 4	119	ω 4	μω	10	10	NV	901	BB
015020 014904 013669	Q47334 Q09140	Q72500 025653 Q70212	Q19931 Q29248	018326 099234	P74405 Q62730	Q15151 P70565	Q15093	Q63473 O28532	ij
KIAA0302 (FRAGMENT). WNT-LIKE PROTEIN WNT14 BASIC TRANSCRIPTION FA	KPSF GENE. UDP-GLC:GLYCOPROTEIN G	VPR PROTEIN. SITE-SPECIFIC RECOMBIN ENVELOPE GLYCOPROTEIN,	z	HUNCHBACK GAP (FRAGMEN CHROMOSOME XV READING	HYPOTHETICAL 62.3 KD P 17-BETA HYDROXYSTEROID	PLAKOGLOBIN. PLAKOGLOBIN.	PLAKOGLOBIN (FRAGMENT)	PARATHYROID HORMONE (F	Description
9.92e+00 1.69e+01 1.69e+01	9.92e+00 9.92e+00	9.92e+00 9.92e+00 9.92e+00	5.79e+00 9.92e+00	5.79e+00 5.79e+00	3.34e+00 5.79e+00	1.92e+00 1.92e+00	1.92e+00	4.94e-03 6.15e-01	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	<b>ω</b> <b>ω</b>	32	31	30	29	28	27	26	25	24	23	22	21
41	41	41	41	41	41	41	41	41	41	42	42	42	42	42	42	42	42	43	43	43	43	43	43	43
σ	σ	66.1	S.	ന	€.	S.	$\alpha$	an.	CD.	-	~	~	v	~	~	~	~	69.4	S	o	S	S	മ	v
2490	2484	2294	1401	831	502	470					979					176		2340						
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Q12923	Q28006	Q15265	Q50177	013705	006585	Q22494	Q90420	Q63778	289195	031783	P93820	028232	P77814	Q84584	021973	Q55024	P88152	Q60705	Q64736	Q63132	Q63130	Q63131	001906	Q22312
PROTEIN TYROSINE PHOSP	BA14 TYROSINE PHOSPHAT	PROTEIN TYROSINE PHOSP	PROBABLE CYCLIC SYNTHE	HYPOTHETICAL 95.0 KD P	HYPOTHETICAL 53.5 KD P	SIMILAR TOS. CEREVISIA	47 KDA HEAT SHOCK PROT	HYPOTHETICAL 43.7 KD P	VACCINA VIRUS GENOMIC	POLYKETIDE SYNTHASE OF	HYPOTHETICAL 110.0 KD	THYMIDYLATE SYNTHASE,	•	SEQUE	HYPOTHETICAL 31.3 KD P	NUTRIENT-STRESS INDUCE	VPR PROTEIN.	ROS1 PROTOONCOGENE (PR	ROS1 PROTOONCOGENE (C-	RAT HEART-DERIVED C-RO	RAT LUNG-DERIVED C-ROS	RAT LUNG-DERIVED LO1 C	COSMID F59E12.	COSMID TO/ES.
4.74e+01	4.74e+01	2.84e+01	2.84e+01				2.84e+01	2.84e+01		1.69e+01		Ξ.	1.69e+01	1.69e+01	1.69e+01	1.69e+01								

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RESULT A SOLUTION OF SOLUTION 
     RESULT
AC 022
AC 022
AC 020
DT 01
DT 01
DT 01
DE Hyp
CS AH
CS AH
CS AH
RA CS
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Best Local Similarity 88.9%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           053473
063473;
063473;
01-NOV-1996
01-NOV-1996
01-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                          O28532 PRELIMINARY; PRT; 421 AA.
O28532;
O1-JAN-1998 (TREMBLREL. O5, CREATED)
O1-JAN-1998 (TREMBLREL. O5, LAST SEQUENCE UPDATE)
O1-JAN-1998 (TREMBLREL. O5, LAST ANNOTATION UPDATE)
HYPOTHETICAL 48.5 KD PROTEIN.
AF1742:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE-THYROID, AND PARATHYROID;
SCHMELLER H.J., GROSS G., MAYER H.;
ADV. GENE TECHNOL. 21:228-229(1984).
EMBL; M54875; G601933; -.
NON_TER 1
KLENK H.P., CLAYTON R.A., TOMB J., WHITE O., NELSON K.E., KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D., RICHARDSON D.L., KERLAVAGE A.R., GRAHAM D.E., KYRPIDES N.C., FLEISCHMANN R.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                         ARCHAEOGLOBUS FULGIDUS.
ARCHAEDACTERIA; EURYARCHAEOTA; ARCHAEOGLOBALES; ARCHAEOGLOBACEAE.
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(TREMBLREL. 01, LAST SEQUENCE UPDATE)
(TREMBLEL. 05, LAST ANNOTATION UPDATE)
HORMONE (FRAGMENT).
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Pred. No. 4.94e-03;
0; Mismatches 1
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RA DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOPTUS B., PETERSON S.,
RA GOCAYNE J.D., WEIDMAN J.F., MCDONALD L., UTTERBACK T., COTTON M.D.,
RA GOCAYNE J.D., WEIDMAN J.F., MCDONALD L., UTTERBACK T., COTTON M.D.,
RA SPRIGGS T., ARTIACH P., KAINE B.P., SYERS S.M., SADOW P.W.,
RA SPRIGGS T., ARTIACH P., KAINE B.P., SYERS S.M., SADOW P.W.,
RA CLENK G.J., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.;
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RE SEQUENCE FROM N.A.
RA KLENK H.P., CLAYTON R.A., TOME J., WHITE O., NELSON K.E., KETCHUM K.A.,
RA KLENK H.P., CLAYTON R.A., TOME J., WHITE O., NELSON K.E., KETCHUM K.A.,
RA KLENK M.P., GRAHAM D.E., KYRFIDES N.C., FLEISCHMANN R.D.,
RA KERLANAGE A.R., GRAHAM D.E., KYRFIDES N.C., FLEISCHMANN R.D.,
RA GOCAYNE J., LEE N.H., SUTTON G.G., GILL S., KIRNESS E.F.,
RA REICH C.I., MCNENEY K., ADAMS M.D., LOFTUS B., PETESON S.,
RA REICH C.I., MCNENEY K., BADGER J.H., GLODEK A., ZHOU L., OVERBEEK R.,
RA REICH C.I., MCNENEY K., BADGER J.H., GLODEK A., ZHOU L., OVERBEEK R.,
RA REICH C.I., MCNENEY K., ADAMS M.D., UTTERBACK T., COTTON M.D.,
RA REICH C.I., MCNENEY K., ADAMS M.D., UTTERBACK T., COTTON M.D.,
RA GOCAYNE J.D., WEIDMAN J.F., MCDONALD L., GARLAND S.A., MASON T.M.,
RA GOCAYNE J.D., WEIDMAN C., FUJII C., GARLAND S.A., MASON T.M.,
RA GOCAYNE J.D., BOWALN C., FUJII C., GARLAND S.A., MASON T.M.,
RA GOCAYNE J.D., BOWALN C., FUJII C., GARLAND S.A., MASON T.M.,
RA GOCAYNE J.D., BOWALN C., FUJII C., GARLAND S.A., MASON T.M.,
RA GOCAYNE J.D., BOWALN C., FUJII C., GARLAND S.A., MASON T.M.,
RA GOCAYNE J.D., BOWALN C., FUJII C., GARLAND S.A., MASON T.M.,
RA GOCAYNE J.D., BOWALN C., FUJII C., GARLAND S.A., MASON T.M.,
RA GOCAYNE J.D., SOTTON M.D. J. FUTERBACK T., COTTON M.D.,
RA GOCAYNE J.D., GARGER J.H., GLODER J.B., STOTON M.D.,
RA GOCAYNE J.D., WEIDMAN C., FUJII C., GARLAND S.A., MASON T.M.,
RA GOCAYNE J.D., WEIDMAN C., FUJII C., GARLAND S.A., MASON T.M.,
RA GOCAYNE J.D., GARGER J.H., GLODER J.B., GARGER J.B.,
RA GOCAYNE J.D., GARGER J.B., GARGER J.B., GARGER J.B.,
RA GOCAYNE J.D., GARGER J.B., GARGER J.B., GARGER J.B.,
RA GOCA
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Psrch\_pp n on: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:29:27 1998; MasPar time 2.68 Seconds 45.741 Million cell updates/sec

Tabular output not generated.

Title:

Description: Perfect Score: Sequence: >US-08-817-547A-14 (1-8) from US08817547A.pep 58 1 HNLGKHLN 8

Scoring table: PAM 150 Gap 15

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 14.991; Variance 49.457; scale 0.303

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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нο.	Parathyroid hormone p	hormone	hormone	Parathyroid hormone p	Human parathyroid hor	Cyclised [Nle 8,18, T	Human parathyroid hor	Human parathyroid-(1-	Human parathyroid hor	Human PTH analogue [D	Human parathyroid hor	[Nle8,18,D-Asn33,D-Ph	Description				
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	0.2
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R75693	R21243	R23245	R21251	R21250	R34460	R30851	W29420	W25687	W21946	P30015	R58162	R58166	R58134	R58122	R58121	R58163	R58282	R24778	R23995	R58263	R58214	R58213	R58071	R58281	RSBL99
	Human parathyroid hor	Human parathyroid hor		Human parathyroid hor		Generic human parathy	Human parathyroid hor	Human parathyroid hor	Fusion protien compri	parathyı	-hPTH(1	]-hPTH(1		]-hPTH(1-	[Met17]-hPTH(1-38)-OH	[Pro33]-hPTH(1-38)-OH	[Trp(SO2Pmc)23]-hPTH(	hPTH(1-37)-amide/ethy	č	[D-Ile5]-hPTH(1-36)-N		17]-hPTH(1-	[Aib3, Gln18]-hPTH(1-	[D-Val21]-hPTH(1-36)-	]-hPTH(1-3
7.41e+00	7.41e+00	7.41e+00	•		•								7.41e+00	7	7	7	7	7		7.41e+00			7.41e+00	7.41e+00	

# ALIGNMENTS

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The present sequence is a specific example of a human parathyroid hormone (hPTH) analogue from fragment 1-34 in which at least one coffice amino acid residues at positions 7, 11, 23, 24, 27, 28 and 31 cc is cyclohexylalanine (cha). In this example the Trp residue at cyclohexylalanine (cha). In this example the Trp residue at cyclohexylalanine (cha). In this example the Trp residue at cyclohexylalanine (cha). In this example the Trp residue at cyclohexylalanine (cha). In this example the Trp residue at cyclohexylalanine (cha). In this example the Trp residue at cyclohexylalanine (cha). In the present sequence is and bone fracture, optionally in conjunction with anti-resorptive therapy (bisphosphonates and calcitonin).

N.B. The present sequence does not appear in the specification. It corresponds to the known hPTH 1-34 fragment with the modifications sequence 34 AA;
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Best Local :
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Best Local S
Matches
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03-JUL-1996; U1292.

13-JUL-1995; US-001105.

06-SEP-1995; US-003305.

29-MAR-1996; US-626186.

(BIOM-) BIOMEASURE INC.
                                                                                                                                                                                                                                                                                                                                           Dong 2X;
WPI; 97-118819/11.

New variants of human parathyroid hormone 1-34 peptide - which
stimulate bone growth and are used for treatment of osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W17949;
29-JUL-1997 (first entry)
Human parathyroid hormone analogue [Cha24,28,31]hpTH(1-34)NH2.
Osteoporosis; agonist; PTH; human; anti-resorptive therapy;
bone fracture.
                                                                                                                                                                                                                                                                                                                                      bone fracture
Claim 7; Page
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  parathyroid hormone variants useful for treating or preventing bone conditions associated with calcium depletion/resorption, in cases where calcium fixation is required (esp. osteoporosis) or to treat hypoparathyroidism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                            y Match 100.0%;
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hes 8; Conservative
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HNLGKHLN 8
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28
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'note- "Cha"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'label- OTHER
                                                        Score 58; DB 22; L
Pred. No. 7.41e+00;
0; Mismatches 0;
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Pred. No. 7.41e+00;
0; Mismatches 0
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Search completed: Thu Jul 30 10:29:43 1998

Job time : 16 secs.

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MPsrch\_pp on: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:28:51 1998; MasPar time 3.31 Seconds 88.370 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-817-547A-14 (1-8) from US08817547A.pep 58 1 HNLGKHLN 8

Scoring table: PAM 150 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 20.760; Variance 25.957; scale 0.800

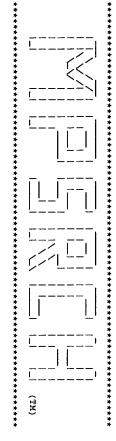
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

1 1 2 3 3 3 3 3 4 4 4 4 7 7 7 7 8 8 8 11 11 11 11 11 11 11 11 11 11 11	sult No.
	Score
100.0 100.0	Query Match
34 34 34 34 35 35 37 37 37 37 37 31 115 115 115 115 215 225 225 225 225 22	Length
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44 75.9 585 2 G64220 ATP-binding protein m 43 74.1 308 5 1AKI ferrochelatase (EC 4. 43 74.1 310 5 1FJI ferrochelatase (EC 4. 43 74.1 310 5 1FJI ferrochelatase (EC 4. 43 74.1 619 2 S54636 probable membrane protein 43 74.1 621 2 S35093 plakoglobin - mouse ( 43 74.1 738 2 S35093 plakoglobin - African 43 74.1 744 A A32905 plakoglobin - African 43 74.1 1021 2 S44644 F3784.7 protein - Cae 42 72.4 180 2 H64310 hypothetical protein 43 74.1 1021 2 S46464 pypothetical protein 42 72.4 243 2 S64361 hypothetical protein 42 72.4 292 2 S64361 hypothetical protein 42 72.4 480 2 F69505 thymidylate synthase 42 72.4 1940 2 S63669 hypothetical protein 42 72.4 1950 2 S12332 ubjquitinprotein H8 41 70.7 417 1 A40968 heat shock protein H8 41 70.7 513 2 S21976 probable RNA-directed 41 70.7 1401 2 S77657 RNA-directed synthase 41 70.7 1444 1 A43377 RNA-directed synthase	45	44	43	42	41	40	39	38	37	36	35	34	ယ္အ	32	<u>3</u>	30	29	28	27	26	25	24
585 2 G64220 ATP-binding pro 308 5 1AK1 ferrochelatase 310 5 1FJI ferrochelatase 310 2 C47045 ferrochelatase 619 2 S54636 probable membra 621 2 S35092 plakoglobin - m 738 2 S35093 plakoglobin - M 748 2 S44644 F3774.7 protein 180 2 H64310 hypothetical pr 243 2 S64361 hypothetical pr 243 2 S64361 hypothetical pr 240 2 S63669 hypothetical pr 241 2 S63669 hypothetical pr 241 2 S12332 ubiquitin -prot 241 1 A40968 heat shock prot 241 1 A40968 heat shock prot 251 2 S21976 probable RNA-di 257657 cyclic peptide 1444 1 A43377 RNA-directed RN	41	41	41	41	41	41	42	42	42	42	42	42	42	43	43	43	43	43	43	43	43	44
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RESULT 2 1ZWE # ENTRY parathyroid ALTERNATE_NAMES HPTH(4-37) PDB_TITLE Structure of structures ORGANISM #formal_name REFERENCE A67860 #authors Roesch, P.; #submission submitted to #cross-references PDB:1ZWE REFERENCE TN001721 #authors in Strukture pp.0, Bayr	Query Match Best Local Simil Matches 8;  Db 9 HNLGKHLN           Qy 1 HNLGKHLN	19-30 SUMMARY	S	REFERENCE A671 #authors Roe. #submission submission references #cross-references TNOO	RESULT 1 ENTRY TITLE ALTERNATE_NAMES PDB_TITLE ORGANISM
parathyroid hormone (residues 4-37) - human HPTH(4-37) structure of human parathyroid hormone fragment 4-37, NMR 10 structures #formal_name Homo sapiens #common_name man A67860 Rossch, P.; Marx, U.G. submitted to the Brookhaven Protein Data Bank, June 1996 ness PDB:1ZWE TN001721 Marx, U.C. in Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth: University of Bayreuth (Thesis), 1996	100.0%; Score 58; DB 5; Length 34; Similarity 100.0%; Pred. No. 1.85e-02; 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0; LGKHLN 16	<pre>#region helix (right hand alpha)\     #region helix (right hand alpha) #length 34 #molecular-weight 4118 #checksum 5629</pre>	Marx, U.C.  Marx, U.C.  in Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0. Bayreuth: University of Bayreuth (Thesis), 1996  Resolution: not applicable Determination: NMR hormone	856 sch, P.; Marx, U.C. plltted to the Brookhaven Protein Dat pDB:1ZWA 01717	12WA #type complete parathyroid hormone (residues 1-34) - human HPTH(1-34) structure of human parathyroid hormone fragment 1-34, NMR 10 structures fragment structures fragment 1-34, NMR 10 structures fragment formal name Homo sapiens #common name man



Psrch\_pp protein - protein database search, using Smith-Waterman algorithm

Thu Jul 30 10:27:45 1998; MasPar time 2.10 Seconds 95.669 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-817-547A-14 (1-8) from US08817547A.pep 58 1 HNLGKHLN 8

Scoring table: PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 21.688; Variance 21.433; scale 1.012

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

45	44	43	42	41	40	39	38	37	3 6	ა 5	34	ω ω	32	ω L	30	29	28	27	26	25	24
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FA5_HUMAN	GP21_RAT	MSH1_YEAST	YSPL_CAEEL	CPT1_RAT	YQZ2_CAEEL	Y187_MYCPN	ST13_SCHPO	Y240_MYCGE	Y240_MYCPN	VIF_HV2D1	YOHD_ECOLI	VPR_HV1N5	CPT1_MOUSE	RRPL_RDV	NAH_YEAST	Y036_HAEIN	CBP2_HUMAN	HS47_HUMAN	HS47_RAT	HS47_MOUSE	HS47_CHICK
COAGULATION FACTOR V P	INTEGRAL MEMBRANE GLYC	MUTS PROTEIN HOMOLOG 1	HYPOTHETICAL 91.0 KD P	MITOCHONDRIAL CARNITIN	HYPOTHETICAL 69.0 KD P	HYPOTHETICAL ABC TRANS	PUTATIVE ATP-DEPENDENT	HYPOTHETICAL PROTEIN M	HYPOTHETICAL PROTEIN M	VIRION INFECTIVITY FAC	HYPOTHETICAL 21.4 KD P	VPR PROTEIN (R ORF PRO	MITOCHONDRIAL CARNITIN	RNA-DIRECTED RNA POLYM	PROBABLE NA(+)/H(+) AN	HYPOTHETICAL ABC TRANS	COLLAGEN-BINDING PROTE	47 KD HEAT SHOCK PROTE			
3.85e+01	2.30e+01																				

	RP SEQUENCE OF 26-37.  RX MEDLINE; 74174967.  RA JACOBS J.W., KEMPER B., NIALL H.D., FRI NATURE 249:155-157(1974).  RN [4]  RN [4]  RN SEQUENCE OF 32-68.  RN MEDLINE; 74111656.  RA NIALL H.D., SAUER R.T., JACOBS J.W., RA NIALL H.D., SAUER R.T., JACOBS J.W., RA O'RIORDAN J.L.H., AUBBACH G.D., POTTE  RA O'RIORDAN J.L.H., AUBBACH G.D., POTTE  RA PROC. NATL. ACAD. SCI. U.S.A. 71:384-  RN [5]	SEQUENCE FROM N.A.  MEDLINE; 82150870.  HENDY G.N., KRONENBERG H.M., POTTS J.  PROC. NATL. ACAD. SCI. U.S.A. 78:736:  [2]  SEQUENCE FROM N.A.  MEDLINE; 83169834.  VASICEK T.J., MCCEVITT B.E., FREEMAN  HENDY G.N., POTTS J.T. JR., RICH A.,  PROC. NATL. ACAD. SCI. U.S.A. 80:2127	SULT 1  PTTY, HUMAN STANDARD; PRT;  P01270;  21-JUL-1986 (REL. 01, CREATED) 21-JUC-1987 (REL. 05, LAST SEQUENCE 13-AUG-1987 (REL. 35, LAST ANNOTATIC PARATHYROID HORMONE PRECURSOR (PARAN PTH. HOMO SAPIENS (HUMAN). EUKARYOTA; METAZOA; CHORDATA; VERTEE EUTHERIA; PRIMATES.
O'RIORDAN J.L.H., , BARLING P.M., HENDY G.N., RADGE R.V., OWEN M., MEDICA FOUNDATION, AMSTERDAM,	LD., HABENER J.F., POTTS J.T. JR.; J.W., KEUTMANN H.T., SEGRE G.V., POTTS J.T. JR.; 1:384-388(1974).	T. JR., RICH A.; ;-7369(1981). M.W., FENNICK B.J., KRONENBERG H.M.; ;-2131(1983).	115 AA. UPDATE) NN UPDATE) HYRIN) (PTH).

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SOURCE STANDS
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A KRONENBERG H.M.;

AL J. CLIN. INVEST. 86:1084-1087(1990).

C. -i- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN

C. -i- DISEASE: DEFECTS IN PTH ARE A CAUSE OF FAMILIAL ISOLATED

C. HYPOPARATHYROLDISM (FIH).

DE EMBL; J00301; G190704; -.

PREMEL; V00597; G37144; -.

PREMEL; V00597; G37144; -.

PREMEL; A29146; E186700; -.

PREMEL; A29146; E186700; -.

PDB; 11HPH; 15-CCT-97.

PDB; 11HPH; 15-CCT-97.

PDB; 12WA; 12-MAR-97.

PDB; 12WA; 12-MAR-97.

PDB; 12WA; 12-MAR-97.

PDB; 12WB; 11-MAR-97.

PDB; 12WB; 12-MAR-97.

PDB; 12WB; 11-MAR-97.

Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 8; Conservative
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VARIANT ARG-18.
MEDLINE; 91009811.
                                                                           CONFLICT
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SYNTHESIS OF
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PROPEP
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MEDLINE; 93345518.
BARDEN J.A., CUTHBERTSON R.M.;
EUR. J. BIOCHEM. 215:315-321(1993).
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MARX U.C., AUSTERMANN
STICHT H., WALTER S.,
ROESCH P.;
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MEDLINE; 91299748.
KLAUS W., DIECKMANN T., WRAY V.,
BIOCHEMISTRY 30:6936-6942(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 75059220.
TREGEAR G.W., VAN RIETSCHOTEN J., GREEN E., NIALL H.D KEUTWANN H.T., PARSONS J.A., O'RIORDAN J.L.H., POTTS HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 355:415-421(1974).
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MEDLINE; 75146516.
KEUTMANN H.T., NIALL H.D., O'RIORDAN J.L.H.,
BIOCHEMISTRY 14:1842-1847(1975).
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                                                                       PARATHYROID HORMONE.

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PROCESSING OF THE PRECU
N -> D (IN REF. 5).

W; 243E87C7 CRC32;
                 Score 58; DB 1;
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RESULT 2

RESULT 2

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DT 21-JUL-190

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DE PARATHYRO:

GN PTH.

OS SUS SCROP;

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RN [1]

RP SEQUENCE |

RA SCHMELZER

RA MEDLINE;

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RA MEDLINE;

RA SEQUENCE |

RA MEDLINE;

RA SCHMERZ

ROTTS J.T

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RA POTTS J.T

RA POSITE;

RA SAUER R.T

BONE

DR PIR; A015

DR PIR; A015

DR PIR; A015

DR PIR; B268

DR PROSITE;

KW HORMONE;

FT SIGNAL

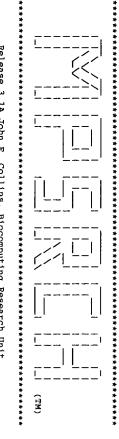
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01-JAN-1988
01-FEB-1996
                                                                                                                                                                                                                                                                     BIOCHEMISTRY 13:1994-1999(1974).

1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING
BONE AND PREVENTING THEIR RENAL EXCRETION.

EMBL; X05722; G1839; -.
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 26-115.

MEDLINE; 76018954.

CHU L.L.H., HUANG W.-Y., LITTLEDIKE
BIOCHEMISTRY 14:3631-3635(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE; 87316938. SCHMELZER H.-J., G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTH.
SUS SCROFA (PIG).
EUKARYOTA; METAZOA;
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Similarity 87.5%;
7; Conservative
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(REL. 05, LAST SEQUENCE UPDATE)
(REL. 3, LAST ANOTATION UPDATE)
HORMONE PRECURSOR (PARATHYRIN) (PTH).
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S. 15:6740-6740(1987).
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MPsrch\_pp on: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:28:08 1998; MasPar time 3.81 Seconds 88.534 Million cell updates/sec

Tabular output not generated

Description: Perfect Score: Title: >US-08-817-547A-14 (1-8) from US08817547A.pep 58 1 HNLGKHLN 8

Sequence:

Scoring table: PAM 150 Gap 15

Searched: 140542 segs, 42109429 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: sptremb15

1:sp\_fungi 2:sp\_human 3:sp\_invertebrate 4:sp\_mammal 5:sp\_mhc 6:sp\_organelle 7:sp\_phage 8:sp\_plant 9:sp\_bacteria 10:sp\_rodent 11:sp\_virus 12:sp\_vertebrate 13:sp\_unclassified

Statistics: Mean 20.802; Variance 21.214; scale 0.981

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result

Result	Score	% Query Match	Length	83	ID	Description	Pred. No.
1	53	91.4	105	10	Q63473	PARATHYROID HORMONE (F	2.85e-02
N	48	82.8	172	ဖ	032112	TRANSCRIPTIONAL REGULA	5.95e-01
ω	45	77.6	381	10	Q62730	17-BETA HYDROXYSTEROID	3.37e+00
4	45	77.6	421	9	028532	HYPOTHETICAL 48.5 KD P	3.37e+00
ر. ن	45	77.6	1817	ω	Q19931	COSMID F31D5.	3.37e+00
O	44	75.9	82	4	Q29248	APOLIPOPROTEIN A-I (FR	5.90e+00
7	44	75.9	96	芦	Q72500	VPR PROTEIN.	5.90e+00
8	44	75.9	301	1	Q70212	ENVELOPE GLYCOPROTEIN,	5.90e+00
9	44	75.9	568	Q	P74405	HYPOTHETICAL 62.3 KD P	5.90e+00
10	43	74.1	123	N	014904	WNT-LIKE PROTEIN WNT14	1.02e+01
11	43	74.1	171	N	Q15093	PLAKOGLOBIN (FRAGMENT)	1.02e+01
12	43	74.1	312	ω	Q22312	COSMID T07E3.	1.02e+01
13	43	74.1	414	w	001906	COSMID F59E12.	1.02e+01
14	43	74.1	619	ᆫ	099234	CHROMOSOME XV READING	1.02e+01
15	43	74.1	745	N	Q15151	PLAKOGLOBIN.	1.02e+01
16	43	74.1	745	10	P70565	PLAKOGLOBIN.	1.02e+01
17	43	74.1	2272	N	015020	KIAA0302 (FRAGMENT).	1.02e+01
18	42	72.4	96	11	P88152	VPR PROTEIN.	1.76e+01
19	42	72.4	283	7	021973	HYPOTHETICAL 31.3 KD P	1.76e+01
20	42	72.4	314	11	Q84584	GENOME, PARTIAL SEQUEN	1.76e+01

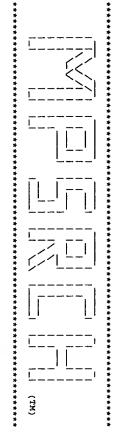
<b>4</b> 5	44	43	42	41	40	39	<u>з</u>	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	1
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			69.0		69.0	70.7	70.7	70.7	70.7	70.7	70.7	70.7	70.7	70.7	70.7	70.7	70.7	70.7	70.7	70.7	72.4	72.4	72.4	12.4
			236		95			1401						502				298			4930			•
N	10	9	2	9	11	N	11	ø	10	<b> </b>	μ	<b>ja</b>	10	9	12	ω	10	ш	φ	4	9	ب	œ	u
000578	035288	P77814	Q15430	025653	037116	Q13535	Q98631	Q50177	P97692	P78585	013705	000061	Q63289	006585	Q90420	018326	Q63778	013669	Q55024	Q29179	031783	209140	P93820	040404
KIAA0167.	IXOLIV	PROLIDASE (EC 3.4.13.9	COAGULATION FACTOR V (	SITE-SPECIFIC RECOMBIN	ENVELOPE GLYCOPROTEIN	FRAP-RELATED PROTEIN (	RNA-DEPENDENT RNA POLY	PROBABLE CYCLIC SYNTHE	L1 RETROTRANSPOSON ORF	PHOSPHOINOSITIDE-SPECI	HYPOTHETICAL 95.0 KD P	CYTOCHROME P-450 MONOO	L1 RETROPOSON, ORF2 MR	HYPOTHETICAL 53.5 KD P	47 KDA HEAT SHOCK PROT	HUNCHBACK GAP (FRAGMEN	HYPOTHETICAL 43.7 KD P	BASIC TRANSCRIPTION FA	NUTRIENT-STRESS INDUCE	CARNITHINE PALMITOYLTR	POLYKETIDE SYNTHASE OF	UDP-GLC:GLYCOPROTEIN G	HYPOTHETICAL 110.0 KD	INIMIDIDATE SINIMAGE,
5.05e+01	5.05e+01	5.05e+01	5.05e+01	5.05e+01	5.05e+01	•	٠	3.00e+01			3.00e+01	3.00e+01	3.00e+01		3.00e+01	3.00e+01	3.00e+01		3.00e+01	3.00e+01	1.76e+01	1.76e+01		T. / 00TO.

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RESULT COMMENTS OF THE COMMENT OF TH
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

TISSUE-THYROID, AND PARATHYROID;
SCHMELZER H.J., GROSS G., MAYER H.;
SCHMELZER TECHNOL. 21:228-229(1984).
EMBL; M54875; G601933; -.
NON_TER 1
SEQUENCE 105 AA; 11746 MW; 6AC3163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q63473;
Q63473;
Q1-NOV-1996
Q1-NOV-1996
Q1-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LT 2
22112 PRELIMINARY; PRT; 172 AA.
032112;
01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
TRANSCRIPTIONAL REGULATOR.
SEQUENCE FROM N.A.
STRALN=168;
KUNST F., OGASAWARA N., MOSZER I., ALBERTINI A.M., ALLONI G.,
AZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,
                                                                                                                                                                                                                                                                                                PROKARYOTA; FIRMICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PARATHYROID HORMONE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                            BACILLUS SUBTILIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 HNLGKHL 36
||||||
1 HNLGKHL 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   y Match 91.4%;
Local Similarity 100.0%;
les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TREMBLREL. 01, CREATED)
(TREMBLREL. 01, LAST SEQUENCE UPDATE)
(TREMBLREL. 05, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                            ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 53; DB 10; Le
Pred. No. 2.85e-02;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6AC3163E CRC32;
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Search completed: Thu Jul 30 10:28:33 1998 Job time : 25 secs.
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                                                                                                                                                                                             Query Match 82.8%; Score 48; DB 9; Length 172; Matches 6; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

STRAIN-168;
KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
KUNST TEL, OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; 299120; E1164294;
EMBL; 299120; E1164294;
SEQUENCE 172 AA; 20015 MW; 2AA7F8CE CRC32;
                                                                                                                                                          105 HGLGKHL 111
                                                                                                                           1 HNLGKHL 7
                                                                                                                                                                                                0;
                                                                                                                                                                                      Gaps
                                                                                                                                                                                      0
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Psrch\_pp protein - protein database search, using Smith-Waterman algorithm

on :: Thu Jul 30 10:31:15 1998; MasPar time 2.62 Seconds 40.993 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Title: (1-7) from US08817547A.pep 53 >US-08-817-547A-15

Sequence: 1 HNLGKHL 7

Scoring table: PAM 150 Gap 15

124785 seqs, 15338987 residues

Post-processing: Minimum Match Listing first 0% 45 summaries

Database:

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 14.515; Variance 42.487; scale 0.342

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

11111111111111111111111111111111111111	Result No.
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	Score
111111111111111111111111111111111111111	Query Match
22 22 22 22 22 22 22 22 22 22 22 22 22	Query Match Length
200 200 200 200 200 200 200 200 200 200	BB
R22064 R62432 R8624310 W1481310 W153673 R415482 R41576 R41576 R34366 R343667 W117958 W117958 W117958 R74444 R74444 R744444 R744444 R74503 R74503 R58242	IJ
Modified hPTH(7-34)NH Accelerator peptide b Human parathyroid hor Cyclic parathyroid hormone/p Parathyroid hormone/p Parathyroid hormone/p Parathyroid hormone/p Parathyroid hormone/p [Lys16]hPTH (1-34)NH2 Human parathyroid hor Human parathyroid hor Human parathyroid hor Human parathyroid hor Parathyroid hormone p	Description
9.01e+00 9.01e+00 9.01e+00 9.01e+00 9.01e+00 9.01e+00 9.01e+00 9.01e+00 9.01e+00 9.01e+00 9.01e+00 9.01e+00 9.01e+00 9.01e+00 9.01e+00	Pred. No.

Query Match 100.0%; Best Local Similarity 100.0%; Matches 7; Conservative

Length

Indels

0

Gaps

0

45	44	43	42	41	40	9	38	37	36	3 5	34	<b>ω</b>	32	<b>3</b>	30	29	28	27	26	25	24	23	22	21	20
53	53	53	53	53	53	53	53	53	υ G	5 3	53	53	53	53	53	53	53	53	53	53	53	53	53	53	53
•	8	8	8	8	8	00.	8	8	8	80.	8	8	8	8	8	8	100.0	8	8	8	8	80.	٠	8	00.
115	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	78	44	38	38	38	38	38	38	36
4	4	4	4	4	4	4	7	7	4	4	4	4	4	7	4	27	σ	26	19	თ	9	φ	9	9	9
P40209	R23452	R21212	R23472	R21176	R23318	R23519	R34453	R34452	R23261	R21195	R23356	R23402	R21215	R34458	R23293	W25687	R30859	P30015	895	P20248	815	R58152	R58156	R58161	822
	Porcine parathyroid h	Human parathyroid hor	Porcine parathyroid h	Human parathyroid hor	Bovine parathyroid ho	Bovine parathyroid ho	Human parathyroid hor	Bovine parathyroid ho	Bovine parathyroid ho	Human parathyroid hor	Bovine parathyroid ho	_	Human parathyroid hor	Bovine parathyroid ho	ጠ	μ	~	parathyro	-	Ř	-hPTH(1-	[Arg22]-hPTH(1-38)-OH	[Leu27]-hPTH(1-38)-OH	[Pro3,Thr33]-hPTH(1-3	[Nle8,18,27]-hPTH(1-3
	•	9.01e+00	•	.016					•					•		9.01e+00	9.01e+00	•		9.01e+00	•	9.01e+00	9.01e+00	9.01e+00	9.01e+00

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osteoporosis and hyperparathyroidism.

Claim 1; Column 10; 6pp; English.

The peptide is modified at Lys13 (of the parent PTH) in the epsilon amino acid gp. by N,N-diisobutyl or 3-phenylpropanoyl. The PTH analogue binds with high affinity to the peptide hormone receptor without activating the 2nd messenger mol. The modification of the Lys residue stabilises the bioactive conformation of PTH to enhance the activity. The peptide may be used in in vitro bioassays to measure naturally occurring PTH and to diagnose the etiology of or to treat hyperthyroidism and diseases caused by abberrent produ. of hormone-like substances, such as tumours. It may also be used to treat immune diseases such as inflammation. It is prepd. by solid
                                                                                                                                                                                                                                                                                                                                                                                                         US5093233-A.
03-MAR-1992.
25-APR-1990; 514394.
25-APR-1990; US-514394.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified hPTH(7-34)NH2.
Parathyroid hormone; analogue; osteoporosis; hyperthyroidism; tumours; hypercalcaemia; renal failure; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R22064;
14-JUL-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R22064 standard; Protein;
                                                               Sequence
                                                                               phase synthesis.
See also R22058-75.
                                                                                                                                                                                                                                                                                                                          New parathyroid hormone analogues - useful for treatment and vitro diagnosis of PTH-dependent tumours, immune disorders,
                                                                                                                                                                                                                                                                                                                                                            WPI; 92-096233/12.
                                                                                                                                                                                                                                                                                                                                                                           (MERI ) MERCK & CO INC. Rosenblatt M, Roubini E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified_site
                                                               28 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "OTHER = see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label- NH2
                                                                                                                                                                                                                                                                                                                                                                             Chorev M, Nutt RF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28
Score 53; DB 4; Leng
Pred. No. 9.01e+00;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₽
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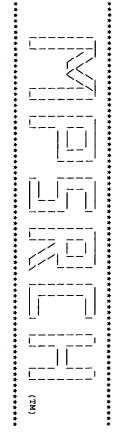
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Search completed: Thu Jul 30 10:31:31 1998 Job time: 16 secs.
                                                                         Š
                                                                                                           밁
                                                                                                                                                                                                                RESULT
1 R62432; standard; peptide; 34 AA.
AC R62432;
DT 31-UTL-1995 (first entry)
DE Accelerator peptide basic region peptide, P-8.
Accelerator; basic amino acid; cell growth factor; growth; gingiva;
KW Accelerator; basic amino acid; cell growth factor; growth; gingiva;
KW down growth; epithelium; fibre adhesion; cement.

OS Synthetic,
PN J06334653-A.
PD 23-AUG-1994.
PF 10-FEB-1993; J0-045998.
10-FEB-1993; JP-045998.
10-FEB-1993; JP-045998.
PR 10-FEB-1993; JP-045998.
10-FEB-1993; JP-045998.
PR 10-FEB-1993; JP-045998.
10-FEB-1993; JP-045998.
CSUNZ) SUNSTAR CHEM IND CO LTD.
WPI; 95-157631/21.
Accelerator for regenerating periodontal tissue - comprises
PT aminoacid residues
PT peptide having 3-34 aminoacid residues having connected basic
CC The sequences in R62423-36 are peptide fragments of an accelerator
CC also comprises a cell growth factor. The accelerator may be used to
CC accelerator is applied by opening the gingiva, treating the tissue
CC destroyed by periodontitis and applying the accelerator in the
CC destroyed by periodontitis and applying the accelerator in the
CC epithelium and accelerates fibre adhesion and regenerates cement.

SQ Sequence 34 AA;
                                                                                                                                 Query Match

Best Local Similarity 100.0%;

Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      å
                                                                 9 hnlgkhl 15
|||||||
1 HNLGKHL 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 hnlgkhl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                            Score 53; DB 26; Le
Pred. No. 9.01e+00;
0; Mismatches 0;
                                                                                                                                                             Length 34;
                                                                                                                            Indels
                                                                                                                          0;
                                                                                                                      Gaps
                                                                                                                      0;
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Psrch\_pp protein - protein database search, using Smith-Waterman algorithm

n on: Thu Jul 30 10:30:52 1998; MasPar time 4.09 Seconds 62.524 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Title: >US-08-817-547A-15 (1-7) from US08817547A.pep 53 1 HNLGKHL 7

Sequence:

Scoring table: PAM 150 Gap 15

Searched: 120441 segs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 20.217; Variance 24.497; scale 0.825

Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

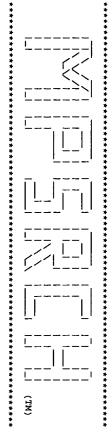
### SUMMARIES

20 21														æ	7	o	u	4	w	N	<b>_</b>	sult No. Score
			43							53	53	5	53	53	53	53	<b>ω</b>	53	53	53	53	re
2	81.1			83.0			94.3		100.0	100.0	100.0	•	100.0	٠	100.0	100.0	100.0	100.0	100.0	100.0	100.0	Query Match Length
2	744	738	621	585	172	172	34	115	115	115	115	115	105	37	37	36	35	34	34	34	34	
s	N	N	N	N	N	N	σı	۳	_	_	2	N	N	ഗ	ហ	U	ഗ	ഗ	ഗ	u	σı	B
	A32905	S35093	S35092	G64220	E69671	A35145	1HTH	PTPG	PTBO	PTHU	A05091	JC4202	151851	12WC	1HPH	12WB	1ZWD	12WA	12WE	12WF	1ZWG	Ħ
Ė	a a	plakoglobin – African	plakoglobin - mouse (	ATP-binding protein m			4	hormone	hormone	parathyroid hormone p	parathyroid hormone p	parathyroid hormone -	parathyroid hormone -	parathyroid hormone (	_	parathyroid hormone (	_	parathyroid hormone (	-	parathyroid hormone 4	parathyroid hormone 4	Description
<b>—</b>	<u></u>	1.91e+01	1.91e+01	_ ⊢	 	. 1.62e+00		_	) 1.17e-01	۲.	.17€	1.17e-01	1.17e-01	1.17e-01	1.17e-01	1.17e-01	1.17e-01	1.17e-01	1.17e-01	1.17e-01	1.17e-01	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
40	40	40	40	40	40	40	40	40	40	40	41	41	41	41	41	41	41	41	41	42	42
75.5	75.5	75.5	75.5	75.5	75.5	75.5	75.5	75.5	75.5	75.5	77.4	77.4	77.4	77.4	77.4	77.4	77.4	77.4	77.4	79.2	79.2
1447	1444	1401	773	513	421	292	291	209	180	160	4930	568	418	417	417	417	405	386	246	619	480
N	۳	N	N	N	N	N	N	N	N	N	N	N	N	۲	_	1	ب	N	N	N	N
S63669	A43377	S77657	A46627	S21976	E69467	E64226	S73826	D35119	H64310	S58066	E69679	S76244	I52968	S20608	A40968	A42843	A41252	D42528	S01789	S54636	F69505
UDPglucoseglycoprot	RNA-directed RNA poly	cyclic peptide synthe	carnitine palmitoyltr	probable RNA-directed		hypothetical protein	MG240 homolog F10_orf	protocatechuate 3,4-d	hypothetical protein	probable olfactory re	polyketide synthase p	hypothetical protein	colligin-2 - human	heat shock protein Hs	heat shock protein 47	heat shock protein Hs	heat shock protein 47	B23R protein - vaccin	pyruvate formate-lyas	probable membrane pro	thymidylate synthase
7.71e+01	7.71e+01	7.71e+01	7.71e+01	7.71e+01	7.71e+01	7.71e+01	7.71e+01	7.71e+01	7.71e+01	7.71e+01	4.89e+01	4.89e+01	4.89e+01	4.89e+01	4.89e+01	4.89e+01	4.89e+01	4.89e+01	4.89e+01	3.07e+01	3.07e+01

RESULT 2 ENTRY TITLE ALTERNATE_NAMES PDB_TITLE ORGANISM REFERENCE #authors #submission #cross refere #authors #authors #book	Db 6 HNLGKHL         Qy 1 HNLGKHL	Query Match Best Local Simi Matches 7;	FEATURE 2-9 15-25 SUMMARY	COMMENT RESOL COMMENT Deter KEYWORDS	#cross-refere REFERENCE #authors #book	REFERENCE #authors #submission	ALTERNATE_NAMES PDB_TITLE ORGANISM	RESULT 1 ENTRY TITLE
ULY 2  IZWF #type complete  RY parathyroid hormone 4 37 mutant N-TERMINAL ACETYLATED -  Synthetic Synthetic  ERNATE_NAMES n-acetyl-hyth(4-37)  _TITLE NMR, 10 structures  ANISM #formal_name synthetic  ERENCE A67742  #authors Roesch, P.; Marx, U.C.  #submission submitted to the Brookhaven Protein Data Bank, June 1996  #cross-references PDB:1ZWF  TN003318  #authors Marx, U.C.  #submission submitted to the Brookhaven Protein Data Bank, June 1996  #cross-references PDB:1ZWF  TN003318  #authors Notukturen Verschiedener Parathormonfragmente in Loesung,  #book in Strukturen Verschiedener Parathormonfragmente in Loesung,	II. 12 	Query Match 100.0%; Score 53; DB 5; Length 34; Best Local Similarity 100.0%; Pred. No. 1.17e-01; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	<pre>#region helix (right hand alpha)\ #region helix (right hand alpha) #length 34 #molecular-weight 4128 #checksum 5508</pre>	pp.0, Bayreuth: University of Bayreuth (Thesis), 1996 Resolution: not applicable Determination: NMR disease mutation; hormone; signal		A67743 Roesch, P.; Marx, U.C. submitted to the Brookhaven Protein Data Bank, June 1996	<pre>synthetic n-succinyl-hpth(4-37) succinyl-hpth(4-37) succinyl human parathyroid hormone 4-37, NMR, 10 structures #formal_name synthetic</pre>	12WG #type complete parathyroid hormone 4 37 mutant N-TERMINAL SUCCINYLATED -

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COMMENT
COMMENT
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RESOLUTION: not applicable
COMMENT
REWORDS
PEATURE
PATURE
14-27
SIMMARY
Query Match
Matches 7;
Conservative
Db 6 HNLCKHL 12
Qy 1 HNLCKHL 17
Search completed: Thu Jul 30 10:30:57 1998
Tob time: 5 secs.
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Psrch\_pp on: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:30:01 1998; MasPar time 2.13 Seconds 82.367 Million cell updates/sec

Tabular output not generated.

Title:
Description:
Perfect Score:
Sequence: >US-08-817-547A-15 (1-7) from US08817547A.pep 53 1 HNLGKHL 7

Scoring table: PAM 150 Gap 15

Searched: 69111 segs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 21.123; Variance 20.163; scale 1.048

### SUMMARIES

sult	Sco	Query Match		1	ID PTHY_BOVIN	Description PARATHYROID HORMONE PR	Pred. No. 8.04e-03
	3 2 53		115	<b></b>			z z z :
	53		115	<b>–</b> ,	PTHY_RAT	٠.	
	5 53		115	_	PTHY_HUMAN	HORMONE	
	6 48		171	_	PAIA_BACSU	PROTEASE SYNTHASE AND	
	7 44	83.	585	_	Y187_MYCGE	HYPOTHETICAL ABC TRANS	
	8 43	81.1	621	٢	PLAK_MOUSE	JUNCTION PLAKOGLOBIN (	
			738	1	PLAK_XENLA	JUNCTION PLAKOGLOBIN (	
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L			1021	_	YPT7_CAEEL	HYPOTHETICAL 111.7 KD	
_		79.2	246	۲	SR1A_PHYPO	SPHERULIN 1A PRECURSOR	
<b></b>		79	381	1	DHB2_MOUSE	ESTRADIOL 17 BETA-DEHY	
<b>_</b>	4 41	77.4	105	بر	YBXF_STAAU	PROBABLE RIBOSOMAL PRO	
_		77.4	245	-	PFLA_ECOLI	PYRUVATE FORMATE-LYASE	
<u></u>		77.4	386	ب	VC17_VACCC	PROTEIN C17/B23.	
_	7 41	77.4	405	۲	HS47_CHICK	47 KD HEAT SHOCK PROTE	
_	8 41	77.4	417	۲	HS47_RAT	47 KD HEAT SHOCK PROTE	
_	9 41	77.4	417	بر	HS47_MOUSE	47 KD HEAT SHOCK PROTE	
N	0 41	77.4	417	Н	HS47_HUMAN		
N	1 41	77.4	418	_	CBP2_HUMAN		
N	22 40	75.5	40	_	CPT1_MOUSE	MITOCHONDRIAL CARNITIN	
N	3 40	75.5	96	س	VPR_HV1N5	VPR PROTEIN (R ORF PRO	

40 75.5 180 1 YOSM_METJA HYPOTHETICAL PROTEIN M 40 75.5 299 1 Y240_MYCPU HYPOTHETICAL PROTEIN M 40 75.5 291 1 Y240_MYCPU HYPOTHETICAL PROTEIN M 40 75.5 292 1 Y240_MYCPU HYPOTHETICAL PROTEIN M 40 75.5 586 1 Y187_MYCPU HYPOTHETICAL ABC TRANS 40 75.5 614 1 YOZZ_CAEEL HYPOTHETICAL ABC TRANS 40 75.5 614 1 YOZZ_CAEEL HYPOTHETICAL CARNITIN 40 75.5 773 1 CPTI_RAT MITOCHONDRIAL CARNITIN 40 75.5 1444 1 RRPL_RDV MITOCHONDRIAL CARNITIN 40 75.5 1444 1 YOZZ_CAEEL HYPOTHETICAL PROTEIN M 39 73.6 135 1 Y315_METJA HYPOTHETICAL PROTEIN M 39 73.6 192 1 YOHD_ECOLI HYPOTHETICAL TRANSCRIP 39 73.6 251 1 YOHD_ECOLI HYPOTHETICAL TRANSCRIP 39 73.6 251 1 YOHD_ECOLI HYPOTHETICAL TRANSCRIP 39 73.6 251 1 YOHD_ECOLI HYPOTHETICAL TRANSCRIP 39 73.6 330 1 RCEM_ERYSP REACTION CENTER PROTEIN 39 73.6 416 1 CCA_HAEIN TRANS PRACTIOR YENG METALLO 39 73.6 188 1 YSPL_CAEEL HYPOTHETICAL 91.0 KD P 39 73.6 1886 1 GP21_RAT INTEGRAL MEMBRANE GLYC 39 73.6 2224 1 FAS_HUMAN CAGGUATION FACTOR V P	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
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1 Y088 METJA 1 PCXA_ACICA 1 Y240_MYCPA 1 Y240_MYCGE 1 Y187 MYCGE 1 Y187 MYCGE 1 Y187 MYCGE 1 Y072_CAEEL 1 CPT1_RAT 1 CPT1_RAT 1 RTL_HAEIN 1 Y315 METJA 1 Y51L_HAEIN 1 Y0HD_ECOLI 1 Y0FL_HY2D1 1 Y07H_MYCTU 1 Y07H_MYCTU 1 Y07H_BCSU 1 Y07H_MTTTU 1 Y07H_ATTTGA 1 YSPL_CAEEL 1 YSPL_CAEEL 1 YSPL_CAEEL 1 YSPL_CAEEL 1 GP21_RAT 1 GP21_RAT 1 GP21_RAT	73.6				•	•	•	•	•	•	•	73.6	73.6	73.6	75.5	75.5	75.5	75.5	75.5	75.5	75.5	75.5
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	COAGULATION FACTOR V P	INTEGRAL MEMBRANE GLYC	LAMININ ALPHA-3 CHAIN	HYPOTHETICAL 91.0 KD P	PUTATIVE VENOM METALLO	TRNA NUCLEOTIDYLTRANSF	3-DEHYDROQUINATE SYNTH	REACTION CENTER PROTEI	HYPOTHETICAL 34.0 KD P		VIRION INFECTIVITY FAC				RNA-DIRECTED RNA POLYM	MITOCHONDRIAL CARNITIN					PROTOCATECHUATE 3,4-DI	

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	SHOULENCE OF 32-115	S Z. PHYSIO	AURBACH G.D., POTTS J.T. JR.;	CATTER D. HOCAN K. T. DANGOW D	SEQUENCE OF 32-115.	PROC. NATL. ACAD. SCI. U.S.A. /1:653-656(1974).	D.V.;		MEDLINE: 74142666.	[5]	E 28:319-329(1984).	WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;	MEDITUE BADDARS	EBOM N A	. CELL. ENDOCRINOL. 28:	.A., GORDON D.	MEDLINE; 83105964.	UENCE	[3]	WART ACADON C.F., ARME		SEQUENCE FROM N.A.		PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).	T M TO STOUR A .	B F MA.TZOTIB		[1]	ARTIODACTYLA.	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	BOS TAURUS (BOVINE).	THE TOTAL PROPERTY OF THE PROP	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).	(REL. OL,	01, CREATED)	P01268;	PTHY_BOVIN STANDARD; PRT; 115 AA.	LT 1

BREWER H.B. JR., RONAN R.; PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).

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RESULT
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AC PE
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, PTHY_CANFA STANDARD;
, PTS2212;
T 01-0CT-1996 (REL. 34, CREATED)
JT 01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
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Best Local S
Matches
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A POTTS J.T. JR., TRECEAR G.W., KEUTMANN H.T., NIALL H.D., SAUER R.,

B DEFTOS L.J., DAWSON B.F., HOGAN M.L., AUBBACH G.D.;

L PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).

C I- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN

C BONE AND PREVENTING THEIR RENAL EXCRETION.

PREMBL; V00106; G85; -.

R EMBL; V00124; E18249; ALT_SEQ.

DR EMBL; J00024; E18249; ALT_SEQ.

DR EMBL; C01938; G163643; -.

DR EMBL; C01938; G163645; -.

DR EMBL; M10024; E18249; ALT_INIT.

DR EMBL; M10024; E18249; ALT_INIT.

DR EMBL; M10024; E18249; ALT_INIT.

DR EMBL; M1004; PTBO.

DR PIR; A01534; PTBO.

PRIR; A01534; PTBO.
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HORMONE;
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TISSUE-PARATIYROID;
MEDLINE; 95369696;
ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,
DEWILLE J.W., CAPEN C.C.;
GENE 160:241-243(1995).
-i- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS
BONE AND PREVENTING THEIR RENAL EXCRETION.
EMBL; U15662; G558916; -
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HORMONE: SIGNAL.
SIGNAL 1
PROPEP 26
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CONFLICT
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
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115 AA;
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31
115 PARATHYROID HORMONE.
106 V -> G (IN REF. 4).
AA; 12980 MW; 673EA5F2 CRC32;
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31 B
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BY SIMILARITY.
PARATHYROID HORMONE.
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Pred. No. 8.04e-03;
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Search completed: Thu Jul 30 10:30:06 1998 Job time : 5 secs.

00.0 105 10 10.6 172 9 10.6 171 2 11.1 171 2 11.1 745 2 11.1 745 10 11.1 2272 1 12.1 2272 1 13.1 23 1 14.1 2272 1 15.1 2272 1 16.1 2272 1 17.4 10 17.4 10 17.4 20 17.4 20 17.4 40 17.4 40 17.4 40 18.5 568 9 17.4 40 18.5 568 9 19.5 568 9	pred. No. is the number of res score greater than or equal to and is derived by analysis of sum Result Query No. Score Match Length DB ID	Database: sptremb15 1:sp_fung1 2:sp_huma 5:sp_mtc 6:sp_organe 9:sp_bacteria 10:sp_ 13:sp_unclassified Statistics: Mean 20.260; Variance	Title: SUS-08-817-547A-15 Description: (1-7) from USO8817547A. Perfect Score: 53 Sequence: 1 HNLGKHL 7  Scoring table: PAM 150 Gap 15 Searched: 140542 seqs, 42109429 r Post-processing: Minimum Match 0% Listing first 45 summar	Release 3.1A John F. Collins Copyright (c) 1993-1998 Uni Distribution rights Distribution rights non:  Thu Jul 30 10:30:24 1 Tabular output not generated.	
PARATHYROID HORMONE (F 1.38e-0 TRANSCRIPTIONAL REGULA 3.17e-0 VPR PROTEIN. 3.38e+0 PLAKOGLOBIN (FRAGMENT) 5.98e+0 PLAKOGLOBIN (FRAGMENT). 5.98e+0 PLAKOGLOBIN. 5.98e+0 PLAKOGLOBIN. 5.98e+0 PLAKOGLOBIN. 5.98e+0 PLAKOGLOBIN. 5.98e+0 PROTEIN WNT14 1.05e+0 WNT-LIKE PROTEIN WNT14 1.05e+0 WNT-LIKE PROTEIN WNT14 1.05e+0 HYPOTHETICAL 11.0 KD 1.05e+0 HYPOTHETICAL 11.0 KD 1.05e+0 HYPOTHETICAL 31.3 KD P 1.82e+0 PCLYKETIDE SYNTHASE OF 1.82e+0 POLYKETIDE GLYCOPROTEIN 3.12e+0 GNYELOPE GLYCOPROTEIN 3.12e+0	results predicted by chance to have a to the score of the result being printed, of the total score distribution.  SUMMARIES  D Description Pred. No.	<pre>p_human 3:sp_invertebrate 4:sp_mammal organelle 7:sp_phage 8:sp_plant 10:sp_rodent 11:sp_virus 12:sp_vertebrate fied riance 20.374; scale 0.994</pre>	7547A.pep 9429 residues summaries	, Biocomputing Research Unit. versity of Edinburgh, U.K. by Oxford Molecular Ltd search, using Smith-Waterman algori search, using 3.61 Seconds 998; MasPar time 3.61 Seconds 81.661 Million cell updates/se	(ME)

45	44	43	42	41	40	39	38	37	36	35 5	34	33	32	31	30	29	28	27	26	25	24	23	22	7.1
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MODIFICATION METHYLASE	PREPRO-HALYSTATIN PREC	BETA-B PROTEIN.	EN-2/LACZ FUSION PROTE	COSMID F31D5.	UDP-GLC:GLYCOPROTEIN G	RNA-DEPENDENT RNA POLY	PROBABLE CYCLIC SYNTHE	WERNER SYNDROME.	L1 RETROTRANSPOSON ORF	93.7 KD	HYPOTHETICAL 95.0 KD P	CARNITINE PALMITOYLTRA	HOMOLOG OF HUMAN WERNE	MOBILISATION PROTEIN.	KIAA0134 PROTEIN (KIAA	RELAXASE.	, ORF2 M	C 3.4.	.5 XD	HYPOTHETICAL 43.7 KD P	OLFACTORY RECEPTOR 33	VPR PROTEIN.	VPR PROTEIN.	ISOLATE NYS, COMPLETE
	•	٠	٠		3.12e+01	3.12e+01			L			٠	٠		3.12e+01	<u></u>	3.12e+01	3.12e+01	3.12e+01	3.12e+01	3.12e+01	3.12e+01	3.12e+01	3.12e+01

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RESULT 1
063473;
DO 063473;
AC 053473;
AC 053473;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
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DE PARATTUS NOBVEGICUS (RAT).

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RA BROUILLET S., BRUSCHI C.V., CALDWELL B., CAPUANO V., CARTER N.M.,
RA CHOI S.K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J., DANIEL R.A.,
RA CHOI S.K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J., DANIEL R.A.,
RA DENIZOT F., DEVINE K.M., DUSTERHOFT A., EHRLICH S.D., EMMERSON P.T.,
RA ENTIAN K.D., ERRINGTON J., FABRET C., FERRARI E., FOULGER D., FRITZ C.,
RA GLASER P., GOFFERNU A., GOLIGHTLY E.J., GRANDI G., GUISEPPI G., GUY B.J.,
RA HAGA K., HAIECH J., HARWOOD C.R., HENAUT A., HILBERT H., HOLSAPPEL S.,
RA KASAHARA Y., KLAERR-BLANCHARD M., KLEIN C., KOBAYASHI Y., KOETTER P.,
RA KASAHARA Y., KLAERR-BLANCHARD M., KLEIN C., KOBAYASHI Y., KOETTER P.,
RA KASAHARA Y., KLAERR-BLANCHARD M., KURITA K., LAPIDUS A., LIU H.,
RA MASUDA S., MAUGEL C., MEDIGUE C., MEDINA N., MELLADOR R.P., MIZUNO M.,
RA MASUDA S., MAUGEL C., MEDIGUE C., MEDINA N., MELLADOR R.P., MIZUNO M.,
RA MOESTL D., NARAI S., NOBACK M., NOONE D., O'REILLY M., OGAWA K.,
RA POWOLLIK S., PRESCOTT A.M., PRESECAN E., PUJIC P., PURNELLE D.,
RA ROCHE B., ROSE M., RADAIE Y., SATO T., SCANLAN E., SCHLEEICH S.,
RA SCHROETER R., SCOFFONE F., SERIGUCHI J., SEKOWSKA A., SEROR S.J.,
RA SCHROETER P., TAKEMARU K., TAKEUCHI M., TAMAKOSHI A., TANAKA T.,
TAKAHASHI H., TAKEMARU K., TAKEUCHI M., TAMAKOSHI A., TANAKA T.,
VANNIER F., VASSAROTTI A., VIARI A., WEDLER E., WEDLER H.,
RA YASUMOTO K., YATA K., YOSHIDA K., YOSHIKAWA H.F., ZUMSTEIN E.,
RA YOSHIKAWA H., DANCHIN A.,
RA YASUMOTO K., YATA K., YOSHIDA K., YOSHIKAWA H.F., ZUMSTEIN E.,
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RA YOSHIKAWA H., DANCHIN A.,
RA YASUMOTO K., YATA K., YOSHIDA K., YOSHIKAWA H.F., ZUMSTEIN E.,
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RA YOSHIKAWA H., DANCHIN A.,
RA YASUMOTO K., YATA K., YOSHIDA K., YOSHIKAWA H.F., ZUMSTEIN E.,
RA YOSHIKAWA H., DANCHIN A.,
                                                                                                     Best Local Similarity 85.7%;
Matches 6; Conservation
                                                                                                                                                                                                          KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; Z99120; E1184294; -.
SEQUENCE 172 AA; 20015 MW; 2AA7F8CE CRC32;
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-168;
                                105 HGLGKHL 111
1 HNLGKHL 7
                                                                                                  Score 48; DB 9; L
Pred. No. 3.17e-01;
0; Mismatches 1
                                                                                                                                                       Length 172;
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Search completed: Thu Jul 30 10:30:35 1998 Job time: 11 secs. Ş В

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Psrch\_pp 92: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:33:38 1998; MasPar time 2.52 Seconds 36.475 Million cell upda

cell updates/sec

Tabular output not generated

Description: Title: >US-08-817-547A-16 (1-6) from US08817547A.pep 45

Sequence: Perfect Score: 1 HNLGKH 6

Scoring table: PAM 150 Gap 15

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 13.446; Variance 33.754; scale 0.398

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result
<b></b>	Score
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R91656 R62840 R628433 R34339 R88834 R07291 R07291 R727291 R727291 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74521 R74522 R74522 R74522 R74522 R74522 R74522 R74522 R74522 R74522 R74522 R74522 R74522 R74522 R74522 R74522 R74522 R74522 R74522 R7452 R74522 R74522 R74522 R74522 R74522 R74522 R74522 R74522 R74522 R74522 R74522 R74522 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7452 R7	Π
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1. 82e+01 1. 82e+01	Pred. No.

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P80305	R21212	R23468	R23280	R23413	R23285	R23513	R23284	R23274	R23393	R23291	39	R21154	S	R29564	R23287	R23449	N	R23357	W25687	P30015	R58036	R58283	P20248	R58238	R58257
	Human parathyroid hor	Porcine parathyroid h	Bovine parathyroid ho	Porcine parathyroid h	Bovine parathyroid ho	parathyroid	Bovine parathyroid ho	5	Porcine parathyroid h	Bovine parathyroid ho	Porcine parathyroid h	Human parathyroid hor	Oxidation resistant [	Oxidation resistant [	Bovine parathyroid ho	Porcine parathyroid h	Bovine parathyroid ho	Bovine parathyroid ho		Human parathyroid hor	[Gln16]-hPTH(1-38)-OH	]-hPTH(1	ř.	[D-Asp30]-hPTH(1-36)-	ř
			1.82e+01			-					-		1.82e+01		÷		1.82e+01			1.82e+01			1.82e+01		

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Best Local S
Matches
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DE4434551-A1.

04-APR-1996.

28-SEP-1994; 434551.

28-SEP-1994; DE-434551.
R88840;
07-OCT-1996 (first entry)
07-OCT-1996 (first entry)
Human parathyroid hormone analogue, [Leu27]-hPTH(1-32)-NH2.
Parathyroid hormone; PTH; analogue; osteoporosis; bone cell
Parathyroid regulation; reduced PKC activity; protein kinase C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 96-180391/19.

New antigenic peptide(s) from human parathyroid hormone - and antibodies generated using them, able to distinguish between active and inactive forms of the hormone claim 2; Page 5; 5pp; German.

The present sequence is a specific example of claimed immunogenic peptides having a sequence from hPTH(1-37) which includes the N-octoreminal alpha-helical region and/or the non-structured region of the hormone. Antibodies and their binding fragments generated by injecting an animal with the peptides are useful as diagnostic reagents for determination of biologically active hPTH(1-37). Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R91656 standard; peptide; 9 AA.
R91656;
R91656;
R06.NOV-1996 (first entry)
Human parathyroid hormone antigenic peptide hPTH 9-17.
Human parathyroid hormone; hPTH; antigen; alpha-helix;
diagnosis; active hPTH 1-37.
                                                                                                                                                                                                                  R88840 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adermann K, Forssmann W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (FORS/) FORSSMANN W.
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||||||
1 HNLGKH 6
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Local Similarity 100.0%;
hes 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 45; DB 18;
Pred. No. 1.82e+01;
0; Mismatches 0
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                               bone cell;
kinase C;
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Search completed: Thu Jul 30 10:33:53 1998 Job time: 15 secs.
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PD 21-DEC-1995.

PP 20-JUN-1994; 126299.

PF 20-JUN-1994; CA-126299.

PR 20-JUN-1994; CA-126299.

PR 20-JUN-1994; CA-126299.

PR (WILL/) WILLICK G E.

PI Neugebauer W, Sung WL, Surewicz W, Whitfield JF;

PI Willick GE;

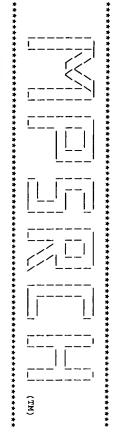
PI Willick GE;

PI Willick GE;

PI Wer human parathyroid hormone analogues - which have increased adenylyl cyclase activating activity, used for treating osteoporosis Claim 2; Page -; 21pp; English.

CR 88829-R88841 are human parathyroid hormone (hPTH) analogues. The Canalogues increase G-protein coupled adenylyl cyclase (cAMPase) activity and reduce protein kinase C (PKC) activity. The analogues without undesirable effects. They are useful for the treatment of osteoporosis and other bone related disorders and disorders of involving bone cell calcium regulation.
                                                                                                                                          Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Increased adenylyl cyclase activity; cAMPase; bone loss.
Synthetic.
Key
Location/Qualifiers
                                                                  9 hnlgkh 14
||||||
1 HNLGKH 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "amidated"
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                                                                                                                                Score 45; DB 18; Length 32;
Pred. No. 1.82e+01;
0; Mismatches 0; Indels
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APsrch\_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Jul 30 10:33:02 1998; MasPar time 3.01 Seconds 72.782 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Title: >US-08-817-547A-16 (1-6) from US08817547A.pep 45 1 HNLGKH 6

Sequence:

Scoring table: PAM 150 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 18.479; Variance 19.656; scale 0.940

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

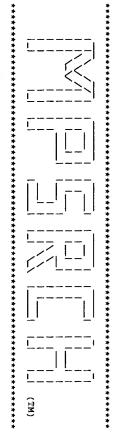
# SUMMARIES

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	8.24e+01	8.24e+01		8.24e+01	8.24e+01	8.24e+01	8.24e+01	8.24e+01	4.93e+01	4.93e+01	4.93e+01	4.93e+01	4.93e+01	4.93e+01	4.93e+01	4.93e+01	4.93e+01	4.93e+01	4.93e+01	4.93e+01	4.93e+01

ORGANISM #formal_name REFERENCE A67742 #authors Roesch, P; #submission submitted to #cross-references PDB:1ZWF REFERENCE TN003318 #authors Marx, U.C. #book in Strukture	RESULT 2 ENTRY TITLE ALTERNATE_NAMES PDB_TITLE	HNLO	Matc] Local	FEATURE 2-9 15-25 SUMMARY	#cross-references PDB:12WG REFERENCE TN003319 #authors Marx, U.C. #book in Strukture	REFERENCE #authors #submission	ALTERNATE_NAMES PDB_TITLE ORGANISM	RESULT 1 ENTRY TITLE
#formal_name synthetic A67742 Roesch, P.; Marx, U.C. submitted to the Brookhaven Protein Data Bank, June 1996 nces PDB:1ZWF TN003318 Marx, U.C. in Strukturen Verschiedener Parathormonfragmente in Loesung,	12WF #type complete parathyroid hormone 4 37 mutant N-TERMINAL ACETYLATED - synthetic n-acetyl-hpth(4-37) structure of n-terminal acetylated human parathyroid hormone, NMP 10 attructures	11	0%; Score 45; DB 5; Length 34; 0%; Pred. No. 5.80e-01; ve 0: Mismatches 0: Indels 0: Gaps	<pre>#region helix (right hand alpha)\ #region helix (right hand alpha) #length 34  #molecular-weight 4128  #checksum 5508</pre>	nces PDB:1ZWG 1003319 Marx, U.C. in Strukturen Verschiedener Parathormonfragmente in Loesung.	A67743 Roesch, P.; Marx, U.C. submitted to the Brookhaven Protein Data Bank, June 1996	synthetic n-succinyl-hpth(4-37) succinyl-human parathyroid hormone 4-37, NMR, 10 structures #formal_name synthetic	12WG #type complete parathyroid hormone 4 37 mutant N-TERMINAL SUCCINYLATED -

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COMMENT COMMENT Resolution: not applicable
COMMENT COM
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Jul 30 10:31:49 1998; MasPar time 2.04 Seconds 73.883 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Title: >US-08-817-547A-16 (1-6) from US08817547A.pep 45 1 HNLGKH 6

Sequence:

Scoring table: PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 19.288; Variance 15.923; scale 1.211

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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HEAVY CHAIN	MYOSIN HEAVY CHAIN D (	TOLL PROTEIN PRECURSOR	REACTION CENTER PROTEI		PARATHYROID HORMONE PR	NERVE GROWTH FACTOR (N	NERVE GROWTH FACTOR (N	HYPOTHETICAL 69.0 KD P	VPR PROTEIN (R ORF PRO	PUTATIVE VENOM METALLO	PROTEIN C17/B23.	PROTEASE SYNTHASE AND	PROBABLE RIBOSOMAL PRO	PYRUVATE FORMATE-LYASE	HYPOTHETICAL 111.7 KD	PARATHYROID HORMONE PR	Description					
1.12e+01 1.12e+01	1.12e+01 1.12e+01	1.12e+01	1.12e+01	1.12e+01	1.12e+01	1.12e+01	1.12e+01	5.90e+00	5.90e+00	3.08e+00	3.08e+00	1.58e+00	1.58e+00	8.04e-01	2.00e-01	4.76e-02	4.76e-02	4.76e-02	4.76e-02	4.76e-02	Pred. No.	

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                                               Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 6; Conservative
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A DEFTOS L.J., DAWSON B.F., HOGAN M.L., AURBACH G.D.;
U. PROC. NATL ACAD. SCI. U.S.A. 68:63-67(1971).
C. -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
EMBLY VOO106, G85;
DR EMBL; VO0102; G163641; -.
REMBL; J00024; G163641; -.
REMBL; J00024; E18249; ALT_SEO.
REMBL; J00024; E18250; ALT_INIT.
BEMBL; MO1938; G163647; -.
DR EMBL; MO5082; G163645; -.
DR EMBL; MO5082; G163647; -.
DR EMBL; MO5082; G163645; -.
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Best Local Similarity 100.0%;
Matches 6; Conservative
                                                                                                      SIGNAL
PROPEP
CHAIN
SEQUENCE
                                                                                                                                                           SEQUENCE FROM N.A.

TISSUE-PARATHYROID;

MEDLINE: 953696.

ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,

DEWILLE J.W., CAPEN C.C.;

GENE 160:241-243(1995).

-1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN

EMBL, U15662; G558916; -

PROSITE; PS00335; PARATHYROID; 1.
                                                                                                                                                       HORMONE; SIGNAL.
                                                                                                                                                                                                                                                                                                  CANIS FAMILIARIS (DOG).
EUKARYOTA; METAGOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; CARNIYORA.
                                                                                                                                                                                                                                                                                                                                                       PTHY_CANFA STANDARD; PRT; 115 AA.
P52212;
01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HORMONE; SIGNAL.

1 25
SIGNAL 1 25
PRODEP 26 31
CHAIN 32 115
CONFLICT 106 106
CONFLICT 106 106
CONFLICT 106 106
SEQUENCE 115 AA; 12980 MW; 673EA5F2 CRC32;
               40 HNLGKH 45
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PIR; A24949; A2494
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PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
1 HNLGKH 6
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115 AA;
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31 B:
115 P.
; 12957 MW;
                                                                                             BY SIMILARITY.
BY SIMILARITY.
PARATHYROID HORMONE.
W: 16ED0EBC CRC32;
                                          Score 45; DB 1; Length 115;
Pred. No. 4.76e-02;
0; Mismatches 0; Indels
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Pred. No. 4.76e-02;
0; Mismatches 0; Indels
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Search completed: Thu Jul 30 10:31:56 1998 Job time: 7 secs.

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05 10 Q63473 PARATHYROID HORMO 96 11 P08152 VPR PROTEIN. 96 11 P08152 VPR PROTEIN. 72 9 O32112 TRANSCRIPTIONAL R 64 9 O25591 HYPOTHETICAL 30.8 53 11 Q83077 BETA-5 PROTEIN. 80 12 Q90220 PREPRO-HALYSTATIN 96 11 Q79723 ISOLATE NY5, COMP 96 11 Q79233 VPR PROTEIN. 96 11 Q79233 VPR PROTEIN. 97 Q54077 PUTATIVE. NCBI GI 97 Q74777 ISOLATE 891-1, VP 97 Q18840 ACTID SHOCK PROTEI 98 Q42966 ACID SHOCK PROTEI 99 Q54077 PUTATIVE. NCBI GI 97 Q18840 ACTID SHOCK PROTEI 90 Q54077 PUTATIVE. NCBI GI 91 Q18840 ACTID SHOCK PROTEI 91 Q10568 ACID SHOCK PROTEI 92 Q55210 ALPHA-SMOOTH MUSC 93 Q60171 T18D3.4 (FRACKENT 93 Q10574 T18D3.4 (FRACKENT 93 Q105863 FUSION PROTEIN (F	SUMMARIES  DB ID Description	554; Variance 16.504; scale 1.124 imber of results predicted by chance to have or equal to the score of the result being inalysis of the total score distribution.	l 2:sp_human 3:sp_invertebrate 4:sp_ 5:sp_organelle 7:sp_phage 8:sp_plant sria 10:sp_rodent 11:sp_virus 12:sp_ lassified	Match 0% first 45 summar	egs, 42109429 residues	817-547A-16 :rom US08817547A.pep :H 6	tein database search, using Smith-Water 30 10:32:12 1998; MasPar time 3.65 Sec 69.257 Million cell ted.	F. Collins, Biocomputing Research Unit. 3-1998 University of Edinburgh, U.K. ion rights by Oxford Molecular Ltd	
	Pred. No.	re a printed,	mammal vertebrate				man algorithm onds updates/sec		(TM)

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THREE ROWS PROTEIN.	HYPOTHETICAL PROTEIN.	METHYLENETETRAHYDROFOL	BJ6 PROTEIN.	Þ	LIPOXYGENASE (FRAGMENT	COSMID F59E12.	55151	B-CREATINE KINASE (EC	NEF PROTEIN.		NEF (NEF).	NEF (NEF).	NEF (NEF).	NEF.	NEF.	ORF C04015.	A670R PROTEIN.	K12F2.1.	SIMILARITY TO C. ELEGA	T18D3.4 (FRAGMENT).	TOLL PROTEIN.	F11C3.3 (FRAGMENT).	RO6C7.10 (FRAGMENT).	ORF3.
			3.65e+01	•		3.65e+01	•	•	3.65e+01	3.65e+01	3.65e+01	3.65e+01	3.65e+01		3.65e+01	3.65e+01	3.65e+01	2.00e+01	2.00e+01	2.00e+01	2.00e+01	2.00e+01	2.00e+01	2.00e+01

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RESULT 2

PRELIMINARY; PRT; 96 AA.

AC 072500;
AC 072500;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
OX VPR.
GN VPR.
GN VPR.
OC VIRIDAE; SS-RNA ENVELOPED VIRUS TYPE 1 (HIV-1).
OC VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
OC LENTIVIRINAE.
RP SEQUENCE FROM N.A.
RC STRAIN=NL4-3;
RX MEDLINE; 96036482.
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10 063473;
AC 063473;
AC 063473;
DT 01-NOV-1996 (TREMBLREL 01, CREATED)
DT 01-NOV-1998 (TREMBLREL 05, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL 05, LAST ANNOTATION UPDATE)
DE PARATHYROID HORMONE (FRAGMENT).
3N PTH.
3N PTH.
3N PTH.
C EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
N [1]
N [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 6; Conservative
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TISSUE-THYROID, AND PARATHYROID;
TISSUE-THYROID, AND PARATHYROID;
SCHMELZER H.J., GROSS G., MAYER H.;
ADV. GENE TECHNOL. 21:228-229(1984).
EMBL, M54875; G601933; -.

NON_TER 1
SEQUENCE 105 AA; 11746 MW; 6AC3163
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||||||
1 HNLGKH 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 45; DB 10; Length 105; Pred. No. 1.06e-01; 0; Mismatches 0; Indels
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RA MICHAEL N.L., CARR J.K., BURKE D.S., MCCUTCHAN F.E.;
RL VIROLOGY 213:80-86(1995).

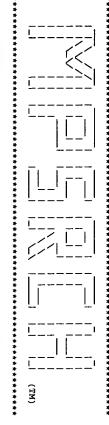
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN-NLA-3;
RX MEDLINE; 86281827.
RA ADACHI A., GENDELMAN.A.;
RL J. VIROL. 59:284-291(1986).
RR RABSON A., MARTIN M.A.;
LJ. VIROL. 59:284-291(1986).
PT CONFLICT 44 44 44 59 SEQUENCE 96 AA; 11391 MW; 035C4D/5 CRC32;

Query Match 93.3%; Score 42: DB 11: Length 96;
Best Local Similarity 83.3%; Pred. No. 8.18e-01;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 40 HNLGRH 45 1111-111 MISMATCHES 0; Indels 1111-111 HNLGRH 6

Search completed: Thu Jul 30 10:32:45 1998

Search completed: Thu Jul 30 10:32:45 1998
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MPsrch\_pp 9 9 1 protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:36:04 1998; MasPar time 2.57 Seconds 29.790 Million cell upda

Tabular output not generated

cell updates/sec

Description: Perfect Score: Title: (1-5) from US08817547A.pep 36 1 HNLGK 5 >US-08-817-547A-17

Sequence:

Scoring table: PAM 150 Gap 15

Searched: 124785 segs, 15338987 residues

Post-processing: Minimum Match Listing first 0% 45 summaries

Database:

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 12.815; Variance 28.014; scale 0.457

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

1 2 3 3 4 4 4 4 4 1 1 1 1 1 1 1 1 1 1 1 1 1	Result
<b></b>	Score
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& & & & & & & & & & & & & & & & & & &	Length I
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R62432 R758189 R758189 R758187 R34455 R34455 W117958 W117953 W117953 W117953 R74489 R74489 R74489 R758166 R758166 R758165 R758165 R758165 R758165 R758165 R758165	ID
Accelerator peptide b [F23,H25,H26,L27,128, Lys15,16 H1527]hPTH [Phe23,H1525,H1526,Le Bovine parathyroid hor Human parathyroid hor Human parathyroid hor Human parathyroid hor Parathyroid hormone parathyroid	Description
1.04e+02 1.04e+02 1.04e+02 1.04e+02 1.04e+02 1.04e+02 1.04e+02 1.04e+02 1.04e+02 1.04e+02 1.04e+02 1.04e+02 1.04e+02 1.04e+02 1.04e+02 1.04e+02 1.04e+02 1.04e+02 1.04e+02	Pred. No.

45	44	43	42	41	40	39	38	37	36	3 5	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36
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R23297	340	7	R23477	116	σ	R23261	æ	J	339	4	9	95	956	9	341	342	326	4	568	$\mathbf{\mu}$	R58078	R58077	R58108	R58105	R58124
ĭ	Ω	Porcine parathyroid h	roid	id ho	Human parathyroid hor	Bovine parathyroid ho	Porcine parathyroid h	5	n.	parathyroid h	Bovine parathyroid ho	ion	resistant	Stability-enhanced hu	parathyroid	O.	D.	ne parathy	roid	parathyro	3]-hPTH(1-38	u33]-hPTH(1-38)-	4]-hPTH(1-	4]-hPTH(1-	19]-hPTH(1-
.04e+0	.04e+0	1.04e+02	.04e+0	.04e+0	.04e+0	1.04e+02	.04e+0	.04e+0	.04e+0	.04e+0	.04e+0	.04e+0	.04e+0	.04e+0	.04e+0	.04e+0	.04e+0	.04e+0	2	e+0	ന	1.04e+02		1.04e+02	1.04e+02

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RESULT
ID RE
AC RE
DT 20
                                                                                                                        ğ
                                                                                                                                                           밁
                                                                                                                                                                                            Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                             Disclosure; Page 3; 7pp; Japanese.

The sequences in R62425-36 are peptide fragments of an accelerator protein which contain at least two basic amino acids. The accelerat also comprises a cell growth factor. The accelerator may be used to accelerate the growth of periodontal tissue regeneration. The accelerator is applied by opening the gingiva, treating the tissue destroyed by periodontitis and applying the accelerator in the periodontal pocket. The accelerator reduces the down growth of the periodontal pocket.
JT 2
JT 2
Standard; peptide; 34 AA.
R58189;
20-SEP-1994 (first entry)
[F23,H25,H26,L27,I28,A29,E30,I31,T33,A34]-hPTH(1-34)-NH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-FEB-1993; JP-045998.
(SUNZ ) SUNSTAR CHEM IND CO LTD.
WPI; 95-157631/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-JUL-1995 (first entry)
Accelerator peptide basic region peptide, P-8.
Accelerator; basic amino acid; cell growth factor; growth; gingiva;
periodontal tissue; regeneration; periodontitis; periodontal pocket;
down growth; epithelium; fibre adhesion; cement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R62432 standard; peptide;
R62432;
31-JUL-1995 (first entry
                                                                                                                                                                                                                                                                 epithelium and accelerates fibre adhesion and regenerates cement. Sequence 34~\mathrm{AA};
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Accelerator for regenerating periodontal tissue - comprises peptide having 3-34 aminoacid residues having connected basic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-AUG-1994.
10-FEB-1993; 045998
10-FEB-1993; JP-045!
                                                                                                                                                                                                                                                                                                                                                                                                                                         aminoacid residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J06234653-A.
                                                                                                                                              9 hnlgk 13
                                                                                                                        1 HNLGK 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34 AA.
                                                                                                                                                                                                              Score 36; DB 26;
Pred. No. 1.04e+02;
                                                                                                                                                                                              0;
                                                                                                                                                                                              Mismatches
                                                                                                                                                                                              0
                                                                                                                                                                                                                              Length 34;
                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                    accelerator
                                                                                                                                                                                              0
                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                         ដ
                                                                                                                                                                                              0
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Search completed: Thu Jul 30 10:36:20 1998 Job time : 16 secs.
                                                                                                                                              Ş
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PD 02-FEB-1994

PF 12-UUL-1993; 014384.

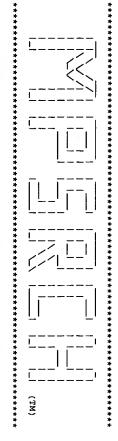
PR 15-UUL-1992; GB-015009

PR 23-DEC-1992; GB-026415.

PR 23-DEC-1992; GB-026861.

PR 23-DEC-1922; GB-026862.

PR 23-
                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 hnlgk 13
|||||
1 HNLGK 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human parathyroid hormone; hPTH; variant; analogue; calcium; depletion; fixation; resorption; osteopathy; osteoporosis; synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                            Score 36; DB 9; Length 34;
Pred. No. 1.04e+02;
0; Mismatches 0; Indels
                                                                                                                                                                            0;
                                                                                                                                                                   Gaps
                                                                                                                                                                0;
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MPsrch\_pp 9n: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:35:29 1998; MasPar time 2.99 Seconds 61.109 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-817-547A-17 (1-5) from US08817547A.pep 36 1 HNLGK 5

Scoring table: PAM 150 Gap 15

Searched:

120441 segs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 17.484; Variance 16.519; scale 1.058

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	თ	u	4	ω	N	۳	ult No:	-
34	34	34	34	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	Score	
94.4	94.4	94.4	94.4	100.0	100.0	100.0	•	100.0	٠		100.0		100.0		•	100.0	•	100.0	100.0	•	100.0		Query Match	dР
146	146	146	142	1209	1172	1097	894	123	115	115	115	115	115	105	37	37	36	35	34	34	34	34	Length	
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JU0163	HBOZ	нвну	C70059	A49440	S42622	JQ0301	B42372	S75382	PTHU	PTBO	A05091	JC4202	PTPG	I51851	12WC	1HPH	1ZWB	1ZWD	1ZWA	1ZWE	1ZWF	1ZWG	Ħ	
beta	hemoglobin beta chain	æ.	hypothetical protein	chromosome disjunctio	roteir		regulatory protein Kd	1 protein	hormone	parathyroid hormone p	parathyroid hormone p	hormone	parathyroid hormone p	parathyroid hormone -	parathyroid hormone (	parathyroid hormone f	parathyroid hormone (	parathyroid hormone (	_	parathyroid hormone (	parathyroid hormone 4	parathyroid hormone 4	Description	;
6.05e+01	6.05e+01	6.05e+01	6.05e+01	1.89e+01	1.89e+01	1.89e+01	1.89e+01	1.89e+01		•	1.89e+01	1.89e+01	<u>.</u>	1.89e+01		1.89e+01	1.89e+01	1.89e+01	1.89e+01	1.89e+01	1.89e+01	Φ T	Pred. No.	

45	44	43	42	41	40	39	မ	37	36	<u>3</u> 5	34	<b>ω</b>	32	31	30	29	28	27	26	25	24
33	33	<b>ω</b>	ω ω	ω ω	33	33	ω ω	34	34	34	34	34	34	34	34	34	34	34	34	34	34
91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	94.4	94.4	94.4	94.4	94.4	94.4	94.4	94.4	94.4	94.4	94.4	94.4	94.4	94.4
578	274	273	273	147	147	146	34	3135	1021	830	759	711	573	573	573	573	416	412	348	314	147
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E69259	I52851	1QRDB	1QRDA	S34719	HBMS	HBOL	1HTH	A48584	S44644	C69011	G69258	E69953	A34173	HHMS60	A32800	HHRT60	B64132	RNECTA	F69831	G69818	S22336
aldehyde ferredoxin o	NAD(P)H dehydrogenase	quinone-reductase (EC	quinone-reductase (EC	hemoglobin beta-2.0 c	hemoglobin beta major	hemoglobin beta chain	cyclic parathyroid ho	transmission-blocking	F37A4.7 protein - Cae	conserved hypothetica		***		chaperonin groEL prec		chaperonin groEL prec	tRNA adenylyltransfer	nylyltrans	iron(III) dicitrate-b	CMP-binding factor ho	hemoglobin beta chain
1.06e+02	6.05e+01	6.05e+01	6.05e+01	6.05e+01	6.05e+01	6.05e+01	6.05e+01	6.05e+01	6.05e+01	6.05e+01		6.05e+01	6.05e+01	6.05e+01							

NATE_NAMES n -acetyl-hpth(4-37)  ITLE structure of n-terminal acetyla  NNR, 10 structures  ISM #formal_name synthetic  ENCE A67742  uthors Roesch, P.; Marx, U.C.  ubmission submitted to the Brookhaven Pro- ross references PDB:12WF ENCE TN00318:12WF ENCE TN00318:12WF ENCE Marx, U.C.  ook in Strukturen Verschiedener Pari	Db 6 HNLGK 10       Qy 1 HNLGK 5  RESULT 2  ENTRY 12WF #type complete ENTRY 12WF #type complete	Query Match 100.0%; Score 36; DB 5; I Best Local Similarity 100.0%; Pred. No. 1.89e+01; Matches 5; Conservative 0; Mismatches 0	#region helix (right hand 5 #region helix (right hand #length 34 #molecular-weight.	#DOOK IN STRUKTUREN VERSCHIEDERF FARACHOFMONIZISHENE IN COMMENT Resolution: not applicable COMMENT Determination: NMR KEYWORDS disease mutation; hormone; signal	rs ssion referen	1ZWG parathyroid parathyroid synthetic synthetic n-succinyl-large succinyl human formal name A67743	RESULT 1
ylated human parathyroid hormone, Protein Data Bank, June 1996	ANT N-TERMINAL ACETYLATED -	3 5; Length 34; 99e+01; nes 0; Indels 0; Gaps 0;	nd alpha)\ nd alpha) t 4128 #checksum 5508	Y of Bayreuth (Thesis), 1996 19nal	une	<pre>htype complete hormone 4 37 mutant N-TERMINAL SUCCINYLATED - pth(4-37) parathyroid hormone 4-37, NMR, 10 structures synthetic</pre>	

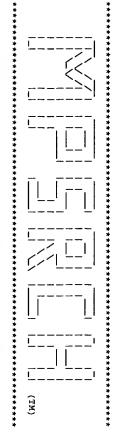
```
COMMENT Resolution: not applicable
COMMENT Determination: NUR
KEYWORDS
FEATURE

3-6
14-27
3-6
14-27
SUMMARY
Query Match
Best Local Similarity 100.0%; Score 36; DB 5; Length 34;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 6 HNLGK 10
[111]
Oy 1 HNLGK 5

Search completed: Thu Jul 30 10:35:46 1998

Search completed: Thu Jul 30 10:35:46 1998
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MPsrch\_pp on: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:34:11 1998; MasPar time 2.00 Seconds 62.590 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: ritle: >US-08-817-547A-17 (1-5) from US08817547A.pep 36 1 HNLGK 5

Scoring table: PAM 150 Gap 15

Searched: 69111 segs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 l:swiss1

Statistics: Mean 18.208; Variance 13.355; scale 1.363

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

3 3 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	ٔ د د	No.
	36	Score
100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0	100.0	Query Match
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	. p.	₽B
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PARATHYROLD HORMONE PR PARATHYROLD HORMONE PR PARATHYROLD HORMONE PR PARATHYROLD HORMONE PR PARATHYROLD HORMONE PR PARATHYROLD KOPPONEN SENSOR PROTEIN KDPD (E PROBABLE DNA POLYMERAS THREE ROWS PROTEIN. HEMOGLOBIN BETA CHAIN. HEMOGLOBIN BETA CHAIN. HEMOGLOBIN BETA MAJOR NUCLEOTIDYLITRANSF TRNA NUCLEOTIDYLITRANSF TRNA NUCLEOTIDYLITRANSF TRNA NUCLEOTIDYLITRANSF YOP PROTEINS TRNASLOCA MITOCHONDRIAL MATRIX P MITOCHONDRIAL MATRIX P MITOCH	HORMONE	Description
3.42e+00 3.42e+00 3.42e+00 3.42e+00 3.42e+00 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.41e+01 1.4	3.42e+00	Pred. No.

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976 979	972 974	836	797	788	700	100	409	274	273	273	235	146	146	146	146	146	146	146
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AMD_RAT	AMD_BOVIN	DPOL_HPBDU	DPOM_AGABT	DPOL HPBDW	טפסד הפסבר	CP5I_CANTR	TRPB_METVO	DHQU_HUMAN	DHQU_RAT	DHQU_MOUSE	REEP_CSV	HBB_MARMA	HBB_SPAEH	HBB2_MOUSE	HBB1_RAT	HBB_SPECI	HBB_MICXA	HBB2_RAT
	PEPTIDYL-GLYCINE ALPHA	DNA POLYMERASE (EC 2.7	BABLE DNA POLYME	POLYMERASE	DAY BOLKEDAGE (EC 4.7	OCHROME P450 LI	TRYPTOPHAN SYNTHASE BE	NAD(P)H DEHYDROGENASE	NAD(P)H DEHYDROGENASE	NAD(P)H DEHYDROGENASE	REPEAT ELEMENT PROTEIN	HEMOGLOBIN BETA CHAIN.	HEMOGLOBIN BETA CHAIN.	HEMOGLOBIN BETA-2 CHAI	HEMOGLOBIN BETA CHAIN,	HEMOGLOBIN BETA CHAIN.	HEMOGLOBIN BETA CHAIN.	HEMOGLOBIN BETA CHAIN,
2.78e+01 2.78e+01	2.78e+01 2.78e+01	2.78e+01	2.78e+01	2.78e+01	3 785+01	2.78e+01	2.78e+01	2.78e+01	2.78e+01	2.78e+01	2.78e+01	2.78e+01	•	2.78e+01	2.78e+01	2.78e+01	2.78e+01	2.78e+01

PTHYLBOVIN STANDARD; PRT; 115 AA. PO1266; 21-JUL-1986 (REL. 01, CREATED) 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE) 21-JUL-1986 (REL. 01, LAST SEQUENCE (PARATHYRIN) (PTH). PTH.  BOS TAURUS (BOVIND). EUKARYOTA; METRACA, CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; ARTIODACTYLA.  [1] SEQUENCE FROM N.A. MEDLINE; 80056617. MEDLINE; 80056617. MEDLINE; 8037785. MEDLINE; 8037785. MEDLINE; 8037785. MEDLINE; 8037785. MEDLINE; 83105964. MEDLINE; 83105964. MEDLINE; 83105964. MEDLINE; 84262483. MEDLINE; 84262483. MEDLINE; 84262483. MEDLINE; 84626483. MEDLINE; 84626483. MEDLINE; 74142666. MEDLINE; 74142666. MEDLINE; 74142666. MEDLINE; 74142666. MEDLINE; 74142666. MEDLINE; 71076162. MEDLINE; 71076162. MEDLINE; 71076162. MEDLINE; 71076162. MIALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWSON B.F., AURBEL G.D., POTTS J.T. SEQUENCE OF 32-115. MEDLINE; 71076162. MEDLINE; 71076162. MEDLINE; 71076162. MEDLINE; 71076162. MEDLINE; 71076163. MEDLINE		RP SEQ RX MED RA NIA							DT 21- DT 01- DT PAR	SUL
REATED) RAST SEQUENCE UPDATE) AST ANNOTATION UPDATE) AST ANNOTATION UPDATE) CURSOR (PARATHYRIN) (PTH).  PRDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  PROBATA; VERTEBRATA; TETRAPODA; MAMMALIA;  PROBATA; VERTEBRATA; TETRAPODA; MAMMALIA;  PROBATA; VERTEBRATA; TETRAPODA; MAMMALIA;  PROBATA; VERTEBRATA; TETRAPODA; MAMMALIA;  SHARP  O.S.A. 76:4981-4985(1979).  PROBATA; VERTEBRATA; TETRAPODA; MAMMALIA; SHARP  O.S.A. 76:4981-4985(1979).  PROBATA; VERTEBRATA; HOGAN M.L., DAWSON B.F.,  OL. CHEM. 351:1586-1588(1970).	PE-SEYLER'S	UENCE OF 32-1 LINE; 710761 LL H.D., KEU!	ENCE OF 26- INE; 741426 ITON J.W., D.V.; NATI. ACA	ENCE FRO INE; 842 ER C.A., 28:319-	ENCE FR INE; 83 ER C.A.	UENCE FROM N LINE; 8203771 VER C.A., GOI C. NATL. ACAI	NCE FI NE; 8( NBERG J.T. NATL	TAURUS (BOV ARYOTA; META: HERIA; ARTIO	_	NIAC
PRT; 115 AA.  DUENCE UPDATE)  UCTATION UPDATE)  (PARATHYRIN) (PTH).  VERTEBRATA; TETRAPODA; MAMMALIA;  VERTEBRATA; TETRAPODA; MAMMALIA;  PER B.;  76:4981-4985(1979).  PER B.;  78:4073-4077(1981).  PER B.;  -424(1982).  SIL M.S., MEAD D.A., KEMPER B.;  SIL M.S., MEAD D.A., KEMPER B.;  71:653-656(1974).  DUER R., HOGAN M.L., DAWSON B.F.,  MER R., HOGAN M.L., DAWSON B.F.,  MEM. 351:1586-1588(1970).	HYSIOL.	NN H.T.,	LL H.D., SCI. U.S.	ON D.F.,	NOL.	U.S.	ITT B.	INE). ZOA; CHORDATA; DACTYLA.	01, CREAS 01, LAST 35, LAST NE PRECURS	STANDARD;
PTH).  TRAPODA; MAMMALIA;  NATHANS J., SHARP  979).  D.A., KEMPER B.;  D.A., KEMPER B.;  ANANN H.T., POTTS J.T  MANN H.T., POTTS J.T  4).	351:	R .,	J.W.,	M. S. ,	PER B.; -424(1982).	יטי	7 :	VERTEBRATA;	) QUENCE UPDAT NOTATION UPD (PARATHYRIN	115
	-1588(1970).	M.L., DAWSON B.	N H.T., POTTS J	D.A., KEMPER B.		7(1981).	THANS J., SHARP		E) ATE) ) (PTH).	AA.

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RESULT ID PT AC PC DT 21 DT 01 DT 01 DT 02 DT 02
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X MEDLINE; 74,253317.

AS SAUER R.T., NIALL H.D., HOGAN M.L., KEUTMANN H.T., O'RIORDAN J.L.H.,

POTTS J.T. JR.;

LBIOCHEMISTRY 13:1994-1999(1974).

C -1- FUNCTION. PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN

EMBL; X05722; G1839; -.

REMAL; X05723; G1839; -.

REMAL; X05722; G1839; -.

REMAL; X05722
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**MEDILINE; 71091588.

**POTTS J.T. JR., TREGEAR G.W., KEUTMANN H.T., NIALL H.D., SAU DEFTOS L.J., DAWSON B.F., HOGAN M.L., AURRACH G.D.;

**PROC. NATL. ACAD. SCI U.S. A. 68:63-67(1971).

**C-!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SEMBL; VO0106; 685; -.

**EMBL; VO0106; 685; -.

**R EMBL; J00024; G163641; -.

**R EMBL; J00024; G163643; -.

**R EMBL; J00024; E18250; ALT_INIT.

**R EMBL; J00024; E18250; ALT_INIT.

**R EMBL; J00024; G163647; -.

**R EMBL; K01938; G163647; -.

**R EMBL; K01938; G163645; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 26-115.

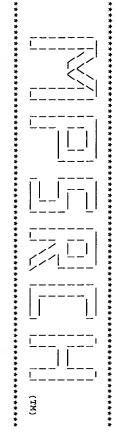
MEDLINE; 76018954.

CHU L.L.H., HUANG W.-Y., LITTLEDIKE
BIOCHEMISTRY 14:3631-3635(1975).

[3]
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HORMONE; SIGNAL.
SIGNAL 1
PROPEP 26
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MEDLINE; 87316938.
SCHMELZER H.-J., GROSS G., WIDERA G.,
SCHMELZER ACIDS RES. 15:6740-6740(1987).
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CONFLICT
SEQUENCE
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SUS SCROFA (PIG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (REL. 01, CREATED)
01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
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PARATHYROID HORMONE
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Search completed: Thu Jul 30 10:34:18 1998 Job time: 7 secs.
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esrch\_pp 9 : protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:34:37 1998; MasPar time 3.52 Seconds 59.805 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-817-547A-17 (1-5) from US08817547A.pep 36 1 HNLGK 5

Scoring table: РАМ 150 Gap 15

Searched: 140542 seqs, 42109429 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb15
1:sp\_fungi 2:sp\_human 3:sp\_invertebrate 4:sp\_mammal
5:sp\_mhc 6:sp\_organelle 7:sp\_phage 8:sp\_plant
9:sp\_bacteria 10:sp\_rodent 11:sp\_virus 12:sp\_vertebrate
13:sp\_unclassified

Statistics: Mean 17.545; Variance 13.620; scale 1.288

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2 2 3 3 3 3 3 5 5 5 5 5 5 5 5 5 5 5 5 5	Result
	Score
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PARATIYYOID HORMONE (F ORF CO4015. LIPOXYGENASE (FRAGMENT ER LUMENAL CHAPERONE B THREE ROWS PROTEIN. YWIA, SBO, YWIB, ARGS CC3 (CC3). HYPOTHETICAL 35.7 KD P RETINAL HOMEOBOX PROTE HYPOTHETICAL 38.6 KD P 60 KD CHAPERONIN (PROT ATP-DEPENDENT RNA HELI CONSERVED PROTEIN. RANSMISSION-BLOCKING T RHOPTRY PROTEIN (FRAGM RAT HEMOGLOBIN BETA-CH VPR PROTEIN. ZERO BETA-GLOBIN. 2ERO BETA-1 GLOBIN. DETA-2 GLOBIN.	Description
5.59e+00 5.59e+00 5.59e+00 5.59e+00 5.59e+00 5.59e+00 2.24e+01 2.24e+01 2.24e+01 2.24e+01 2.24e+01 2.24e+01 2.24e+01 2.24e+01 2.24e+01 2.24e+01 2.24e+01 2.24e+01 3.7e+01 4.37e+01 4.37e+01 4.37e+01 4.37e+01 4.37e+01 4.37e+01 4.37e+01 4.37e+01 4.37e+01 4.37e+01	Pred. No.

45	44	43	42	41	40	39	38	37	36	35 5	34	33	32	31	30	29	28	27	26	25	24	23	22	21
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YOUNG F., SCHENK M.E., GAASTERLAND T., DOOLITTLE W.F. CHARLEBOIS R.L.;	.W., KLENK H.P., SINGH R.K., ALLARD G.,	[1] SEQUENCE FROM N.A.	SULFOLOBUS SOLFATARICUS. ARCHAEBACTERIA; CRENARCHAEOTA; SULFOLOBALES.		O1-MAY-1997 (TREMBEREEL O3, LAST SEQUENCE UPDATE)	1997 (TREMBLREL. 03, CREATED)		DOSOSA DEFT.THINADO. DDT. 123 AA	1 HNLGK 5	30 HNLGK 34	Query Match 100.0%; Score 36; DB 10; Length 105; Best Local Similarity 100.0%; Pred. No. 5.59e+00; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	NON_TER 1 1 1 1 SEQUENCE 105 AA; 11746 MW; 6AC3163E CRC32;	, M54875; G601	TECHNOL. 21	SCHMELZER H.J., GROSS G., MAYER H.:	Ä		* Liki bukata,	CUCCOATA: VERTERBATA: TETRABODA:		HORMONE (FRAGMENT).	(TREMBLREL.	1996 (TREMBLREL. 01, CREATED)		JT 1 O63473 PRELIMINARY: PRT: 105 AA.

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RL MOL. MICROSTOL. 22:175-191(1996).

DR EMPL; Y08257; E28388; -.

Query Match

Best Local Similarity 100.09; Score 36; DB 9; Length 123;

Best Local Similarity 100.09; Pred. No. 5.59e+00;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 6 HNLGK 10

Qy 1 HNLGK 5

Search completed: Thu Jul 30 10:35:11 1998

Job time : 34 secs.
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Database:	Searched: Post-processing:	Scoring table:	Title: Description: Perfect Score: Sequence:	MPSTCh_pp protein  on: Thus  Tabular output not of	Releas Copyri	
eq31-2 t1 2:part2 t8 9:part9 rt14 15:pa rt19 20:pa	124785 seqs, 15338987 residues Minimum Match 0% Listing first 45 summaries	PAM 150 Gap 15	>US-08-817-547A-18 (1-14) from US08817547A.pep 103 1 LRKKLQDVHNFVAL 14	otein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:38:52 1998; MasPar time 2.75 Seconds 78.050 Million cell updates/sec not generated.	1A John F. Collins, Biocomputing (c) 1993-1998 University of Edilerthian of Edilerthian rights by Oxford Mole	

Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Mean 19.363; Variance 67.336; scale 0.288

# SUMMARIES

Result	Score	Query Match	Length	B	ΠĐ	Description	Pred. No.
<b>-</b>	103	100.0	38	و	R58283	[Trp(Pmc)23]-hPTH(1-3	1.80e-03
2	103	100.0	38	9	R58151	22]-hpri	1.80e-03
ω	103	100.0	38	ø	R58134	[Ile19]-hPTH(1-38)-OH	1.80e-03
4	103	100.0	38	ø	R58133	[Asp19]-hPTH(1-38)-OH	1.80e-03
<sub>5</sub>	103	100.0	38	ø	R58138	[Ala21]-hPTH(1-38)-OH	1.80e-03
0	103	100.0	38	ø	R58137	[Phe20]-hPTH(1-38)-OH	1.80e-03
7	103	100.0	44	26	P30015	Human parathyroid hor	1.80e-03
8	103	100.0	47	25	W21946	Fusion protien compri	1.80e-03
9	103	100.0	84	27	W25687	Human parathyroid hor	1.80e-03
10	103	100.0	84	4	R23387	Porcine parathyroid h	1.80e-03
11	103	100.0	84	4	R23262	Bovine parathyroid ho	1.80e-03
12	103	100.0	84	4	R21188	Human parathyroid hor	1.80e-03
13	103	100.0	84	4	R21189	Human parathyroid hor	1.80e-03
14	103	100.0	84	4	R21156	Human parathyroid hor	1.80e-03
15	103	100.0	84	4	R21157	Human parathyroid hor	1.80e-03
16	103	100.0	84	4	R23429	Porcine parathyroid h	1.80e-03
17	103	100.0	84	4	R23259	Bovine parathyroid ho	1.80e-03
18	103	100.0	84	4	R23384	Porcine parathyroid h	1.80e-03
19	103	100.0	84	4	R23246	Human parathyroid hor	1.80e-03

DT 20-SEP-1994 DE [Trp(Pmc)23]-		SU										36																
pmc)				103	03	103	03	3	103	103	3 5	103	103	103	103	03	103	03	103	103	103	103	103	103	103	103	103	03
20-SEP-1994 (first entry) [Trp(Pmc)23]-hPTH(1-38)-NH2 Human parathyroid hormone;	tandard;			•	•	•				•	•	100.0	•	•	•	•	•	•	•	•	•	•	•	•	•	•	•	•
st en (1-38	peptide;			115	84	84	84	8 4	8 4	œ o	α α	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84
try)	de;	•		N	4	4	۰ 4	. م	۰ م	ء م	٠.	4.	4	4	4	4	4	4	4	4	4	4	25	4	4	4	4	4
hPTH: variant:	38 AA.	)	ALIGNMENTS	P80275	R23449	R23313	R23344	R23326	R23299	R23394	R234U2	R23290	R21168	R23258	R21227	R23439	R21192	R23237	R23378	R23241	R23415	R23317	W29420	R21240	R23441	R23265	R21222	R21223
ant: analogue:			•	Sequence of human pre	parathyroid	parathyroid	parathyroid	parathyroid	parathyroid	Porcine parathyroid h	paratnyroid	Bovine parathyroid ho	Human parathyroid hor	Bovine parathyroid ho	Human parathyroid hor	ne parathyro		parathyroid h	Bovine parathyroid ho	arathyroid ho	parathyroid	e parathyroid		Human parathyroid hor	Porcine parathyroid h	ወ	parathyroid	
				. 806	. 806	. 806	. 806	. 806	806		1.006	1.80e-03	. 806	. 80€	80e	. 80€	80e	. 806	. 806	. 80€	. 806	. 806	. 80€	. 806	. 80€	. 806	.80€	. 80e

#### CCCCCCCTTRHHAPPPRRRRRRRRRRHHHHHHK& PN GB2269176-A. PD 02-FEB-1994. PF 12-UUL-1993; 014384. PF 15-UUL-1992; GB-015009. PR 15-UUL-1992; GB-015009. PR 18-DEC-1992; GB-026415. PR 28-DEC-1992; GB-026859. PR 28-DEC-1992; GB-026861. PR 28-DAN-1993; GB-001691. PR 28-DAN-1993; GB-001691. PR 28-DAN-1993; GB-001691. PR 28-DAN-1993; GB-001691. PR 19-APR-1993; GB-001691. PR 19-APR-1993; GB-008033. PR 19-APR-1993; GB-008033. PR 19-APR-1993; GB-008033. PR 19-APR-1993; GB-00803. PA (SANO) SANDOZ-ERFINDUNCSN VERW GES MBH. PA (SANO) SA Key modified\_site calcium; depletion; fixation; hypoparathyroidism. Synthetic. modified\_site 2,2,5,7 38 /note= /label= Other /note= "Trp(Pmc) where Pmc is 2,2,5,7,8-Pentamethylchroman-6-sulphonyl." Location/Qualifiers 23 "in amide form" resorption; osteopathy; osteoporosis; bone

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Search completed: Thu Jul 30 10:39:16 1998 Job time: 24 secs.
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PF 12-JUL-1993; 014384.

PR 15-JUL-1993; GB-015009.

PR 18-DEC-1992; GB-026859.

PR 23-DEC-1992; GB-026859.

PR 23-DEC-1992; GB-026861.

PR 28-JAN-1993; GB-001691.

PR 14-APR-1993; GB-001691.

PR 14-APR-1993; GB-001691.

PR 16-APR-1993; GB-001691.

PR 16-APR-1993; GB-001691.

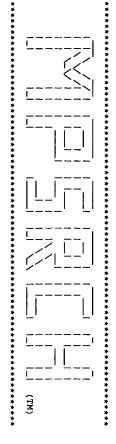
PR 16-APR-1993; GB-001692.

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PR 16-APR-1993; GB-001692.

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PR 16-APR-1993; GB-
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Best Local Similarity 100.0%;
Matches 14; Conservative
                                                                                                                                                                                                       Matches
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[Ser22] hprH(1-38)-OH.
Human parathyroid hormone; hPTH; variant; analogue;
calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
hypoparathyroidism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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R58151 standard; peptide; 38
R58151;
                                                                                                                           24 lrkklqdvhnfval 37
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1 LRKKLQDVHNFVAL 14
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les 14; Conservative
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                                                                                                                                                                                            Score 103; DB 9; Lo
Pred. No. 1.80e-03;
0; Mismatches 0;
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Pred. No. 1.80e-03;
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                                                                                                                                                                                                                                              Length 38;
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Psrch\_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Jul 30 10:38:07 1998; MasPar time 3.41 Seconds 150.175 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Title: >US-08-817-547A-18 (1-14) from US08817547A.pep 103

1 LRKKLQDVHNFVAL 14

Sequence:

Scoring table: PAM 150 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 26.838; Variance 43.748; scale 0.613

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

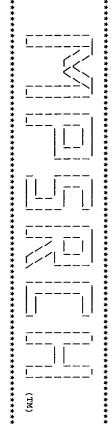
3 5 5 6 6 7 7 7 10 11 11 11 11 11 11 11 11 11 11 11 11	21	NO.
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34 35 36 37 37 37 31 115 115 115 115 115 115 145 247 462 2475 4475 4475 4475 4475 4475 4475 447	34	Length
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d then t	parathyroid hormone (	Description
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COMMENT KEYWORDS FEATURE 2-9 15-25 SUMMARY Search completed: Thu Jul 30 10:38:34 1998 Job time: 27 secs. δõ Query Match 100.0%; Score 103; DB 5; Length 34; Best Local Similarity 100.0%; Pred. No. 8.54e-08; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps Determination: NMR disease mutation; hormone; signal #region helix (right hand alpha)\
#region helix (right hand alpha)
#length 34 #molecular-weight 4128 #checksum 5508 0;

Page 2



MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Jul 30 10:36:38 1998; MasPar time 2.28 Seconds 153.724 Million cell updates/sec

Tabular output not generated.

Title: Description: Perfect Score: Sequence: >US-08-817-547A-18 (1-14) from US08817547A.pep 103 1 LRKKLQDVHNFVAL 14

Scoring table:

PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 28.165; Variance 35.949; scale 0.783

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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52.4	52.4	52.4	52.4	52.4	52.4	52.4	52.4	52.4	52.4	52.4	52.4	52.4	52.4	53.4	53.4	53.4	53.4	53.4	53.4	53.4	53.4
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GENOME POLYPROTEIN (CO	KINESIN HEAVY CHAIN.	HPR1 PROTEIN.	FOLLICLE STIMULATING H	FOLLICLE STIMULATING H	SERYL-TRNA SYNTHETASE	CAMP-DEPENDENT PROTEIN	CAMP-DEPENDENT PROTEIN	CAMP-DEPENDENT PROTEIN	CAMP-DEPENDENT PROTEIN	DNA POLYMERASE III, EP	•	HYPOTHETICAL 17.8 KD P	FILENSIN (LENS FIBER C	UBIQUITIN-ACTIVATING E	STE6 PROTEIN.	FOLLICLE STIMULATING H	FOLLICLE STIMULATING H	CALCIUM/CALMODULIN-DEP	HEMOLYSIN E (HEMOLYSIN	PLACENTAL PROLACTIN-LI	DNA-DIRECTED RNA POLYM
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(BOVINE). METAZOA; CHORDATA;	HORMONE	(REL. 35,	(REL OI)	(REI. 01		STANDARD;		LRKKLQDVHNFVAL 14	LRKKLQDVHNFVAL 68	Conservative	100.0%; ilarity 100.0%;	115 AA; 12957 MW;		26 31	1 25	SIGNAL.	PS00335; PARATHYROID;	EMBL; U15662; G558916;	D PREVENTING THEIR RENAL EXCRETION.	FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING	1-243(1995).	DEWILLE J.W., CAPEN C.C.;	STEINMEYER C.L.,	369696.	THYROID:	FROM N.A.			METAZOA; CHORDATA;	IARIS (DOG).		HOMONE DI	(REL 34)	(NUCL OF) CAUSE	/ DFT	STANDAND,		
; VERTEBRATA;	R (PARATH	LAST ANNOTATION UPDATE)	SOTIENCE II	ر		PRT;	1			0; Mism	Score 103; Pred. No.	16ED0EBC	PARATHYROID	BY SIMIL	BY SIMILARITY.		0, 1.		RENAL E	ALCIUM LE			MCCAULEY L.K.,						VERTEBRATA;		, (111111111111111111111111111111111111	/ DABATH	LAST ANNOTATION (IPDATE)	1501	2	771,		
ATA; TETRAPODA;	PRECURSOR (PARATHYRIN) (PTH).	UPDATE)	PDATE			II5 AA.				Mismatches 0; I	DB 1; Len 1.98e-10;	BC CRC32;	OID HORMONE.	ARITY.	ARITY.				XCRETION.	VEL BY DISSOLV			GRONE						ATA; TETRAPODA;		(**************************************	VRIN) (PTH)	ON (IPDATE)	D)ATE)		110 25.		
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RA POTTS J.T. JR., TREGEAR G.W., KEUTMANN H.T., NIALL H.D., SAUER R., DEFTOS L.J., DAWSON B.F., HOGAN M.I., AURBACH G.D.;

RA DEFTOS L.J., DAWSON B.F., HOGAN M.I., AURBACH G.D.;

PROC. NATL ACAD. SCI. U.S.A. 68:63-67(1971).

C.: FUNCTION. PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN BONE AND PREVENTING THEIR RENAL EXCRETION.

EMBL; V00106; G85; -.

EMBL; V001023; G163641; -.

EMBL; J00024; E163643; -.

EMBL; J00024; E163643; ALT_SEQ.

EMBL; J00024; E163645; ALT_SIG.

EMBL; M25082, G163645; -.

EMBL; M25082, G163645; -.

PRE EMBL; M25082, G163645; -.

RENEL; R02582, G163645; -.

RENEL; R02582, G163645; -.
                                                                                                 Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 14; Conservative
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SEQUENCE FROM N.A.
MEDLINE; 82037785.
MEAVER C.A., GORDON
PROC. NATL. ACAD. S
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CONFLICT
SEQUENCE
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HORMONE;
SIGNAL
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SEQUENCE FROM N.A.
MEDLINE; 80056617.
KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A.,
KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A.,
POTTS J.T. JR., RICH A.;
PPOCC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).
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MEDLINE; 71076162.

NIALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWSO AURBACH G.D., POTTS J.T. JR.;
HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 351:1586-1588(1970).
                                                                                                                                                                                                                                                                                              PROPEP
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MEDLINE; 71063634.

BREWER H.B. JR., RONAN R.;

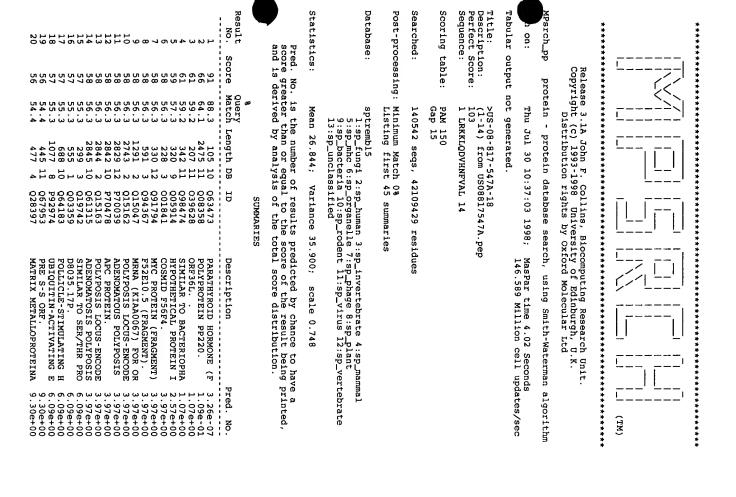
PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
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MEDLINE; 74142666.

HAMLITON J.W., NIALL H.D., JACOBS J.W., KEUTMANN COHN D.V.;

PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).
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MEDLINE; 84262483.
MEAVER C.A., GORDON D.F.,
GENE 28:319-329(1984).
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MEDLINE; 83105964.
WEAVER C.A., GORDON D.F., KEMPER B.;
WEAVER C.A., GORDON D.F., KEMPER B.;
MOL. CELL. ENDOCRINOL. 28:411-424(1982).
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115 AA;
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ACAD. SCI. U.S.A. 78:4073-4077(1981).
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                                                                                              Score 103; DB 1; Le
Pred. No. 1.98e-10;
0; Mismatches 0;
                                                                                                                                                                                                        PARATHYROID HORMONE.
V -> G (IN REF. 4).
; 673EA5F2 CRC32;
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                                                                                                 Gaps
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Search completed: Thu Jul 30 10:36:46 1998 Job time: 8 secs.



1080 8 P9333 UBIQUINU- 231 1 Q05436 CAM KINASE 245 8 Q40969 AGLIS TYPE 265 8 Q39296 AGLIS TYPE 284 9 P72666 DIMETHYLAD 39 3 018530 HYPOTHERIO 453 1 Q04934 HYPOTHERIO 693 12 Q090719 GLYCOGEN P 1167 10 Q63681 ZINC FINGE 1186 10 008961 ZINC FINGE 1186 10 008961 ZINC FINGE 1186 3 Q26216 RHOPTRY PR 2708 3 015791 CHLOROQUIN 2712 3 015791 CHLOROQUIN 2712 3 015791 CHLOROQUIN 2712 3 015791 CHLOROQUIN 2712 3 015791 CHLOROQUIN 2713 3 015791 CHLOROQUIN 2714 3 015791 CHLOROQUIN 2715 3 015791 CHLOROQUIN 2716 3 015791 CHLOROQUIN 2716 3 015791 CHLOROQUIN 2717 3 015801 STRAIN HB3 465 10 Q63341 MACROPHAGE 694 3 Q17150 C0663.9 PR 962 9 P95235 HYPOTHETIC 963 3 Q17150 PRSV YK PO 4162 12 Q98918 CONNECTINY	45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21
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01-NOV-1996
01-NOV-1996
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POLYPROTEIN!
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063473;
064473;
01-NOV-1996
01-NOV-1996
01-JAN-1998
PARATHYROID 1
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AFRICAN
SEQUENCE FROM N.A.
MEDLINE; 93327788.
SIMON-MATEO C., ADDRES G., VINUELA E.;
EMBO J. 12:2977-2987(1993).
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TISSUE-THYROID;
TISSUE-THYROID;
SCHMELZER H.J., GROSS G., MAYER H.;
ADV. GENE TECHNOL. 21:228-229(1984).
EMBL; M54875; G601933; ...
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EUKARYOTA; METAZOA; CHORDATA;
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Local Similarity 85.7%;
nes 12; Conservation
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; DS-DNA NONENVELOPED VIRUSES; IRIDOVIRIDAE.
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(TREMBLREL.)
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(TREMBLREL. 01, LAST SEQUENCE UPDATE)
(TREMBLREL. 05, LAST ANNOTATION UPDATE)
HORMONE (FRAGMENT).
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01, LAST SEQUENCE UPDATE)
02, LAST ANNOTATION UPDATE)
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Pred. No. 3.26e-07;
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RN [2]

RP COMPLETE GENOME.

RA YANGE R.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,

RA YANGE R.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,

RA YANGE R.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,

RA YANGE R.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,

RA YANGE R.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,

RA YANGE R.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,

RA YANGE R.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,

RA YANGE R.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,

RA YANGE R.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,

RA YANGE R.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,

RA YANGE R.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,

RA YANGE R.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,

RA YANGE R.J., RODRIGUEZ C.,

RA YANGE R.J., RODRIGUEZ C., ENRIQUEZ C.,

RA YANGE R.J., NOGAL M.L., YUSTE L., ENRIQUEZ C.,

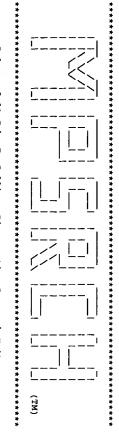
RA YANGE R.J., RODRIGUEZ L., ENRIQUEZ C.,

RA YANGE R.J., PORTAGE R.J., NOGAL M.L., YUSTE L., ENRIQUEZ C.,

RA RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,

RA RODRIGUEZ J.F., VINUELA E.;

RA RODRIGUEZ J.F., VINUELA E.;
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

9 0 1 Thu Jul 30 10:41:57 1998; MasPar time 2.73 Seconds 73.134 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-817-547A-19 (1-13) from US08817547A.pep 95 1 RKKLQDVHNEVAL 13

Scoring table: PAM 150 Gap 15

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 18.828; Variance 67.821; scale 0.278

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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[Ser19]-hPTH(1-38)-OH [I1e19]-hPTH(1-38)-OH Isopropyl-[Lys(Isopro [Ala21]-hPTH(1-38)-OH [Phe20]-hPTH(1-38)-OH [Lys19]-hPTH(1-38)-OH	Description
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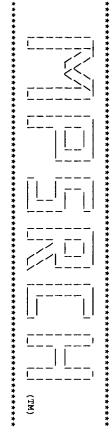
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Query Match 100.0%; Score 95; DB 9; Length 38; Best Local Similarity 100.0%; Pred. No. 1.55e-02; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	nypoparatnyroidism. Sequence 38 AA;				This peptide is an example of a highly generic formula covering			WPI; 94-018352/03.	Waelchli R, Rainer A;	Combert F. Gram H. Lewis T. Bamage D. Schnei	. (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH. Albert R. Baner W. Breckenridge R. Cardinanx F:	(SANO ) SANDOZ PATENT GMBH.	(BAUE/)	(SANO ) SANDO	19-APR-1993;	14-APR-1993;	28-JAN-1993;	28-JAN-1993;	23-DEC-1992; GB-026861.	23-DEC-1992;	18-DEC-1992;	15-JUL-1992;					hynomarathyroidism	calcium; depletion; fixation; resorption; osteopathy; osteoporosis;	(Seriy) -nerh(1-30) -OH.	20-SEP-1994 (IIISC entry)		R58123 standard; peptide; 38 AA.	RESULT 1

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RESULT 2

ID R50134 standard; peptide: 38 AA.
AC R50134,
AC R50134,
DT 20-SEP-1994 (first entry)
DE [11e19]-brH(1-38)-08;
KW Human parathyroldism.
KW Galclum, depletion; fixation; resorption; osteopathy; osteoporosis;
KW pyoparathyroldism.
KW Galclum, depletion; fixation; resorption; osteopathy; osteoporosis;
KW pyoparathyroldism.
Synthetic.
PN GB2269176-A.
PD 20-FEB-1994 (1-1993 00-1509.
PR 12-JUL-1992; GB-026615.
PR 12-JUL-1993; GB-001591.
28-JAN-1993; GB-001591.
29-JAN-1993; GB-001592.
29-J
```



MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Jul 30 10:41:13 1998; MasPar time 3.44 Seconds 138.161 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-817-547A-19 (1-13) from US08817547A.pep 95 1 RKKLQDVHNFVAL 13

Scoring table: PAM 150 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

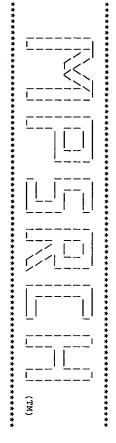
Statistics: Mean 25.919; Variance 39.318; scale 0.659

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

NO.	Score 95 95	Match 100.0	Length 34 34	555	ID 12WE 12WG	Description  parathyroid hormone ( parathyroid hormone 4 parathyroid hormone 4
n 🕰	95		35	n UI	1ZWD	
יט ת	95	•	3 3 7	n U	1ZWB	
70	95 5	100.0	37	u u	1APH	parathyroid hormone (
8	95		115	_	PTHU	
9	95	•	115	N	JC4202	hormone
10	95	•	115	μ.	PTPG	_
11	95	100.0	115	μ.	PTBO	_
12	93	٠	115	N	A05091	parathyroid hormone p
13	83	87.4	105	N	I51851	parathyroid hormone -
14	76	•	34	σ	1HTH	4
15	76	•	34	ഗ	12WA	⋖
16	58	•	183	N	S42547	
17	58	•	2475	N	S35307	polyprotein pp220 pre
18	57	•	555	N	S69641	l prote
19	56	58.9	281	N	S41854	-
20	56	٠	444	2	S09681	citrate transport pro
21	56	•	475	<u>_</u>	KCRTIH	
22	56	•	477	$\vdash$	KCMSS1	stromelysin 1 (EC 3.4
;	ת					

45	44	43	42	41	40	3 9	38	37	36	3 5	34	33	32	31	30	29	28	27	26	25	24
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1321	632	611	611	610	471	471	470	462	271	145	49	3344	1323	752	694	608	525	445	102	692	90-
ຎ	N	N	N	N	ω	N	N	2	N	UI	2	2	N	N	N	N	N	2	2	2	^
S27337	S73824	S65947	JN0066	S20444	A43480	A46400	A49499	A42401	G64698	1ATO	S70651	JQ1899	PN0568	S51866	JC2237	A46312	C64313	S43492	S53076	A34548	664068
multidrug resistance	MG242 homolog H91_orf	leukotriene-A4 hydrol	leukotriene-A4 hydrol	leukotriene-A4 hydrol	segmentation gene hed	segment polarity prot	metalloelastase HME (	macrophage elastase (	16S rRNA - Helicobact	17-hedgehog 17-kda fr	leukotriene-A4 hydrol	genome polyprotein -	connectin 3B - chicke	HPR1 protein - yeast	follitropin receptor,	gag polyprotein – hum	hypothetical protein	surface antigen - hep	probable membrane pro	follitropin receptor	DNA Copoisomerase (EC
3.62e+01	3.62e+01	3.62e+01	3.62e+01	3.62e+01	3.62e+01	3.62e+01	3.62e+01	3.62e+01	3.62e+01		3.62e+01	2.50e+01	2.50e+01		2.50e+01		2.50e+01			1.71e+01	I.I/e+UI



WPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Thu Jul 30 10:39:34 1998; MasPar time 2.25 Seconds 145.141 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-817-547A-19 (1-13) from US08817547A.pep 95 1 RKKLQDVHNFVAL 13

Scoring table: PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 27.177; Variance 32.181; scale 0.844

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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<b>Ტ Ტ Ტ Ტ Დ Ზ Ზ Ზ Ზ Ზ Ზ Ზ Ზ Ზ Ზ Ზ Ზ Ზ Ზ Ზ </b>	Score
100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0	Query Match
115 115 115 115 115 115 115 115 115 115	Length
	BB
PPHY_CANFA PTHY_BOVIN PTHY_HUMAN PTHY_RAT GLG2_ARATH P2C1_YEAST GTT1_KLEPN COG3_RAT COG3_RABT TOP3_HAEIN FSHR_CHICK YM88_YEAST FILS_HUMAN Y107_METJA FSHR_HORSE	ID
PARATHYROID HORMONE PR PARATHYROID HORMONE PR PARATHYROID HORMONE PR PARATHYROID HORMONE PR PARATHYROID HORMONE PR FARATHYROID HORMONE PR GLUCOSE-1-PHOSPHATASE 2C CITRATE-PROTON SYMPORT STROMELYSIN-1 PRECURSO STROMELYSIN-1 PRECURSO OTROMELYSIN-1 PRECURSO DIA TOPOISOMERASE II FOLLICLE STIMULATING H FOLLICLE STIMULATING H VERY HYPOTHETICAL PROTEIN H VERY HYPOTHETICAL PROTEIN H FOLLICLE STIMULATING H PROLLICLE STIMULATING H FOLLICLE STIMULATING H GENOME POLYPROTEIN (CO MACROPHAGE METALLOELAS MACROPHAGE METALLOELAS	, <b>5</b>
8.93e-10 8.93e-10 8.93e-10 8.93e-10 8.93e-10 8.93e-10 8.93e-10 8.18e-00 2.18e-00 2.18e+00 2.18e+00 2.18e+00 3.46e+00 3.46e+00 5.46e+00 5.46e+00 5.46e+00 5.46e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+00 6.55e+	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	33 3	32	31	30	29	28	27	26	25	24
50	51	51	51	51	51	51	51	51	51	52	52	52	52	52	υ	53	53	53	53	53	53
52.6	53.7	53.7	53.7	53.7	53.7	53.7	53.7	53.7	53.7	54.7	54.7	54.7	54.7	54.7	55.8	55.8	55.8	55.8	55.8	55.8	55.8
419	1444	1302	695	636	476	232	227	200	119	925	695	695	476	189	2133	1321	632	610	610	609	471
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MYC1_XENLA	RRPL_RDV	RRPL_BTV10	FSHR_PIG	RPOC_CYAPA	COGX_HUMAN	RM16_YEAST	PRRA_RAT	YIGP_ECOLI	RT13_ACACA	DBL_HUMAN	FSHR_SHEEP	FSHR_BOVIN	COGX_RAT	YNOO_YEAST	FA8_PIG	MDR1_CAEEL	Y242_MYCPN	LKHA_MOUSE	LKHA_HUMAN	LKHA_RAT	HH_DROME
MYC I PROTO-ONCOGENE P	RNA-DIRECTED RNA POLYM	RNA-DIRECTED RNA POLYM	FOLLICLE STIMULATING H	DNA-DIRECTED RNA POLYM	STROMELYSIN-2 PRECURSO	PROBABLE MITOCHONDRIAL	PLACENTAL PROLACTIN-LI	HYPOTHETICAL 22.3 KD P	MITOCHONDRIAL RIBOSOMA	PROTO-ONCOGENE DBL PRE	FOLLICLE STIMULATING H	FOLLICLE STIMULATING H	STROMELYSIN-2 PRECURSO	VERY HYPOTHETICAL 21.7	COAGULATION FACTOR VII	MULTIDRUG RESISTANCE P	HYPOTHETICAL PROTEIN M	LEUKOTRIENE A-4 HYDROL	LEUKOTRIENE A-4 HYDROL	LEUKOTRIENE A-4 HYDROL	HEDGEHOG PROTEIN PRECU
3.16e+01	2.06e+01	1.33e+01	1.33e+01	1.33e+01	1.33e+01	1.33e+01	8.55e+00														

000	BE	1 13	ď	al	ð	RESULT	Y.	?	В	Ма	Be Qu	SQ	FT	H.T	FT	X	DR	DR	ဌ	င္ပ	R.	RΑ	RA	RX X	2	RP	Z (	88	3	000	2 6	DI.	ğ	Ü	ð	ij	RESULT
TH. BOS TAURUS (BOVINE). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	ATHYROID HORMON	(REL. 01,	(REL.		YHY	<u>.</u> 2	I KNALQUVHNE VAL IS		56 RKKLQDVHNFVAL 68	13; Conse	Query Match 100.0%; Score 95; DB 1; Length 115; Best Local Similarity 100.0%; Pred. No. 8.93e-10;	NCE 115 AA; 12957 MW;	32 115 PAF	26 31	1 25 BY	HORMONE; SIGNAL.	; PARA		BONE AND PREVENTING THEIR RENAL EXCRETION.		GENE 160:241-243(1995).		ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,	MEDLINE; 95369696.		SEQUENCE FROM N.A.			EIKARYOTA: METTAZOA: CHORDATA: VERTERRATA: TETTRADODA: MAMMALTA:	CANIS FAMILIARIS (DOG).	DAB DAB		(REL. 34, LAST	(REL.		PTHY_CANFA STANDARD; PRT: 115 AA.	÷ 1

EUTHERIA; ARTIODACTYLA. [1]

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DR DR DR DR FT FT ST
Q
                          밁
                                                   Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 13; Conservative
                                                                                                                                                                                                              EMBL; V00106; G85; -.
EMBL; J00023; G163641; -.
EMBL; J00024; G163643; -.
EMBL; J00024; E18249; ALT_SEQ.
EMBL; J00024; E18250; ALT_INIT.
EMBL; K01938; G163647; -.
EMBL; M25082; G163645; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE; 82037785.

WEAVER C.A., GORDON D.F., KEMPER B.;

PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).

[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

MEDLINE; 80056617.

KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A.,

POTTS J.T. JR., RICH A.;

PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).

[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 32-115.

MEDLINE; 71076162.

NIALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWS AURBACH G.D., POTTS J.T. JR.;

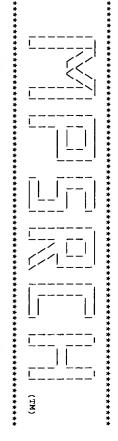
HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 351:1586-1588(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 26-115.
MEDITINE; 74142666.
HAMILTON J.W., NIALL H.D., JACOBS J.W., KEUTMANI
COHN D.V.;
PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE; 84262483.
WEAVER C.A., GORDON D.F.,
GENE 28:319-329(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE; 83105964.
WEAVER C.A., GORDON D.F., KEMPER B.;
MOL. CELL. ENDOCRINOL. 28:411-424(1982).
                                                                                                    CHAIN
CONFLICT
SEQUENCE
                                                                                                                                       PROSITE;
HORMONE;
SIGNAL
PROPEP
                                                                                                                                                                                                                                                                                                    MEDLINE; 71091588.

POTTS J.T. JR., TREGEAR G.W., KEUTMANN H.T., NIALL H.D., SAUER R., DEFTOS L.J., DAWSON B.F., HOGAN M.L., AURBACH G.D.;

PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).

-1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN BONE AND PREVENTING THEIR RENAL EXCRETION.
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 32-115.
MEDLINE; 71063634.
BREWER H.B. JR., RONAN
PROC. NATL. ACAD. SCI.
                                                                                                                                                                                                                                                                                                                                                                               SYNTHESIS OF 32-65.
                          56
  <u>س</u>ا
                 RKKLQDVHNFVAL
                                                                                                                                                                                         A01534; PTBO.
A24949; A24949.
  RKKLQDVHNFVAL
                                                                                                                                                                   SIGNAL.
                                                                                                                                                                             PS00335; PARATHYROID;
                                                                                                     106
115 /
                                                                                                                               26
32
                                                                                                    1 25
26 31
32 115 P2
06 106 V
5 AA; 12980 MW;
   <u>ا</u>
                           89
                                                                                                                                                                                                                                                                                                                                                                                                      R.;
U.S.A. 67:1862-1869(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KISSIL M.S., MEAD D.A., KEMPER B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JACOBS J.W., KEUTMANN
                                                   Score 95; DB 1; L
Pred. No. 8.93e-10;
0; Mismatches 0
                                                                                                     PARATHYROID HORMONE
V -> G (IN REF. 4).
; 673EA5F2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HOGAN M.L., DAWSON B.F.,
                                                                             Length 115;
                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H.T.,
                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTTS J.T. JR.,
                                                       0
                                                        Gaps
                                                         0
```

Search completed: Thu Jul 30 10:39:40 1998 Job time : 6 secs.



MPsrch\_pp on: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:39:58 1998; MasPar time 3.95 Seconds 138.577 Million cell updates/sec

Description: Perfect Score: Title: >US-08-817-547A-19 (1-13) from US08817547A.pep 95

Tabular output not generated.

Sequence: RKKLQDVHNFVAL 13

Scoring table: PAM 150 Gap 15

Searched: 140542 segs, 42109429 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb15
1:sp\_fung1 2:sp\_human 3:sp\_invertebrate 4:sp\_mammal
5:sp\_mhc 6:sp\_organelle 7:sp\_phage 8:sp\_plant
9:sp\_bacteria 10:sp\_rodent 11:sp\_virus 12:sp\_vertebrate
13:sp\_unclassified

Statistics: Mean 25.965; Variance 32.081; scale 0.809

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score 83	72 - 4.	Length	15 B	ID Q63473	Description
ωŅ	61 60		207 342	11	039628 Q98474	ORF36L. SIMILAR TO BACTERIOPHA
4	58	61.1	2475	11	Q08358	POLYPROTEIN PP220.
σı	57	60.0	555	Ц	Q03359	D8035.17P.
σ	57		688	10	Q64183	FOLLICLE-STIMULATING
7	56	58.9	477	4	Q28397	MATRIX METALLOPROTEINA
œ	55		693	12	Q90719	OVARIAN FOLLICLE-STIMU
Q	55		1459	ω	Q218 <b>74</b>	R09E10.5.
10	54	σ	445	11	Q67953	PRE S-S ORF.
11	54	σ	993	ω	Q17162	VINCULIN.
12	54	σ	1002	11	Q85025	HC, P3 AND CI PROTEINS
13	54	σ	1323	12	Q08476	CONNECTIN (TITIN) (FRA
14	54	σ	3344	11	P90213	H
15	54	σ	4162	12	Q98918	CONNECTIN/TITIN (FRAGM
16	53	Ü	269	ω	Q19322	COSMID F10G7.
17	53	ú	271	9	025972	16S RRNA (ADENOSINE-N6
18	53	ú	299	ω	Q19742	SIMILAR TO SER/THR PRO
19	53	55.8	709	w	015783	HYBRID HISTIDINE KINAS
20	υ G	u	1321	u	0313/0	

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LYSE-TYPE BETA-LAC ANNEXIN.  STBA.  STBA.  FROM BASES 1485094  HYD GAMMA.  URA7 CTP SYNTHETAS  URA7 CTP SYNTHETAS  HYPOTHETICAL PROTE  F52E10.5 (FRAGMENI  TARTAN PROTEIN PR  DNA HELICASE-PRIMI  SIMILAR TO MULTIDI  CORE PROTEIN NA E  RNA-DIRECTED RNA E  RNA-DIRECTED RNA E  RNA-DIRECTED RNA E  RNA-DIRECTED RNA E  RNA-DIRECTED SHA E  FRAN-DIRECTED SHA E  RNA-DIRECTED SHA E  STROMELYSIN-1/2-A  ADENOMATOUS POLYPE	12	12	2	9	12	ω	w	N	11	1	1	11	H	ω	H				<b>1</b> -1	φ	9	9	ω	9	u
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	ADENOMATOUS POLYPOSIS	STROMELYSIN-1/2-A.	(EC 4.	SMALL		MEROZOITE		MRNA (KIAA0042) FOR OR	RNA	RNA	RNA	RNA	CORE PROTEIN.	SIMILAR TO MULTIDRUG-R		TARTAN PROTEIN PRECURS			SYNTHETAS	HYD GAMMA.	BASES 1485094	STBA.	ANNEXIN.		27.930.I.

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039628
01-JAN-1998 (TREMBLREL. 05, CREATED)
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SEQUENCE FROM N.A.
JEHLE J.A., VAN DER LINDEN I.F.A.,
VIRUS RES. 0:0-0(1997).
EMBL, AF007732; G2233189; -.
SEQUENCE 207 AA; 23915 MW; D2F0
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PRELIMINARY; PRT; 105 AA.

Q63473;

01-NOV-1996 (TREMBLREL. 01, CREATED)

01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)

01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                               TISSUE-THYROID, AND PARATHYROID; SCHMELZER H.J., GROSS G., MAYER H.; ADV. GENE TECHNOL. 21:228-229(1984). EMBL; M54875; G601933; -. NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                      RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PARATHYROID HORMONE (FRAGMENT).
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                                                                                                                                                                                                               46 RKKLQDGHNFVSL 58
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1 RKKLQDVHNFVAL 13
                                                                                                                                                                                                                                                          87.48;
Local Similarity 84.68;
les 11; Conservation
                                                                                                                                                                                                                                                                                                                  105 AA; 11746 MW; 6AC3163E CRC32;
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Pred. No. 1.95e-06;

    Mismatches

 D2F0E988 CRC32;
                                       VLAK J.M.;
                                                                           BACULOVIRIDAE; GRANULOVIRUS
                                                                                                                                                                                                                                                                                           Length 105;
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Psrch\_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Jul 30 10:44:34 1998; MasPar time 2.69 Seconds 68.390 Million cell upda updates/sec

Description: Perfect Score: Title: >US-08-817-547A-20

Sequence: (1-12) from US08817547A.pep 86 1 KKLQDVHNFVAL 12

Scoring table: PAM 150 Gap 15

124785 seqs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Mean 18.088; Variance 63.020; scale 0.287

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result
& & & & & & & & & & & & & & & & & & &	Score
	Query Match
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[Alal,Ile2]-hPTH(I Human parathyroid Fusion protien con Human parathyroid Bovine parathyroid Porcine parathyroid Bovine parathyroid Bovine parathyroid Bovine parathyroid Bovine parathyroid Bovine parathyroid Bovine parathyroid Porcine parathyroid Porcine parathyroid Bovine parathyroid Bovine parathyroid Bovine parathyroid Bovine parathyroid Bovine parathyroid Human parathyroid Human parathyroid Human parathyroid Human parathyroid Human parathyroid	Description
-38 6.03e-02 ppri 6.03e-02 hor 6.03e-02 hor 6.03e-02 d h 6.03e-02 hor 6.03e-02 hor 6.03e-02 hor 6.03e-02 hor 6.03e-02 hor 6.03e-02 hor 6.03e-02	Pred. No.

В

26 kklqdvhnfval 37

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R23449	R42069	R42067	R23904	R21208	R23394	R23275	R23402	R23290	R21168	R23258	R21164	R21165	R21189	R21188	R23283	R23395	R21212	R21213	R21231	R21230	R21170	R21169	W29420	R23370	K233/1
Porcine parathyroid h	Stability-enhanced hu	Human parathyroid hor	Bovine parathyroid ho	Human parathyroid hor	Porcine parathyroid h	Bovine parathyroid ho	Porcine parathyroid h	Bovine parathyroid ho	Human parathyroid hor	Bovine parathyroid ho	Human parathyroid hor	Human parathyroid hor		Human parathyroid hor	Bovine parathyroid ho	-	Human parathyroid hor	Human parathyroid hor	Human parathyroid hor		Human parathyroid hor		Human parathyroid hor	Bovine parathyroid ho	bovine parachyroid no
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12-JUL-1993; 014384.

15-JUL-1992; GB-015009.

18-DEC-1992; GB-026415.

23-DEC-1992; GB-026859.

23-DEC-1992; GB-026861.

23-DEC-1992; GB-001691.

28-JAN-1993; GB-001691.

28-JAN-1993; GB-001691.

28-JAN-1993; GB-001693.

19-APR-1993; GB-007673.

19-APR-1993; GB-008033.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R58024 standard; peptide; 38 AA. R58024; 20-SEP-1994 (first entry) [Ala1,Ile2]-hPTH(1-38)-OH. Human parathyroid hormone; hPTH; variant; analogue; calcium; depletion; fixation; resorption; osteopathy; osteoporosis; hypoparathyroidism. Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SANO ) SANDOZ LITD.
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(SANO ) SANDOZ PATENT GMBH.
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                                                                                                                                                                                                                                                                                                                                                New active para-thyroid hormone variants - used for treating or preventing osteoporosis etc.

Example 10; Page 35; 92pp; English.

This peptide is an example of a highly generic formula covering parathyroid hormone variants useful for treating or preventing bone conditions associated with calcium depletion/resorption, in cases where calcium fixation is required (esp. osteoporosis) or to treat
                                                                                                                                                                                                                                              hypoparathyroidism.
Sequence 38 AA;
      h 100.0%;
Similarity 100.0%;
12; Conservative
      Score 86; DB 9; L
Pred. No. 6.03e-02;
0; Mismatches 0
            0;
                                                                                                                    Length 38;
            Indels
            0;
            Gaps
            0
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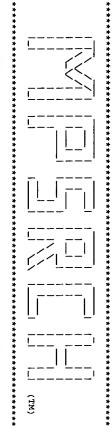
RESULT

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. on: Thu Jul 30 10:43:49 1998; MasPar time 3.30 Seconds 132.749 Million cell updates/sec

Description: Perfect Score: Sequence: Title: >US-08-817-547A-20 (1-12) from US08817547A.pep 86 1 KKLQDVHNFVAL 12

Scoring table: PAM 150 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 25.131; Variance 37.196; scale 0.676

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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59.3	59.3	59.3	59.3	59.3	59.3	60.5	60.5	60.5	60.5	60.5	61.6	61.6	61.6	61.6	61.6	61.6	61.6	61.6	61.6	Ν	N
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A43377	TVHUDB	KCHUS2	S50292	S20583	C65188	I45896	JC1493	S13526	KCRTS2	S66274	S27337	S73824	S65947	JN0066	S20444	A43480	A46400	1ATO	S70651	JQ1899	PNOUGH
RNA-directed RNA poly	transforming protein	stromelysin 2 (EC 3.4	ribosomal protein L16	DNA-directed RNA poly	hypothetical 22.3 kD	imulati	follitropin receptor	hydrogenase homolog,	stromelysin 2 (EC 3.4	annexin - pepper	multidrug resistance	MG242 homolog H91_orf	leukotriene-A4 hydrol		leukotriene-A4 hydrol	ation gene	segment polarity prot	17-hedgehog 17-kda fr	leukotriene-A4 hydrol	genome polyprotein -	connectin 3B - chicke
4.36e+01	4.36e+01	4.36e+01	4.36e+01	4.36e+01	4.36e+01	2.98e+01	2.98e+01	2.98e+01	2.98e+01	2.98e+01		2.03e+01	2.03e+01	2.03e+01	2.03e+01	2.03e+01		2.03e+01		1.37e+01	1.3/e+01

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COMMENT
EXPUTES

Alsease mitation; hormone; signal
TENTER

EVERY

STREAM

STREAM

STREAM

ALIX (right hand alpha)

STREAM

10.04; Stoce 86, DB 5; Length 34;

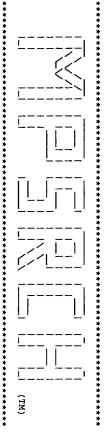
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 13 KILOPHHYVAL 14

Oy 1 KILOPHHYVAL 12

Search completed: The Jul 30 10:44:16 1998

Do time: 27 secs.
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm on:

Thu Jul 30 10:42:38 1998; MasPar time 2.23 Seconds 134.872 Million cell updates/sec

Tabular output not generated.

Title: >US-08-817-547A-20
Description: (1-12) from US08817547A.pep
Perfect Score: 86

Sequence: 1 KKLQDVHNFVAL 12

Scoring table: PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 26.327; Variance 30.652; scale 0.859

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Query No. Score Match Length DB ID    Print
Query Query Atch Length DB ID  PHY_CANFA 100.0  115 1 PTHY_BOVIN 115 1 PTHY_BIG 100.0  115 1 PTHY_BOVIN  100.0  100.0  100.0  115 1 PTHY_BOVIN  100.0  100.0  100.0  100.0  100.0  100.0  100.0  115 1 PTHY_BOVIN  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  100.0  10
Length DB ID  Description  PHY_CANFA  115 1 PTHY_BOVIN  PARATHYROID HORMONE PR  115 1 PTHY_BOVIN  PARATHYROID HORMONE PR  115 1 PTHY_BOVIN  PARATHYROID HORMONE PR  115 1 PTHY_BIG  PARATHYROID HORMONE PR  115 1 PTHY_BIG  PARATHYROID HORMONE PR  PARATHYROI
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Description  PARATHYROID HORMONE PR STROMELYSIN-1 PRECURSO PROTEIN PRECURSO PROTEIN PRECURSO PROTEIN PRECURSO PROTEIN A 4 HYDROL LEUKOTRIENE A 4 HYDROL LEUKOTRIENE A 5 HYDROL LEUKOTRIENE A 5 HYDROL LEUKOTRIENE A 6 HYDROL LEUKOTRIENE A 7 HYDROL LEUKOTRI
G G G G G G G G G G G G G G G G G G G
Pred. No. 5.76e-08 5.76e-08 5.76e-08 5.76e-00 1.06e-00 1.06e-00 1.72e-00 1.72e-00 1.72e-00 2.76e-00 2.76e-00 2.76e-00 2.76e-00 4.42e-00 7.01e-00 7.01e-00 7.01e-00

45	44	43	42	41	40	39	38	37	36	35	34	<u>ω</u> ω	32	31	30	29	28	27	26	25	24
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ATMB_SALTY	DYHC_NECHA	MSP1_PLAFM	MSP1_PLAFF	MSP1_PLAF3	MFD_BACSU	TVID_SALTI	VP61_NPVAC	COG3_HUMAN	COGM_HUMAN	COGM_MOUSE	VSH5_DICDI	RPOC_PROHO	RRPL_RDV	DBL_HUMAN	FSHR_PIG	RPOC_CYAPA	COGX_HUMAN	RM16_YEAST	YIGP_ECOLI	RT13_ACACA	FSHR_SHEEP
MG(2+) TRANSPORT ATPAS	DYNEIN HEAVY CHAIN, CY	MEROZOITE SURFACE PROT	MEROZOITE SURFACE PROT	MEROZOITE SURFACE PROT	TRANSCRIPTION-REPAIR C	VI POLYSACCHARIDE BIOS	61 KD PROTEIN.	STROMELYSIN-1 PRECURSO	MACROPHAGE METALLOELAS	MACROPHAGE METALLOELAS	VEGETATIVE SPECIFIC PR	DNA-DIRECTED RNA POLYM	RNA-DIRECTED RNA POLYM	PROTO-ONCOGENE DBL PRE	FOLLICLE STIMULATING H	DNA-DIRECTED RNA POLYM	STROMELYSIN-2 PRECURSO	PROBABLE MITOCHONDRIAL	HYPOTHETICAL 22.3 KD P	MITOCHONDRIAL RIBOSOMA	FOLLICLE STIMULATING H
2.69e+01	1.73e+01	1.73e+01	1.73e+01	1.73e+01	1.73e+01	1.73e+01	1.73e+01	1.73e+01	1.73e+01	1.73e+01	1.73e+01	1.73e+01	1.11e+01	7.01e+00							

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ACCORDANCE SOLUTION
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RESULT
ID PT
AC PC
DT 21
DT 21
DT 01
DT 91
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Best Local Similarity 100.0%;
Matches 12; Conservative
                                                                                                           PTHY_BOVIN
P01268;
21-JUL-1986
21-JUL-1986
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTHY_CANFA
P52212;
01-OCT-1996
01-OCT-1996
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROPEP
CHAIN
PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
PTH.
BOS TAURUS (BOVINE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS BONE AND PREVENTING THEIR RENAL EXCRETION.

EMBL; U15662; G558916; -...

PROSITE; PS00335; PARATHYROID; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUS-PARATHYROID;
MEDLINE; 95369696.
ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K.,
DEWILLE J.W., CAPEN C.C.;
GENE 160:241-243(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CANIS FAMILIARIS (DOG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EUTHERIA; CARNIVORA.
                                                                                                                                                                                                                                                                                                                                  57 KKLQDVHNFVAL 68
||||||||||||
1 KKLQDVHNFVAL 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26
32 1
115 AA;
                                                                        (REL. 01, CREATED)
(REL. 01, LAST SEQUENCE UPDATE)
(REL. 35, LAST ANNOTATION UPDATE)
HORMONE PRECURSOR (PARATHYRIN) (PTH).
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(REL. 34, LAST SEQUENCE UPDATE)
(REL. 34, LAST ANNOTATION UPDATE)
HORMONE PRECURSOR (PARATHYRIN) (PTH).
                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 B)
31 B)
115 PI
12957 MW;
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BY SIMILARITY.
PARATHYROID HORMONE.
W; 16ED0EBC CRC32;
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Pred. No. 5.76e-08;
0; Mismatches (
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EUTHERIA; ARTIODACTYLA. [1]

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Best Local Similarity 100.0%;
Matches 12; Conservative
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RX MEDLINE; 71091588.

RA DEFTOS L.J. JARSON B.F., MEGRANN H.T., NIALL H.D., SAUER R., DEFTOS L.J. DAWSON B.F., ABORDAN, H.T., AURBACH G.D.;

CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN EMBL; V00106; G85; --

EMBL; V00106; G85; --

EMBL; J00024; G163641; --

EMBL; J00024; G163643; --

EMBL; J00024; E18260; ALT_SEQ.

EMBL; J00024; E18250; ALT_SEQ.

EMBL; J00024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
CONFLICT
SEQUENCE
                                                                                                                                                                                                                          HORMONE; PS00335; PARATHYROID; SIGNAL PROPEP
                      57 KKLQDVHNFVAL 68
1 KKLQDVHNFVAL 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 32-115.
MEDIINE, 71063634.
BREWER H.B. JR., RONAN R.;
PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 32-115.
MEDLINE; 71076162.
NIALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWSC HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 351:1586-1588(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 26-115.

MEDLINE; 74142666.

HAMILTON J.W., NIALL H.D., JACOBS J.W., KEUTMANN H.T., POTTS J.T.

COHN D.V.;

PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE: 84262483.
WEAVER C.A., GORDON D.F.,
GENE 28:319-329(1984).
[5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE; 83105964.
WEAVER C.A., GORDON D.F., KEMPER B.;
MOL. CELL. ENDOCRINOL. 28:411-424(1882).
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MEDLINE: 82037785.
WEAVER C.A., GORDON D.F., KEMPER B.;
PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE, 80056617.
KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A.,
POOTS J.T., FICH A.;
PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).
                                                                                                                                                            26
32
106
115 AA;
                                                                                         25
31
115 PARATHYROID HORMONE.
106 V -> G (IN REF. 4).
4A; 12980 MW; 673EA5F2 CRC32;
                                                 Score 86; DB 1; Length 115;
Pred. No. 5.76e-08;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KISSIL M.S., MEAD D.A., KEMPER B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAUER R., HOGAN M.L., DAWSON B.F.,
                                                                                                                                                                                                                                                                         ۲
                                                 0;
                                            Gaps
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Search completed: Thu Jul 30 10:42:44 1998 Job time : 6 Secs.

1 74 4 57 601 7 55 7 55 8 57 112 113 114 115 115 116 117 118 118 119 119 119 119 119 119 119 119	Pred. No score grand is different No. Score	Database: Statistics:	Scoring table: Searched: Post-processing:	MPSICh_pp pro  on:  Tabular output  Title: Description: Perfect Score: Sequence:	
105 10 0 106.0 2007 10 0 109.8 342 11 0 109.8 342 11 0 109.8 342 11 0 109.8 342 11 0 109.8 12 0	No. is the number of results predicted by chance to have greater than or equal to the score of the result being ps derived by analysis of the total score distribution.  SUMMARIES  Query Query Query Query Pre Match Length DB ID  Description P	<pre>sptremb15 1:sp_fung1 2:sp_human 3:sp_invertebrate 4:sp_mamma. 5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant 9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertel 13:sp_unclassified Mean 25.060; Variance 31.683; scale 0.791</pre>	: PAM 150 Gap 15 140542 seqs, 42109429 residues ng: Minimum Match 0% Listing first 45 summaries	right (c) 193-1998 University of Edinburgh, U.K. right (c) 193-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd  otein - protein database search, using Smith-Watern Thu Jul 30 10:43:01 1998; MasPar time 3.89 Seco not generated.  >US-08-817-547A-20 (1-12) from US08817547A.pep 86 1 KKLQDVHNFVAL 12	
2.00e-04 2.77e-01 1.17e+00 1.87e+00 2.97e+00 2.97e+00 4.70e+00 4.70e+00 4.70e+00 4.70e+00 4.70e+00 7.39e+00 7.39e+01 1.16e+01 1.16e+01 1.16e+01 1.16e+01 1.16e+01 1.16e+01 1.16e+01 1.16e+01 1.16e+01 1.16e+01 1.16e+01 1.16e+01 1.16e+01 1.16e+01 1.16e+01 1.16e+01 1.16e+01 1.16e+01 1.16e+01 1.16e+01 1.16e+01 1.16e+01 1.16e+01 1.16e+01 1.16e+01	printed, pred. No.	p_mammal .nt p_vertebrate		an algorithm nds updates/sec	* 1

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T: 207 AA. SEQUENCE UPDATE) ANNOTATION UPDATE) ANGE; BACULOVIRIDAE; GRANULOVIRUS , VLAK J.M.; SEDE988 CRC32;	; DB 10; Length 105; . 2.00e-04; matches 1; Indels 0;	ED) SEQUENCE UPDATE) ANNOTATION UPDATE) (IEBRATA; TETRAPODA; MAMMALIA; (3).	RIMILAR TO MULTIDRUG-R 1. RNA-DEPENDENT RNA POLY 1 ARYLALKYLAMINE N-ACETY 2. MAJOR MEROZOITE SURFAC 2. MAJOR MAJOR MAJOR MEROZOITE SURFAC 2. MAJOR MAJOR MEROZOITE SURFAC 2. MAJOR MAJ
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Query Match
Query Match
Best Local Similarity 66.7%; Pred. No. 1.70e-01;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 144 RLOEVHDFV 152
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Qy 2 KLODVHNFV 10

Search completed: Thu Jul 30 10:43:30 1998
Job time: 29 secs.
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5	Protein sequence incl	P40251	4	115			\$5
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o	parathyroid	R21169	4	84	•		Ö
•	parathyroid	R21170	4	84	•		39
თ	rathyroid	R21241	4	84	•		88
. 64	Porcine parathyroid h	R23425	4	84	•		37
	Human parathyroid hor	R21168	4	84	•		36
. 64	Bovine parathyroid ho	R23258	4	84	•		35
5	Human parathyroid hor	R21189	4	84			34
		R21188	4	84	•		ω
6	parathyroid	R21183	4	84			32
64		R21238	4	84			31
6		R21212	4	84	•		30
. 64	Human parathyroid hor	R21213	4	84			29
o		R23327	4	84			88
٠	e parathyroid	R23549	4	84			27
. 64	arathyroid	W29420	25	84	•		26
		R23483	4	84	•		25
5	Human parathyroid hor	R21156	4	84	•		24
٠	Human parathyroid hor	R21257	4	84			23
'n		R23485	4	84	•		22
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New parathyroid hormone fragment and its naturally occurring derivs. - used to treat osteoporosis, hypertonia, hypertonia, hyperathyroidism, electrolyte imbalance associated with kidney of failure, etc.

Claim 1; page 6; 22pp; German.

Chaim 2; page 6; 22pp; German.

Chaim 3; page 6; 22pp; German.

Chaim 1; page 6; 22pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 11; Conservative
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DE3938738-A.
D8-MAY-1991.
27-OCT-1989; 935738.
27-OCT-1989; DE-935738.
(FORS/) FORSSMANN W.
R58024 standard; peptide; 38 AA.
R58024;
20-SEP-1994 (first entry)
[Ala1,Ile2]-hPTH(1-38)-OH.
Human parathyroid hormone; hPTH; variant; analogue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R11882 standard; protein; 37 AA.
R11882;
24-JUL-1991 (first entry)
Parathyroid hormone fragment (1-37).
Parathyroid hormone; osteoporosis; hypertonia; hypoparathyroidism; Parathyroid hormone; osteoporosis; hypertonia; hypoparathyroidism; kidney fallure; hypertension; acute renal insufficiency.
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1 KLQDVHNFVAL 11
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KW hypoparathyroidism.

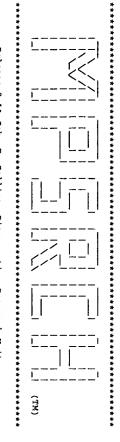
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PD 02-FEB-1994.
PE 12-JUL-1993; 014384.
PF 12-JUL-1993; GB-015009.
PR 15-JUL-1992; GB-026815.
PR 15-JUL-1992; GB-026859.
PR 15-JUL-1992; GB-026861.
PR 23-DEC-1992; GB-026863.
PR 14-APR-1993; GB-001692.
PR 14-APR-1993; GB-001692.
PR 18-JAN-1993; GB-001692.
PR 18-JAN-1993; GB-008033.
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Search completed: Thu Jul 30 10:47:36 1998 Job time: 24 secs.
                                                                                                          В
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Best Local Similarity 100.0%;
Matches 11; Conservative
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Jul 30 10:46:26 1998; MasPar time 3.26 Seconds 123.145 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Title: >US-08-817-547A-21 (1-11) from US08817547A.pep 79 1 KLQDVHNFVAL 11

Sequence:

Scoring table: PAM 150 Gap 15

Searched: 120441 segs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nr13d

Statistics: Mean 24.418; Variance 35.126; scale 0.695

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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62.0	62.0	62.0	62.0	62.0	62.0	62.0	62.0	62.0	62.0	62.0	62.0	62.0	62.0	63.3	63.3	63.3	63.3			63.3	
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JC4172	S22610	JC5145	S50054	G64068	KCRBS1	KCMSS1	KCRTIH	A43480	A46400	A26081	S07569	1ATO	B40535	PN0568	D36892	S28491	S40449	S25128	H40781	A49499	
DNA (cytosine-5-)-met	DNA (cytosine-5-)-met	DNA (cytosine-5-)-met	chloride channel prot	DNA topoisomerase (EC	stromelysin 1 (EC 3.4	1 (EC	stromelysin 1 (EC 3.4	ation gene	segment polarity prot	epoxide hydrolase (EC	protein H5 - slime mo	17-hedgehog 17-kda fr	clathrin-associated p	connectin 3B - chicke	VipC 5'-region hypoth	hypothetical protein	pro-hormone convertas	61K protein - Autogra	hypothetical 60.7K pr	metalloelastase HME (	
5.40e+01	5.40e+01	5.40e+01		5.40e+01	5.40e+01	5.40e+01	5.40e+01	5.40e+01	5.40e+01	5.40e+01	5.40e+01	5.40e+01	5.40e+01	3.67e+01	3.67e+01	3.67e+01	3.67e+01	3.67e+01	3.67e+01	3.67e+01	

succinyl human parathyroid hormo fformal_name synthetic A67743. Roesch, P.; Marx, U.C. submitted to the Brookhaven Protences PDB:1ZWG TN003319 Marx, U.C. in Strukturen Verschiedener Parapp.0, Bayreuth: University of lution: not applicable	RESULT 2  1ZWG #type complete  TITLE parathyroid hormone 4 37 mutant N-TERMI  Synthetic synthetic  ALTERNATE NAMES n-succinyl-hoth(4-37)	Db 24 KLQDVHNFVAL 34           Qy 1 KLQDVHNFVAL 11	Query Match 100.0%; Score 79; DB 5; Length Best Local Similarity 100.0%; pred. No. 7.53e-05; Matches 11; Conservative 0; Mismatches 0; Inc	**PATURE 15-25 #region helix (right hand alpha) SUMMARY #length 34 #molecular-weight 4128 #ch	hors k Resolu Determ	#EFFERENCE TROUTZ12  **REFERENCE A67860  #authors Roesch, P.; Marx, U.C.  #submission submitted to the Brookhaven Protein Data  #cross-references PDB:1ZWE  **REFERENCE TROUTZ21	1 12WE #type complete parathyroid hormone (residues 4-37) - ] E_NAMES HPTH(4-37) Structure of human parathyroid hormone structures formal parathyroid hormone
ne 4-37, NMR, 10 structures ein Data Bank, June 1996 thormonfragmente in Loesung, Bayreuth (Thesis), 1996	ete 37 mutant N-TERMINAL SUCCINYLATED -		Length 34; ; 0; Indels 0; Gaps 0;	) #checksum 5508	ormonfragmente in Loesung, Bayreuth (Thesis), 1996	n Data Bank, June 1996	

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COMMENT
KETHORDS

disease mutation; hormone; signal
EARURE
2-9
15-25
15-25

SUMMARY

Alength 34 #molecular-weight 4128 #checksum 5508

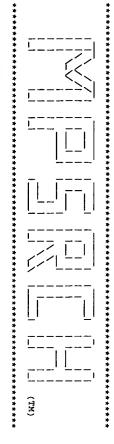
Query Match
Best Local Similarity 100.0%; Score 79: DB 5; Length 34;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 KLOPHNFVAL 14

Oy 1 KLODYHNFVAL 11

Search completed: Thu Jul 30 10:46:54 1998

Job time: 28 secs.
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(Psrch\_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Jul 30 10:45:13 1998; MasPar time 2.26 Seconds 122.035 Million cell updates/sec

Tabular output not generated.

Description:
Perfect Score:
Sequence: Title: >US-08-817-547A-21 (1-11) from US08817547A.pep 79 1 KLQDVHNFVAL 11

Scoring table: PAM 150 Gap 15

Searched: 69111 segs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 25.575; Variance 28.974; scale 0.883

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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77777777777777777777777777777777777777	Score
100.0 100.0 100.0 100.0 100.0 67.1 64.6 64.6 63.3 63.3 63.3 63.3 63.3 63.3	% Query Match
115 115 115 115 1321 2302 2444 462 470 471 142 3142 475 477 477 477	Length
	ВВ
PTHY_CANFA PTHY_BOVIN PTHY_PIG PTHY_PIG PTHY_RAT Y242_MYCPN MDR1_CAEEL YIGP_ECOLI RM16_YEAST RRPL_RDV COGM_MOUSE COGM_MOUSE COGM_HUMAN VP61_NPVAC TVID_SALTI AP17_RAT AP17_RAT AP17_RAT AP17_RAT COG3_RABIT COG3_RABIT COG3_RABIT COG3_RABIT COG3_RABIT	ID
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<b>4</b> 5	44	43	42	41	40	39	ა 8	37	36	35	34	33	32	31	30	29	28	27	26	25	24
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59.5	59.5	59.5	59.5	59.5	60.8	60.8	60.8	60.8	60.8	60.8	60.8	60.8	60.8	60.8	60.8	60.8	60.8	60.8	60.8	62.0	62.0
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POLG_PRSVH	FSHR_HORSE	FSHR_EQUAS	FAF1_MOUSE	CD1_SYLFL	DYHC_DICDI	MIDM_MOUSE	VIVD_BPT7	CC54_YEAST	HELI_VZVD	RED1_YEAST	FSHR_CHICK	FSHR_RAT	NADR_ECOLI	NADR_SALTY	YQFD_BACSU	LDH_STRMU	YG00_HAEIN	ML11_BRARE	Y441_MYCPN	MTDM_HUMAN	GEF1_YEAST
GENOME POLYPROTEIN (CO	FOLLICLE STIMULATING H	FOLLICLE STIMULATING H	FAF1 PROTEIN (FAS-ASSO	T-CELL SURFACE GLYCOPR	DYNEIN HEAVY CHAIN, CY	DNA (CYTOSINE-5)-METHY	INTERNAL VIRION PROTEI	CELL DIVISION CONTROL	PROBABLE HELICASE.	RED1 PROTEIN.	FOLLICLE STIMULATING H	FOLLICLE STIMULATING H	TRANSCRIPTIONAL REGULA	TRANSCRIPTIONAL REGULA	HYPOTHETICAL 45.7 KD P	L-LACTATE DEHYDROGENAS	HYPOTHETICAL PROTEIN H	MELATONIN RECEPTOR TYP	HYPOTHETICAL PROTEIN M	DNA (CYTOSINE-5)-METHY	GEF1 PROTEIN (VOLTAGE-
3.55e+01	3.55e+01	3.55e+01		3.55e+01	2.27e+01	2.27e+01	2.27e+01	2.27e+01	2.27e+01	2.27e+01	2.27e+01	2.27e+01	2.27e+01	2.27e+01	2.27e+01	2.27e+01	2.27e+01	2.27e+01	2.27e+01	1.44e+01	1.44e+01

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PTH. BOS TAURUS (BOVINE). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	THYROID HORMO	(REL. 01, LAST	(REL.		YHT	2	1 KLQDVHNEVAL 11	58 KLQDVHNEVAL 68	Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	atch 100.0%; Score 79; DB 1; Length 115; cal Similarity 100.0%; Pred. No. 1.01e-06;	SEQUENCE 115 AA; 12957 MW; 16ED0EBC CRC32;	32 115 PA	26 31	1 25 BY		PROSITE; PS00335; PARATHYROID; 1.	; G558916;	BONE AND PREVENTING THEIR RENAL EXCRETION.	-!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN	GENE 160:241-243(1995).		ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,	MEDLINE; 95369696.	TISSUE-PARATHYROID;	SEOCIENCE FROM N.A.	[1]	EUNARIOIA; METAEOA; CHORDATA; VERTEBRATA; LEIRAFODA; MARMALIA; RITHERTA: CARNIVORA			HORMONE PRECUR	(REL. 34, LAST	01-001-1996 (REI. 34. LAST SECTIONCE HUDATE)	DET.	DESCRIPTION STANDARD; EXI; III AN.	HUV CANTA CHANTADA. DOM. 115	

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ROTTS J.T. JR., TREGEAR G.W., KEUTMANN H.T., NIALL H.D., SAU POTTS J.T. JR., TREGEAR G.W., AURBACH G.D.;

DEFTOS L.J., DARSON B.F., HOGAN M.L., AURBACH G.D.;

PROC. NATL. ACAD. SCI. U.S.A. 68:63:67(1971).

PROC. NATL. ACAD. SCI. U.S.A. 68:63:67(1971).

PROC. NATL. ACAD. SCI. U.S.A. 68:23-87(1971).

PROC. NATL. ACAD. SCI. U.S.A. 68:23-87(1971).

PROC. NATL. ACAD. SCI. U.S.A. 68:23-87(1971).

REMBL; V00106; G88; -.

REMBL; V00106; G88; -.

REMBL; J00024; E18250; ALT_INIT.

REMBL; V01938; G163643; -.

REMBL; W15082; G163645; -.

REMBL; W15082; G163645; -.
                                                    Query Match
Best Local S
Matches 1
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MEDLINE; 80056617.

KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS POTTS J.T. JR., RICH A.;

POTTS J.T. JR., RICH A.;

PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).
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MEDLINE; 82037785.

WEAVER C.A., GORDON D.F., KEMPER B.;

PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).
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MEDLINE: 84262483.
WEAVER C.A., GORDON D.F.,
GENE 28:319-329(1984).
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MEDLINE; 83105964.
WEAVER C.A., GORDON D.F., KEMPER B.;
MOL. CELL. ENDOCRINOL. 28:411-424(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 32-115.

MEDLINE; 71076162.

MIALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWSON B.F., AURBACH G.D., POTTS J.T. JR.;

AURBACH G.D., POTTS J.T. JR.;

HOPPE-SEXLER'S Z. PHYSIOL. CHEM. 351:1586-1588(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 26-115.

MEDLINE; 74142666.

MEDLINE; 74142666.

MIALL H.D., JACOBS J.W., KEUTMAN CONN D.V.;

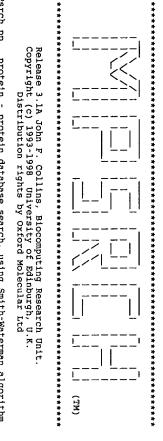
CONN D.V.;

CONN D.V.;

CONN D.V.;

CONN D.V.;
                                                                                                          CHAIN
CONFLICT
SEQUENCE
                                                                                                                                                 PROSITE;
HORMONE;
SIGNAL
PROPEP
                                                                                                                                                                                                                                                                                                                                                                                        SYNTHESIS OF 32-65. MEDLINE; 71091588.
                                                                                                                                                                                                    PIR; A01534; PTBO.
PIR; A24949; A24949.
                           58
                 KLQDVHNEVAL 68
  KLODVHNFVAL 11
                                                      h 100.0%;
Similarity 100.0%;
11; Conservative
                                                                                                                                                                             SIGNAL.
                                                                                                                                                                                          PS00335; PARATHYROID; 1.
                                                                                                          26
32
106
115 AA;
                                                                                                            25
31
115
106
V
1080 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                 R.;
U.S.A. 67:1862-1869(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KISSIL M.S., MEAD D.A., KEMPER B.;
                                                         Score 79; DB 1; L
Pred. No. 1.01e-06;
0; Mismatches 0
                                                                                                             PARATHYROID HORMONE
V -> G (IN REF. 4).
; 673EA5F2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KEUTMANN H.T., POTTS J.T. JR.,
                                                                                      Length 115;
                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J.,
                                                                                                                                                                                                                                                                                                                                               THE SALTS IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SHARP P.A.,
                                                                                                                                                                                                                                                                                                                                                                                       SAUER R.,
                                                                 0
                                                                 Gaps
                                                                   0
```

Search completed: Thu Jul 30 10:45:20 1998 Job time : 7 secs.



(Psrch\_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. on : Thu Jul 30 10:45:37 1998; MasPar time 3.84 Seconds 120.566 Million cell updates/sec

Sequence: Description: Perfect Score: >US-08-817-547A-21 (1-11) from US08817547A.pep 79 1 KLQDVHNFVAL 11

Title:

Scoring table:

PAM 150 Gap 15

Searched: 140542 seqs, 42109429 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb15
1:sp\_fung1 2:sp\_human 3:sp\_invertebrate 4:sp\_mammal
5:sp\_mhc 6:sp\_organelle 7:sp\_phage 8:sp\_plant
9:sp\_bacteria 10:sp\_rodent 11:sp\_virus 12:sp\_vertebrate
13:sp\_unclassified

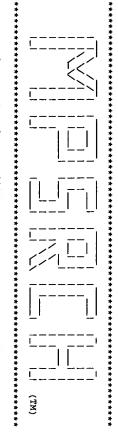
Statistics: Mean 24.328; Variance 30.213; scale 0.805

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

20 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result
55555555555555555555555555555555555555	Score
784 677 677 677 677 677 677 677 677 677 67	Query Match
105 993 993 1325 1325 1325 1325 1232 1232 1233 144 146 146 146 146 146 146 146 146 146	Length
111 111 111 11 11 11 11 11 11 11 11 11	BB
063473 0171628 0171628 0171629 098474 098474 0213349 0213349 021349 077216 0077216 0077216 0077216 0077216 0077216 0077216 0077216 0077216 0077216 0077216 0077216 0077216 0077216 0077216 0077216 0077216 0077216 0077216 0077216 0077216 0077216 0077216 0077216 0077216 0077216 0077216 0077216 0077216 0077216 0077216 0077216 0077216 0077216 0077216 0077216 0077216 0077216 0077216	Ħ
PARATHYROID HORMONE (FOR SELL.) VINCULIN. SIMILAR TO BACTERIOPHA B035.17P. K08E7.9. STBA. HYD GAMMA. HYD GAMMA. URA7 CTP SYNTHETASE. SIMILAR TO MULTIDRUG-R RNA-DEPENDENT RNA POLY ARYLALKYLAMINE N-ACETY HYDROGENASE SMALL SUBUFERCOHGLELATASE (EC 4.9 MACROPHAGE METALLOELAS STROMELYSIN-1/2-A. PREPRO-HORMONE CONVERT PEZO. SIMILAR TO THE ATP-BIN	Description
3.43e-03 7.48e-02 2.47e+00 3.95e+00 3.95e+00 6.29e+00 6.29e+00 9.94e+00 9.94e+00 1.56e+01 1.56e+01 1.56e+01 1.56e+01 1.56e+01 1.56e+01 1.56e+01 1.56e+01 1.56e+01 1.56e+01 1.56e+01 1.56e+01 1.56e+01 1.56e+01 1.56e+01 1.56e+01 1.56e+01	Pred. No.

45	44	43	42	41	40	39	3 8	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	17
48	48	48	48	48	48	49	49	49	49	49	49	49	49	49	49	49	49	49	49	49	49	50	50	50
	•		•	•	•	•	•	•	•	•	•		•	•	•	•		•	•	٠	•	•	63.3	٠
1289	787	693	453	377	232	1918	1774	1564	1537	1490	1190	743	732	726	477	455	299	227	227	227	142	4162	1323	1254
ω	φ	12	ᆫ	ω	9	ω	ω	4	12	12	w	ω	ω	w	4	10	w	4	4	4	w	12	12	u
001495	032799	Q90719	Q04934	017273	P95776	Q93637	Q93636	Q28689	Q92072	P79922	Q20187	017305	P91676	Q27936	Q28397	P97869	Q19742	Q28973	Q28972	Q28974	019123	Q98918	Q08476	026599
SIMILARITY TO THE ATP-	PYRUVATE FORMATE-LYASE	OVARIAN FOLLICLE-STIMU	HYPOTHETICAL 50.0 KD P	T27A1.2 PROTEIN.	DNA FOR DTDP-RHAMNOSE	F29G6.3A.	F29G6.3B.	EPITHELIAL BASOLATELAR	MODIFICATION METHYLASE	≫	F39B1.1 (FRAGMENT).	ZK250.1 PROTEIN.	MCM5 HOMOLOG.	ATP-BINDING CASSETTE P	MATRIX METALLOPROTEINA	MICROSOMAL EPOXIDE HYD	SIMILAR TO SER/THR PRO	CYTOCHROME P450 2C33V2	CYTOCHROME P450 2C33V1	CYTOCHROME P450 2C33V3	SIMILARITY TO CLATHRIN	CONNECTIN/TITIN (FRAGM	CONNECTIN (TITIN) (FRA	SMDR2.
	3.78e+01	3.78e+01	. 7	3.78e+01			2.44e+01	2.44e+01		2.44e+01	2.44e+01			2.44e+01	1.56e+01	1.56e+01								



MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not Thu Jul 30 10:50:05 1998; generated. MasPar time 2.64 Seconds 58.155 Million cell updates/sec

Title:

Description: Perfect Score: >US-08-817-547A-22 (1-10) from US08817547A.pep 72

Sequence: 1 LQDVHNFVAL 10

Scoring table: PAM 150 Gap 15

124785 seqs, 15338987

Post-processing: Minimum Match Listing first 45 summaries

Database: a-geneseq31-2 1:part1 2:pa

i:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 16.979; Variance 58.346; scale 0.291

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

esult No.	Score	Query Match	Length	B	ID	Description	Pred. No
1	72	100.0	38	ٔ و	R58151	[Ser22]-hPTH(1-38)-OH	8.81e-01
2	72	100.0	38	9	R58153	[Arg26]-hPTH(1-38)-OH	
w	72		38	φ	R58022	[Ile1]-hPTH(1-38)-OH.	8.81e-01
4	72		38	9	R58140	1]-hPTH(1	
տ	72	100.0	38	9	R58142	[Asn21]-hPTH(1-38)-OH	8.81e-01
σ	72	100.0	38	φ	R58129	[His19]-hPTH(1-38)-OH	
7	72	100.0	38	ø	R58133	[Asp19]-hPTH(1-38)-OH	.81e-
8	72	100.0	44	26	P30015	Human parathyroid hor	8.81e-01
Q	72	100.0	47	25	W21946	Fusion protien compri	8.81e-01
10	72	100.0	84	27	W25687	Human parathyroid hor	8.81e-01
11	72	100.0	84	4	R23237	Human parathyroid hor	
12	72	100.0	84	4	R21192	Human parathyroid hor	8.81e-01
13	72	100.0	84	4	R23309	Bovine parathyroid ho	8.81e-01
14	72	100.0	84	4	R23276	Bovine parathyroid ho	8.81e-01
15	72	100.0	84	4	R21254	Human parathyroid hor	8.81e-01
16	72	100.0	84	4	R23429	Porcine parathyroid h	8.81e-01
17	72	100.0	84	4	R23259	Bovine parathyroid ho	
18	72	100.0	84	4	R23485	Porcine parathyroid h	8.81e-01
19	72	100.0	84	4	R21257	Human parathyroid hor	8.81e-01

72 100.0 84 4 R33424 72 100.0 84 5 R29568 Oxidation resistant [ 72 100.0 84 5 R29568 Oxidation resistant [ 72 100.0 84 5 R29563 Oxidation resistant [ 72 100.0 84 4 R23483 Porcline parathyroid hor 72 100.0 84 5 R29562 Oxidation resistant [ 72 100.0 84 5 R29562 Oxidation resistant [ 72 100.0 84 5 R29562 Oxidation resistant [ 72 100.0 84 4 R23339 Bovine parathyroid hor 72 100.0 84 4 R23327 Bovine parathyroid hor 72 100.0 84 4 R23272 Bovine parathyroid hor 72 100.0 84 4 R23242 Human parathyroid hor 72 100.0 84 4 R23224 Human parathyroid hor 72 100.0 84 4 R23227 Human parathyroid hor 72 100.0 84 4 R23227 Human parathyroid hor 72 100.0 84 4 R232364 Bovine parathyroid hor 72 100.0 84 4 R23248 Human parathyroid hor 72 100.0 84 4 R23250 Porcline parathyroid hor 72 100.0 84 4 R23456 Porcline parathyroid hor 72 100.0 84 4 R2343 Bovine parathyroid hor 72 100.0 84 4 R23439 Porcline parathyroid hor 72 100.0 84 4 R23439 Porcline parathyroid hor 73 100.0 84 4 R23439 Porcline parathyroid hor 74 100.0 84 4 R23439 Porcline parathyroid hor 75 100.0 84 4 R23439 Porcline parathyroid hor 76 100.0 84 4 R23449 Porcline parathyroid hor 77 100.0 84 4 R23449 Porcline parathyroid hor 78 100.0 84 4 R23449 Porcline parathyroid hor 79 100.0 84 4 R23449 Porcline parathyroid hor	45	44	43	42	41	40	39	38	37	36	35	34	<u>ω</u>	32	31	30	29	28	27	26	25	24	23	22	21	20
.0 84 4 R23424 Porcine parathyrol .0 84 5 R29568 Oxidation resistan .0 84 5 R29563 Oxidation resistan .0 84 6 R23483 Porcine parathyrol .0 84 7 R23483 Porcine parathyrol .0 84 8 R29562 Oxidation resistan .0 84 8 R29562 Oxidation resistan .0 84 4 R23333 Bovine parathyrol .0 84 4 R23372 Bovine parathyrol .0 84 4 R23272 Bovine parathyrol .0 84 4 R23294 Bovine parathyrol .0 84 4 R23294 Bovine parathyrol .0 84 4 R23294 Human parathyrol .0 84 4 R23297 Human parathyrol .0 84 4 R23297 Human parathyrol .0 84 4 R23181 Human parathyrol .0 84 4 R23287 Bovine parathyrol .0 84 4 R23289 Human parathyrol .0 84 4 R23363 Bovine parathyrol .0 84 4 R23489 Bovine parathyrol .0 84 4 R23489 Bovine parathyrol .0 84 4 R23489 Bovine parathyrol .0 84 4 R23449 Porcine parathyrol .0 84 4 R23449 Porcine parathyrol .0 84 4 R23429 Porcine parathyrol	72	72	72	72	72	72	72	72	72	72	72	72	72	72	72	72	72	72	72	72	72	72	72	72	72	72
4 R23424 Porcine parathyroid 4 R23383 Porcine parathyroid 5 R29568 Oxidation resistan 5 R29563 Oxidation resistan 4 R23483 Porcine parathyroid 25 W29420 Oxidation resistan 6 R29562 Oxidation resistan 7 R29562 Oxidation resistan 8 R29562 Oxidation resistan 9 R29562 Oxidation resistan 10 R23272 Bovine parathyroid 11 R23273 Bovine parathyroid 12 R23294 Human parathyroid 13 R23129 Human parathyroid 14 R23240 Human parathyroid 14 R23127 Human parathyroid 15 R29561 Bovine parathyroid 16 R23561 Human parathyroid 17 R23561 Human parathyroid 18 R23561 Bovine parathyroid 18 R23463 Bovine parathyroid 18 R23464 Bovine parathyroid				٠	٠	•				•	٠	•				•	•			٠			00.			00.
4 R23424 Porcine parathyrol R2383 Porcine parathyrol R29568 Oxidation resistan R29563 Oxidation resistan R23483 Porcine parathyrol R23460 Porcine parathyrol R23561 Coxidation resistan R23561 Coxidation resistan R23561 Coxidation resistan R23572 R29562 R23373 R2964 R23373 R2364 R23242 R23394 R23180 R23264 R23273 R2364 R23276 R232864 R232864 R23264 R232664 R236664 R236666 R236666666666666666666666666666	115	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84
Porcine parathyroid Oxidation resistan Oxidation resistan Oxidation resistan Oxidation resistan Porcine parathyroid Human parathyroid Bovine parathyroid Bovine parathyroid Human parathyroid Porcine parathyroid Porcine parathyroid Bovine parathyroid Porcine parathyroid	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	5	S	25	4	σı	ഗ	4	4
	P40251	R23449	R23423	R21180	Oi	R23456	R21250	R23248	26	R23507	R23227	R21181	R21229	R23242	R23294	R23301	R23272	R23339	R29561	R29562	W29420	R23483	R29563	R29568	R23383	R23424
	sequence	parathyroid	parathyroid	parathyroid	parathyroid	parathyro	parathyroid	parathyroid	parathyroid	parathyroi	parathyroid	4			2	resistant	resistant	parathyroid	parathyroid							

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밁
                                                                             Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                            12-JUL-1993; 014384.

15-JUL-1992; GB-015009.

18-DEC-1992; GB-026415.

23-DEC-1992; GB-026859.

23-DEC-1992; GB-026861.

23-DEC-1992; GB-001691.

28-JAN-1993; GB-001692.

14-APR-1993; GB-001693.

19-APR-1993; GB-007673.
                                                                                       New active para-thyroid hormone variants - used for treating or preventing osteoporosis etc.

Example 148; Page 40; 92pp; English.

This peptide is an example of a highly generic formula covering parathyroid hormone variants useful for treating or preventing bone conditions associated with calcium depletion/resorption, in cases where calcium fixation is required (esp. osteoporosis) or to treat hypoparathyroidism.
                                                                                                                                                                                                    (SANO) SANDOZ PATENT GMBH.
(SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
Albert R, Bauer W, Breckenridge R, Ca
Gombert F, Gram H, Lewis I, Ramage P,
Waelchii R, Rainer A;
WPI; 94-018352/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R58151;
20-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                       GB2269176-A.
02-FEB-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypoparathyroidism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R58151 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [Ser22]-hPTH(1-38)-OH.
Human parathyroid hormone; hPTH; variant;
calcium; depletion; fixation; resorption;
                                                                                                                                                                                                                                                                                     (BAUE/)
                                                                                                                                                                                                                                                                                                   SANO )
28 lqdvhnfval 37
                                                                                                                                                                                                                                                                                                  SANDOZ LTD.
                                                                                                                                                                                                                                                                                     BAUER W.
                                                                               A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38
                        Score 72; DB 9; Lei
Pred. No. 8.81e-01;
0; Mismatches 0;
                                                                                                                                                                                                                                 η,
                                                                                                                                                                                                                                             Cardinaux
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     analogue;
osteopathy; osteoporosis;
                                                                                                                                                                                                                               dinaux F;
Schneider
                                                  Length
                                                                                                                                                                                                                                 Ξ
                          0
                          Gaps
                          0;
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Page 2

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RESULT 2

ID R58153 standard: peptide: 38 AA.

AC R58155; Standard: peptide: 38 AA.

BC R58155; Standard: peptide: 38 AA.

AC R58155; Standard: peptide: 38 AA.

BC R58155; Control of the standard: peptide: 38 AA.

BC R58155; Control of the standard: peptide: 38 AA.

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BC R58155; Control of the standard: peptide: 38 AA.

BC R58155; Control of the standard: peptide: 38 AA.

BC R58155; Control of the standard: peptide: peptide: 38 AA.

BC R58155; Control of the standard: peptide: peptide: 38 AA.

BC R58155; Control of the standard: peptide: peptide:
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MPsrch\_pp 9 2 3 protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:49:12 1998; MasPar time 3.29 Seconds 111.059 Million cell updates/sec

Tabular output not generated.

Title: Description: Perfect Score: Sequence: >US-08-817-547A-22 (1-10) from US08817547A.pep 72 1 LQDVHNFVAL 10

Scoring table: PAM 150 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 23.774; Variance 33.625; scale 0.707

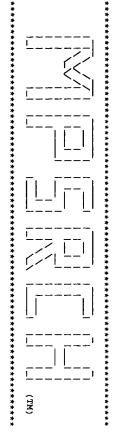
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

100 0 115 1 5 5	.0 115 1 PTPG parath .0 115 1 PTBO parath .2 115 2 A05091 parath .3 105 2 I51851 parath .6 34 5 IFWA parath .6 34 5 IFWA Cyclic .6 632 2 S73824 Mydrog .2 606 2 S13526 hydrog .2 606 2 C65188 hypoth .4 217 2 E70126 hypoth .4 543 2 H40781 hypoth .4 543 2 S25128 61K pr .4 653 2 S28491 hypoth .4 731 2 S28491 hypoth	9ult No. 1 2 3 3 5 6 6	Score 72 72 72 72 72 72 72 72 72 72 72 72 72		; <sub>0</sub>	» + σ σ σ σ σ σ σ σ σ σ σ σ σ σ σ σ σ σ	ID 12WE 12WG 12WF 12WF 11ZWD 11EWB 11EWB 11EWB 11EWC 1	Description parathyroi	ion  roid hormone eroid hormon
0 115 1 DEDC	.0 115 2 JC42/2 parath .0 115 1 PTBO parath .2 115 2 N5591 parath .3 105 2 I51851 parath .6 34 5 IFWA parath .6 34 5 IHTH CYClic .6 632 2 S73824 MG242 .2 606 2 S13526 hygoth .4 217 2 E70126 hygoth .4 543 2 H40781 hypoth .4 543 2 S40449 pro-h .4 731 2 S28491 hypoth .4 731 2 S28491 hypoth	72 72 72 72 72 72 72		00000000	:	:	12WE 12WE 12WG 12WF 12WD 12WB 11WC 11WC PTHU	parathyroid	
100.0 115 1 FIBO	97.2 115 2 A05091 parath 83.3 105 2 I51851 parath 73.6 34 5 IZWA parath 73.6 34 5 IHTH cyclic 73.6 632 2 S73824 Mc2v21 73.6 632 2 S13526 hydrog 72.2 606 2 S13526 hydrog 70.8 201 2 C65188 hypoth 69.4 217 2 E701126 hypoth 69.4 543 2 H40781 hypoth 69.4 543 2 S25128 61K pr 69.4 653 2 S26491 hypoth 69.4 731 2 S28491 hypoth	177777777777777777777777777777777777777		0000000000		11215555555	12WE 12WG 12WF 12WF 12WD 11EWD 11HPH 11HPH 11HO 71HO 9THO 9THO 9THO	parathyroid	1
92 2 105 3 TE1951	73.6 632 2 873824 MG242 72.2 606 2 813826 hydrog 70.8 201 2 C65188 hypoth 69.4 217 2 E70126 hypoth 69.4 543 2 8404781 hypoth 69.4 553 2 840449 pro-ho 69.4 731 2 828491 hypoth		, 5 0			лию	151851 12WA 14TH	~ ~	hormone hormone
73.6 34 5 12WA	72.2 606 2 S13526 7 70.8 201 2 C65188 1 69.4 217 2 E70126 1 69.4 543 2 H40781 1 69.4 553 2 S40499 1 69.4 731 2 S28491 1		5 5 5 5 5 5			, <b>N</b> G	1HTH S73824	റ	
73.6 34 5 1HTH cyclic 73.6 34 5 1HTH cyclic 73.6 632 2 S73824 MG242	69.4 217 2 E70126 1 69.4 543 2 H40781 1 6 69.4 653 2 S25128 6 69.4 653 2 S40449 1 69.4 731 2 S28491 1		52 51	- :-		NN	S13526 C65188	hydrogenase hypothetica	ase homolog, ical 22.3 kD
73.6 34 5 12WA parath 73.6 34 5 1HTH cyclic 73.6 32 2 873824 MG27 73.6 632 2 813526 hydrog 70.8 201 2 C65188 hypoth	69.4 543 2 S25128 6 69.4 653 2 S40449 F 69.4 731 2 S28491 F		50 50	99		ผผ	E70126 H40781	hypothet	prote
73.6 34 5 1EWA parath 73.6 34 5 1HTH Cyclic 73.6 632 2 \$73824 MG242 73.6 632 2 \$13526 hydrog 72.2 606 2 \$13526 hydrog 70.8 201 2 C65188 hypoth 69.4 217 2 E70126 hypoth 69.4 543 2 H40781 hypoth	69.4 653 2 S40449 I 69.4 731 2 S28491 I		50	69.4		N	S25128	61k prot	
73.6 34 5 1ZWA parath 73.6 34 5 1HTH cyclic 73.6 632 2 S73824 Mcyclic 72.2 606 2 S13526 hydrog 70.8 201 2 C65188 hypoth 69.4 217 2 E70126 hypoth 69.4 543 2 S25128 61K pr			50 50	69.4 69.4		NN	S40449 S28491	pro-hormone hypothetical	ione convertas

4000HH00000000000000000000000000000000	45	44	43	42	41	40	39	38	37	36	ω 5	34	ၗ	32	31	30	29	28	27	26	25	4
1142 2 B40535 1 142 2 B40535 1 145 2 R26081 1 1321 2 S27337 1 1490 2 S725145 1 1490 2 S725145 1 1490 2 S73520 1 1537 2 UC4172 1 36 2 S73520 7 145 2 S73520 7 145 2 S743598 3 240 2 S7435 7 471 3 A43598 7 491 3 A44400 7 653 2 S77436 7 471 3 A46400 7 653 2 S77636	47	47	48	48	48	48	48	48	48	48	48	48	48	48	49	49	49	49	49	49	49	000
2 B40535 2 S07569 2 A26681 2 S27337 2 S27610 2 S73520 5 1ATO 5 1ATO 2 S74554 2 R43598 2 R43598 2 R56400 2 S77436 3 R43480 2 S77436 3 R43480 3 R4348	65.3	65.3	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	68.1			•		•	•	٠
B40535 B40535 S07569 A26081 S27337 JC25145 S27316 S273520 JA705 JA7520 JA7520 JA7520 JA7520 JA7520 JA7520 S73520 JA7520 S73520 S73520 JA7520 S73520 JA7520 S73520 JA7520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S73520 S7352	494	240	1612	1318	881	653	471	471	452	398	328	326	145	136	1537	1495	1490	1321	455	316	142	000
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clathrin-associated protein H5 - slime mo epoxide hydrolase (EC multidrug resistance DNA (cytosine-5-)-met blotin synthesis prote cytochrome P450 cl17	S13101	F64676	JC5210	HIBPD7	WZBE55	S27270	A46400	A43480	S77436	D69953	A43598	S76954	1ATO	S73520	JC4172	S22610	JC5145	S27337	A26081	S07569	B40535	00000
	cytochrome P450 c117	biotin synthesis prot	(cytosine-5-		•	prohormone convertase	segment polarity prot	gene	sibG	conserved hypothetica	L-lactate dehydrogena	hypothetical protein	17-hedgehog 17-kda fr	homolog E09_	(cytosine-5-	(cytosine-5-	_	tidrug	hydrolase (	H5 - slime	3	

Roesch, P.; Marx, U.C. sission submitted to the Brookhaven Protein Data Bank, June references PDB:1ZWG TN003319  ors Marx, U.C.  in Strukturen Verschiedener Parathormonfragmente in pp.0, Bayreuth: University of Bayreuth (Thesis), Resolution: not applicable	RESULT 2  IZWG #type complete  TITLE parathyroid hormone 4 37 mutant N-TERMINAL SUCCINYLATED  synthetic synthetic  ALTERNATE_NAMES n-succinyl-hpth(4-37)  PDB_TITLE succinyl human parathyroid hormone 4-37, NMR, 10 struct  ORGANISM #formal_name synthetic	Query Match 100.0%; Score 72; DB 5; Length 34; Best Local Similarity 100.0%; Pred. No. 1.05e-03; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps Db 25 LQDVHNFVAL 34	#BOOK MAIX, U.C. #book in Strukturen verschiedener Parathormonfragmente in I pp.0, Bayreuth: University of Bayreuth (Thesis), 1 COMMENT Resolution: not applicable COMMENT Determination: NMR KEYWORDS hormone 15-25 #region helix (right hand alpha) SUMMARY #length 34 #molecular-weight 4128 #checksum 5508	AMES HPTH(4-37)  structure of human parathyroid hormone fragment 4-3:  structures  structures  #formal_name Homo sapiens #common_name man  A67860  Roesch, P.; Marx, U.C.  Roesch, P.; Marx, U.C.  ion submitted to the Brookhaven Protein Data Bank, June eferences PDB:1ZWE TN001721  MERT IC	RESULT 1  ENTRY 12WE #type complete  TITLE parathyroid hormone (residues 4-37) - human
1996 Loesung, 1996	WLATED - structures	š O;	1996	7, NMR 10	



MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Thu Jul 30 10:47:53 1998; MasPar time 2.15 Seconds 116.508 Million cell updates/sec

Tabular output not generated.

Description:
Perfect Score:
Sequence: Title: >US-08-817-547A-22 (1-10) from US08817547A.pep

1 LQDVHNEVAL 10

Scoring table: PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 24.901; Variance 27.707; scale 0.899

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

No.	Score	Query Match	Length	DB	Ħ	Description	Pred. No.
_	72	100.0	115	- 5	PTHY_CANFA	PARATHYROID HORMONE PR	2.56e-05
2	72	100.0	115	ᆫ	PTHY_BOVIN	PARATHYROID HORMONE PR	
ω	72	100.0	115	Н	PTHY_PIG	PARATHYROID HORMONE PR	2.56e-05
4	72	100.0	115	Н	PTHY_HUMAN	PARATHYROID HORMONE PR	.566
տ	70	97.2	115	ш	PTHY_RAT	PARATHYROID HORMONE PR	8.57e-05
o	53	73.6	632	ᆫ	Y242_MYCPN	HYPOTHETICAL PROTEIN M	1.14e+00
7	51	70.8	200	ب	KIGP_ECOLI	HYPOTHETICAL 22.3 KD P	3.11e+00
80	50	69.4	543	ᅩ	VP61_NPVAC	61 KD PROTEIN.	5.08e+00
9	50	69.4	831	ᆫ	TVID_SALTI	VI POLYSACCHARIDE BIOS	5.08e+00
10	49	68.1	142	ب	AP17_HUMAN	CLATHRIN COAT ASSEMBLY	8.24e+00
11	49		142	ш	AP17_RAT	CLATHRIN COAT ASSEMBLY	8.24e+00
12	49	68.1	316	ب	VSH5_DICDI	VEGETATIVE SPECIFIC PR	8.24e+00
13	49	68.1	455	<u>ب</u>	HYEP_RAT	EPOXIDE HYDROLASE (EC	8.24e+00
14	49	68.1	1321	Н	MDR1_CAEEL	MULTIDRUG RESISTANCE P	
15	49	68.1	1495	щ	MTDM_HUMAN	DNA (CYTOSINE-5)-METHY	
16	48	66.7	136	<b>ب</b>	Y441_MYCPN	HYPOTHETICAL PROTEIN M	1.32e+01
17	48	66.7	153	_	ML11_BRARE	MELATONIN RECEPTOR TYP	1.32e+01
18	48	66.7	328	۳	LDH_STRMU	L-LACTATE DEHYDROGENAS	1.32e+01
19	48	66.7	398	_	YQFD_BACSU	HYPOTHETICAL 45.7 KD P	1.32e+01
20	48	66.7	471	<u>مـــر</u>	HH_DROME	HEDGEHOG PROTEIN PRECU	1.32e+01
21	48	66.7	881	ᆫ	HELI_VZVD	PROBABLE HELICASE.	1.32e+01
22	48	66.7	1318	Н	VIVD_BPT7	INTERNAL VIRION PROTEI	1.32e+01
23	48	66.7	1620	-	MTDM_MOUSE	DNA (CYTOSINE-5)-METHY	1.32e+01

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
45	45	45	45	45	45	45	45	45	45	46	46	46	46	47	47	47	47	47	47	47	47
62.5	62.5	62.5	62.5	62.5	62.5	62.5	62.5	62.5	62.5	63.9	63.9	63.9	63.9	65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3
2505	2504	1247	687	505	490	303	297	120	104	4344	964	469	435	1444	925	700	589	494	274	251	125
	<u> </u>	<u> </u>	1	_	<u> </u>	щ	۳	Ь	μ.	۳	_	<u>ب</u>	_	_	1	₩	4	۲	دسو	Н	Н
FAS_RAT	FAS_HUMAN	YMF6_CAEEL	CSTA_HELPY	YXD2_CAEEL	CPCQ_MESAU	APPC_BACSU	YMY9_YEAST	YGX0_YEAST	YHV2_LACHE	DYHC_EMENI	YBS9_YEAST	NIFN_RHISN	PEPC_LACIC	RRPL_RDV	DBL_HUMAN	ADB1_YEAST	KY28_MYCTU	CPCN_RAT	CD1_SYLFL	AGAI_ECOLI	Y4WJ_RHISN
FATTY ACID SYNTHASE (E	FATTY ACID SYNTHASE (E	HYPOTHETICAL 139.9 KD	CARBON STARVATION PROT	PUTATIVE SERINE CARBOX	CYTOCHROME P450 IIC26	TRANSPORT	HYPOTHETICAL 34.0 KD P	HYPOTHETICAL 14.1 KD P	HYPOTHETICAL 11.8 KD P	DYNEIN HEAVY CHAIN, CY	HYPOTHETICAL 110.3 KD	NITROGENASE IRON-MOLYB	AMINOPEPTIDASE C (EC 3	RNA-DIRECTED RNA POLYM	PROTO-ONCOGENE DBL PRE	PROBABLE BETA-ADAPTIN	PROBABLE SERINE/THREON	CYTOCHROME P450 IIC23	T-CELL SURFACE GLYCOPR	PUTATIVE GALACTOSAMINE	HYPOTHETICAL 13.3 KD P
5.24e+01	5.24e+01	5.24e+01	5.24e+01	5.24e+01	5.24e+01	5.24e+01	5.24e+01	5.24e+01	5.24e+01	3.34e+01	3.34e+01	3.34e+01	3.34e+01	2.11e+01	2.11e+01	2.11e+01	2.11e+01	2.11e+01	2.11e+01	2.11e+01	2.11e+01

88	GN	DE	UT	DŢ	DI	2	3 6	;	RESULT	Qу	В	M. Be	ဝ	SQ	FT	ГŦ	FΤ	ΚW	DR	DR	ဂ္ဂ	ဂ္ဂ	RL	RA	RΑ	RX	RC.	RP	RN	റ്റ	8	SO	GN	DE	Dī	D.T.	DI	AC	ij	RESULT
BOS TAURUS (BOVINE). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;		HORMONE PR	(REL. 35, LAST ANNOTATION	01,	(REL.		PTHY_BOVIN STANDARD; FRT; 113 AA.	THE POLITY CHANDADA DOT 115	ULT 2	1 LQDVHNEVAL 10	59 LQDVHNFVAL 68	2.56e-05; atches 0; In	100.0%; Score 72;	NCE 115 AA;	32 115 PAF	26 31 BY	ш	SIGNAL.	PROSITE; PS00335; PARATHYROID; 1.	EMBL; U15662; G558916;	BONE AND PREVENTING THEIR RENAL EXCRETION.	-!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN		., CAPEN C.C.;	ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,	MEDLINE; 95369696.	TISSUE-PARATHYROID;	SEQUENCE FROM N.A.	[1]		YOTA; METAZOA; CH	CANIS FAMILIARIS (DOG).		HORMONE PR	34, LAST ANNOTATIO	(REL. 34,	(REL.		PTHY_CANFA STANDARD; PRT; 115 AA.	ULT 1

EUTHERIA; ARTIODACTYLA. [1]

SEQUENCE FROM N.A.

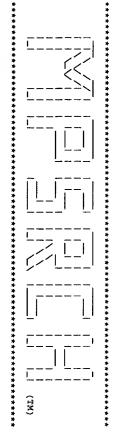
MEDILINE, 80056617.

KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A.,

POTTS J.T. JR., KICH A.;

PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).

Search completed: Thu Jul 30 10:47:59 1998 Job time : 6 secs.



Psrch\_pp 9 :: protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Thu Jul 30 10:48:18 1998; MasPar time 3.79 Seconds 111.185 Million cell updates/sec

Title: Description: Perfect Score: Sequence: >US-08-817-547A-22 (1-10) from US08817547A.pep

1 LQDVHNFVAL 10

Scoring table: PAM 150 Gap 15

Searched: 140542 seqs, 42109429 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb15
1:sp\_fungi 2:sp\_human 3:sp\_invertebrate 4:sp\_mammal
5:sp\_mhc 6:sp\_organelle 7:sp\_phage 8:sp\_plant
9:sp\_bacteria 10:sp\_rodent 11:sp\_virus 12:sp\_vertebrate
13:sp\_unclassified

Statistics: Mean 23.635; Variance 29.603; scale 0.798

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

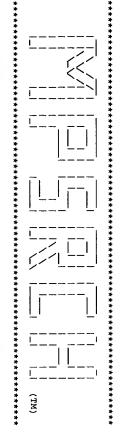
Result

1 3 3 3 3 3 3 3 4 4 4 7 7 7 7 1 1 1 1 1 1 1 1 1 1 1 1 1	esult No.
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Score
83.3 75.0 75.0 75.0 69.4 68.1 68.1 68.1 68.1 68.1 68.1 68.1 68.1	Query
105 993 345 653 653 653 663 663 1432 1143 1143 1143 1143 11537	Length
110 111 112 112 112 112 113 113 114 114 117 117 117 117 117 117 117 117	DΒ
063473 017162 017162 016606 016606 016672 016972 018845 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 019123 01	ij
PARATHYROID HORMONE (FORE36L. VINCULIN. STBA. HYD GAMMA. PREPRO-HORMONE CONVERT NEUROENDOCRINE CONVERT PC2. SIMILARITY TO CLATHRIN ARYLALKYLAMINE N-ACETY CYTOCHROME P450 2C33V3 CYTOCHROME P450 2C33V3 CYTOCHROME P450 2C33V3 CYTOCHROME P450 2C33V3 CYTOCHROME P450 2C33V1 SIMILAR TO SER/THR PROMICROSOMAL EPOXIDE HYD F39B1.1 (FRAGMENT). KOBE7.9. MODIFICATION METHYLASE MODIFICATION METHYLASE GENOME, PARTIAL SEQUEN	Description
8.41e-02 3.80e-01 1.64e+00 4.22e+00 1.06e+01 1.06e+01 1.06e+01 1.67e+01 1.67e+01 1.67e+01 1.67e+01 1.67e+01 1.67e+01 1.67e+01 1.67e+01 1.67e+01 1.67e+01 1.67e+01 1.67e+01 1.67e+01 1.67e+01 1.67e+01 1.67e+01 1.67e+01 1.67e+01 1.67e+01 1.67e+01 1.67e+01 1.67e+01 1.67e+01 1.67e+01 1.67e+01 1.67e+01	Pred. No.

45	44	43	42	41	40	39	3 8	37	<u>ა</u>	35	34	33	32	31	30	29	28	27	26	25	24	23	22	17
46	46	46	46	47	47	47	47	47	47	47	47	47	48	48	48	48	4.8	48	48	48	48	48	48	4
63.9	63.9	63.9	63.9	65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	σ	σ	66.7	66./
1825	1758	709				939					240	207	1612	1149	787	787							377	
10	w	ω	2	11	ω	w	ω	10	10	1	9	4	ω	ω	9	ø	N	ω	11	ω	9	9	w	۷
P97394	Q22830	015783	042479	Q98631	015788	015790	015799	035488	Q64534	Q05160	025846	002785	Q27746	Q23315	032799	032797	Q92542	Q25409	011448	Q18198	P73256	Q55301	017273	P/4/46
ACTIN-CROSSLINKING PRO	SIMILAR TO HUMAN SREBP	HYBRID HISTIDINE KINAS	FERROCHELATASE (EC 4.9	RNA-DEPENDENT RNA POLY	STRAIN HB3 CG9 (CG9) A	STRAIN 7G8 CG9 (CG9) A	STRAIN DD2 HEAT SHOCK	VERY-LONG-CHAIN ACYL-C	CYTOCHROME P450 (EC 1.	ALPHA-AGGLUTININ (AG-A	BIOTIN SYNTHESIS PROTE	ARYLALKYLAMINE-N-ACETY	MODIFICATION METHYLASE	ZC434.5.	PYRUVATE FORMATE-LYASE	PYRUVATE FORMATE-LYASE	MYELOBLAST KIAA0253 (F	STAGNALIS LPC2.	VP78.	SIMILAR TO K12H4.7 AND	SIGMA FACTOR SIBG REGU	COTA GENE (ORF440), CO	T27A1.2 PROTEIN.	HYPOTHETICAL 30.0 KD P
6.22e+01	6.22e+01	6.22e+01	6.22e+01	4.04e+01	4.04e+01	4.04e+01	4.04e+01	4.04e+01	4.04e+01	4.04e+01	4.04e+01	4.04e+01	2.61e+01	2.61e+01	2.61e+01	2.61e+01	2.61e+01	2.61e+01	2.61e+01	2.61e+01	2.61e+01	2.61e+01	2.61e+01	2.61e+01

RP SEQUENCE FROM N.A.  RP SEQUENCE FROM N.A.  RA JEHLE J.A., VAN DER LINDEN I.F.A., VLAK J.M.;  RL VIRUS RES. 0:0-0(1997).  RL VIRUS RES. 0:0-0(2997).  RD EMBL; AF002732; G2232189;  SQ SEQUENCE 207 AA; 23915 MW; D2F0E988 CRC32;	OS CYDIA POMONELLA GRANULOVIRUS. OC VIRUSES; DSDNA VIRUSES, NO RNA STAGE; BACULOVIRIDAE; GRANULOVIRUS.	RESULT 2 ID 039628 PRELIMINARY; PRT; 207 AA. AC 039628.	Db 49 LQDGHNEVSL 58	Query Match 83.3%; Score 60; DB 10; Length 105; Best Local Similarity 80.0%; Pred. No. 8.41e-02; Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps	OS RATTUS NORVEGICUS (RAT). OS RATTUS NORVEGICUS (RAT). OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; OC EUTHERIA; RODENTIA. RN [1]	DT 01-NOV-1996 (TREMBLREL. 01, CREATED) DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE) DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE) DE PARATHYROID HORMONE (FRAGMENT).	SU
				0;			

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Db 145 LQEVHDFV 152
||:||:||
Qy 1 LQDVHNFV 8
Search completed: Thu Jul 30 10:48:55 1998 Job time: 37 secs.
                                                                                                                                                                                                    Query Match 79.2%; Score 57; DB 11; Length 207; Best Local Similarity 75.0%; Pred. No. 3.80e-01; Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm on:
Thu Jul 30 10:52:34 1998; MasPar time 2.61 Seconds 52.799 Million cell updates/sec

Tabular output not generated.

Title: >US-08-817-547A-23
Description: (1-9) from US08817547A.pep
Perfect Score: 64

Sequence: 1 QDVHNFVAL 9

Scoring table: PAM 150 Gap 15

earched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq31-2

i:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27

Statistics: Mean 16.221; Variance 50.458; scale 0.321

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result
00000000000000000000000000000000000000	Score
11111111111111111111111111111111111111	Query Match I
8 C C C C C C C C C C C C C C C C C C C	Length DB
R58140 R58140 R58140 R58133 R58133 P3015 W21046 W21046 W21046 R21190 R23309 R231190 R23120 R23120 R23420 R23420 R23493 R23493	ij
[Ser22]-hPTH(1-38)-OH [Asn21]-hPTH(1-38)-OH [Phe21]-hPTH(1-38)-OH [His19]-hPTH(1-38)-OH [His19]-hPTH(1-38)-OH Human parathyroid hor Fusion protien compri Human parathyroid hor Human parathyroid hor Human parathyroid hor Bovine parathyroid hor Bovine parathyroid hor Bovine parathyroid hor Bovine parathyroid hor Porcine parathyroid hop Porcine parathyroid hop Porcine parathyroid hop Porcine parathyroid hop Porcine parathyroid hop	Description
1.84e+00 1.84e+00 1.84e+00 1.84e+00 1.84e+00 1.84e+00 1.84e+00 1.84e+00 1.84e+00 1.84e+00 1.84e+00 1.84e+00 1.84e+00 1.84e+00 1.84e+00 1.84e+00 1.84e+00 1.84e+00 1.84e+00 1.84e+00 1.84e+00	Pred. No.

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29

qdvhnfval 37

45	44	43	42	41	40	39	38 8	37	36	35 5	34	3 3	32	31	30	29	28	27	26	25	24	23	22	21	0
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R47971	P40251	R23449	R21211	R21210	R23363	R23456					w	R23227	R23248	R23339	R23242	R23272	R21181	R21250	95	R29562	W29420	R21240	R29563	R29568	20000
Sequence of a full-le	Protein sequence incl	Porcine parathyroid h	ğ	id	O.	Porcine parathyroid h		Bovine parathyroid ho	Q,	Human parathyroid hor		Human parathyroid hor		Bovine parathyroid ho	Human parathyroid hor	Bovine parathyroid ho	-		Oxidation resistant P	ņ	athyroid	Human parathyroid hor	Oxidation resistant P	Oxidation resistant [	POTCINE PATACHYTOTA II
				1.84e+00									1.84e+00				1.84e+00								

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RESULT RE
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A (SANO) SANDOZ PATENT GMBH.

A (SANO) SANDOZ ERFINDUNGEN VERW GES MBH.

I Albert R, Bauer W, Breckenridge R, Cardinaux F;

I Gombert F, Gram H, Lewis I, Ramage P, Schneider H;

Waelchli R, Rainer A;

Rapit 494-01852/03.

Proventing osteoporosis etc.

SExample 148; Page 40; 92pp; English.

Example 148; Page 40; 92pp; English.

This peptide is an example of a highly generic formula covering conditions associated with calcium depletion/resoxption, in cases where calcium fixation is required (esp. osteoporosis) or to treat thypoparathyroidism.
Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-JUL-1993; 014384.

15-JUL-1992; GB-015009.

18-DEC-1992; GB-026415.

23-DEC-1992; GB-026859.

23-DEC-1992; GB-026861.

23-DAN-1993; GB-001691.

28-JAN-1993; GB-001692.

14-APR-1993; GB-007673.

19-APR-1993; GB-008033.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [Ser22]-hPTH(1-38)-OH.
Human parathyroid hormone; hPTH; variant; analogue; calcium; depletion; fixation; resorption; osteopath
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
GB2269176-A.
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                                                                                                                                                                    38 AA;
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8
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Pred.
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        re 64; DB 9; Leng
l. No. 1.84e+00;
Mismatches 0;
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                                                                                Length
            Indels
                                                                                    38;
            0
            Gaps
                                                                                                                                                                                                                                                                                                                        bone
            0;
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RESULT

RESULT

AC REA

AC RE

Search completed: Thu Jul 30 10:52:49 1998 Job time: 15 secs.
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PF 12-JUL-1993; 014384.

PF 15-JUL-1992; GB-015009.

PR 15-DUL-1992; GB-026859.

PR 23-DEC-1992; GB-026861.

23-DEC-1992; GB-026861.

28-JAN-1993; GB-001691.

28-JAN-1993; GB-001691.

28-JAN-1993; GB-001692.

PR 14-APR-1993; GB-008033.

PA (SANO) SANDOZ LTD.

PA (SANO) SANDOZ PATENT GMBH.

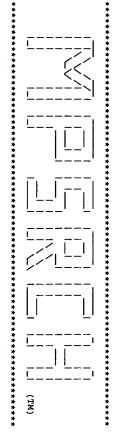
PA (SANO) SANDOZ GRATINT GB-001691

PA (SANO) SANDOZ GRATINT GMBH.

PA (SANO) SANDOZ GRATINT GMBH.

PA (SANO) SANDOZ GRATINT GMBH.

PA (SANO) SANDOZ G
                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative
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[Asn21]-hPTH(1-38)-OH.
Human parathyroid hormone; hPTH; variant; analogue;
calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypoparathyroidism.
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R58142;
                                                                                                                                                                                                                                                     29 qdvhnfval 37
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                                                                                                                                                                                                  QDVHNFVAL 9
                                                                                                                                                                                                                                                                                                                                                                                          Score 64; DB 9; Ler
Pred. No. 1.84e+00;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 38;
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                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                     0;
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Psrch\_pp protein - protein database search, using Smith-Waterman algorithm

900 Thu Jul 30 10:51:51 1998; MasPar time 3.32 Seconds
99.175 Million cell updates/sec

Tabular output not generated.

Title:
Description:
Perfect Score:
Sequence: >US-08-817-547A-23 (1-9) from US08817547A.pep 64 1 QDVHNFVAL 9

Scoring table: PAM 150 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 22.614; Variance 30.162; scale 0.750

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

22222222223333333333333333333333333333	NO.
00000000000004444444444444444444444444	Score
100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0	Query Match
344 344 343 343 343 343 343 343 343 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443 3443	Length
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	BG
12WE 12WE 12WG 12WD 12WD 12WB 11PPH 12WB 11PPH 12WC PTBO PTBO PTBO A05091 151851 C65185 873520 805688 73520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 8173520 81	ID
parathyroid hormone ( parathyroid hormone 4 parathyroid hormone 4 parathyroid hormone ( parathyroid hormone p parathyroid hormone l parathyroid hormone l parathyroid hormone l parathyroid hormone l pupothetical 22.3 kD possible possible possible l pupothetical 12K hlv hypothetical 12K hlv peptidylprolyl isomer triose-phosphate isom	Description
9.27e-03 9.27e-03 9.27e-03 9.27e-03 9.27e-03 9.27e-03 9.27e-03 9.27e-03 9.27e-03 9.27e-03 9.27e-03 9.27e-03 1.16e+01 1.16e+01 1.16e+01 1.75e+01 2.75e+01 6.36e+01 6.36e+01 6.36e+01 6.36e+01	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24
43	43	43	43	44	44	44	44	44	44	44	44	44	44	45	45	45	45	45	45	45	40
67.2	67.2									68.8				70.3	70.3	70.3	70.3	70.3	70.3	70.3	70.0
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S60228	S44798	S77073	B64153	SYASAA	JN0781	S54289	S13526	JC2032	S76954	S33143	S33956	H64961	A69445	G01880	XYRTFA	B57788	A57788	S40178	H64665	S73824	00000
glutamate synthase (f	F09G8.5 protein - Cae	hypothetical protein	ribose-5-phosphate is	acetateCoA ligase (	acetateCoA ligase (	phosphoglycerate kina	hydrogenase homolog,	regulatory protein Ac	hypothetical protein	superantigen Mtv - mo	ubiquitin thiolestera	hypothetical protein	hypothetical protein	fatty-acid synthase (	<pre>fatty-acid synthase (</pre>	fatty-acid synthase (	fatty-acid synthase (	isoleucinetRNA liga	carbon starvation pro	'n	nypornected procern
1.43e+02	1.43e+02	1.43e+02	1.43e+02	9.57e+01	9.57e+01	9.57e+01	9.57e+01	9.57e+01	9.57e+01	9.57e+01	9.57e+01	9.57e+01	9.57e+01	6.36e+01	6.36e+01	6.36e+01	6.36e+01	6.36e+01	6.36e+01	6.36e+01	0.000701

#book COMMENT Resc	REFERENCE #authors	#authors #submission #cross-refer	ALTERNATE_NAMES PDB_TITLE ORGANISM REFERENCE	RESULT 2 ENTRY TITLE	Db 26 QDVHNEVAL           Qy 1 QDVHNEVAL	Query Match Best Local Similarity Matches 9; Conse	15-25 SUMMARY	ß	#authors #book	#submission #cross-refer REFERENCE	ORGANISM REFERENCE #authors	RESULT 1 ENTRY TITLE ALTERNATE_NAMES PDB_TITLE
in Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth : University of Bayreuth (Thesis), 1996 Resolution: not applicable	IN003319 Marx, U.C.	#authors Roesch, P.; Marx, U.C. #submission submitted to the Brookhaven Protein Data Bank, June 1996 #cross-references PDB:12WG	- synthetro s n-succinyl-hpth(4-37) succinyl human parathyroid hormone 4-37, NMR, 10 structures #formal_name synthetic A67743	12WG #type complete parathyroid hormone 4 37 mutant N-TERMINAL SUCCINYLATED -	QDVHNEVAL 34          QDVHNEVAL 9	100.0%; Score 64; DB 5; Length 34; Similarity 100.0%; Pred. No. 9.27e-03; 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	<pre>#region helix (right hand alpha) #length 34 #molecular-weight 4128 #checksum 5508</pre>	PP.U, BAYFEUTH: UNIVERSITY OF BAYFEUTH (Thesis), 1990 Resolution: not applicable Determination: NMR hormone	C. turen Verschiedener Parathormonfragmente in	ed to the I :12WE	<pre>#formal_name Homo sapiens #common_name man A67860 Roesch, P.: Marx, U.C.</pre>	12WE #type complete parathyroid hormone (residues 4-37) - human HPTH(4-37) structure of human parathyroid hormone fragment 4-37, NMR 10 structures

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COMMENT Determination: NMR
KEYWORDS disease mutation; hormone; signal
FEATURE
2-9 #region helix (right hand alpha)\
15-25 #region helix (right hand alpha)
SUMMARY #length 34 #molecular-weight 4128 #checksum 5508

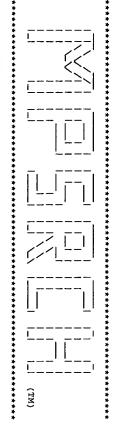
Query Match 100.0%; Score 64; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 9.27e-03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 26 ODPHNEVAL 34
[||||||||||||
Qy 1 ODVHNEVAL 9

Search completed: Thu Jul 30 10:52:17 1998

Job time: 26 secs.
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MPsrch\_pp 02: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:50:38 1998; MasPar time 2:13 Seconds 106.097 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-817-547A-23 (1-9) from US08817547A.pep 64 1 QDVHNFVAL 9

Scoring table: PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 23.654; Variance 24.782; scale 0.954

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24
43	43	43	43	43	43	43	43	43	43	43	43	4.	43	43	43	43	43	43	43	44	44
67.2	67.2	67.2	67.2		67.2	67.2	67.2	67.2	67.2	67.2	67.2	67.2	67.2	67.2			67.2	67.2	67.2	68.8	σä. α
2511	1550	962	752	741	493	493	490	490	490	483	449	447	444	411	309	302	264	219	117	2133	266
ب	Н	Ь	۲	ш	بر	ш	μ	μ	ب	<b>μ.</b>	μ	سر	Н	Н	۳	Н	Н	Ь	Н	<b>_</b>	۲
FAS_CHICK	GLTB_SYNY3	YAXA_SCHPO	CUL1_HUMAN	CH12_YEAST	CPE1_MESAU	CPE1_HUMAN	CPC6_RAT	CPCP_MESAU	CPCQ_MESAU	GLYC_RABIT	CPE1_MACFA	CLUS_RAT	CADB_ECOLI	YLBB_ECOLI	VP62_MRDV	D3D2_HUMAN	YQHG_BACSU	RPIA_HAEIN	KV5H_MOUSE	FA8_PIG	Y Z S 4 _ HUMAN
FATTY ACID SYNTHASE (E	FERREDOXIN-DEPENDENT G	HYPOTHETICAL 112.7 KD	CULLIN HOMOLOG 1 (CUL-	CHL12 PROTEIN.	CYTOCHROME P450 IIE1 (	CYTOCHROME P450 IIE1 (	CYTOCHROME P450 IIC6 (	CYTOCHROME P450 IIC25	CYTOCHROME P450 IIC26	SERINE HYDROXYMETHYLTR	CYTOCHROME P450 IIE1 (	CLUSTERIN PRECURSOR (S	PROBABLE CADAVERINE/LY	HYPOTHETICAL 45.7 KD P	PROBABLE NONSTRUCTURAL	3,2-TRANS-ENOYL-COA IS	HYPOTHETICAL 30.8 KD P	RIBOSE 5-PHOSPHATE ISO	IG KAPPA CHAIN PRECURS	COAGULATION FACTOR VII	HYPOTHETICAL PROTEIN K
4.43e+01	4.43e+01	4.43e+01	4.43e+01	4.43e+01	4.43e+01	4.43e+01	4.43e+01	4.43e+01	4.43e+01	4.43e+01	4.43e+01	4.43e+01	4.43e+01	4.43e+01	4.43e+01	4.43e+01	4.43e+01	4.43e+01	4.43e+01	2.75e+01	2./5e+U1

RESULT 2  ID PTHY_BOVIN STANDARD; PRT; 115 AA.  AC P01268; DT 21-JUL-1986 (REL. 01, CREATED) DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE) DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).  GN PTH.  OS BOS TAURUS (BOVINE).  OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	Query Match 100.0%; Score 64; DB 1; Length 115; Best Local Similarity 100.0%; Pred. No. 3.54e-04; Matches 9; Conservative 0; Mismatches 0; Indels 0; Ob 60 ODVHNFVAL 68	SEQUENCE FROM N.A. TISSUE-PARATHYROID; MEDLINE; 9536966. ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A., ROSOL T.J., STEINMEYER C.C.; GENE 160:241-243(1995)!- FUNCTION: PPH ELEVATES CALCIUM LEVEL BY DISSOLVING THE BONE AND PREVENTING THEIR RENAL EXCRETION. EMBL; U15662; G558916; PROSITE; PS00335; PARATHYROID; 1. HORMONE; SIGNAL. SIGNAL 1 25 BY SIMILARITY. SIGNAL 1 25 BY SIMILARITY. PROPEP 26 31 BY SIMILARITY. SEQUENCE 115 AA; 12957 MW; 16ED0EBC CRC32;	RESULT 1  ID PTHY_CANFA STANDARD; PRT; 115 AA.  AC P52212; DT 01-0CT-1996 (REL. 34, CREATED) DT 01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE) DT 01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE) DT 01-PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).  GN PTH.  OS CANIS FAMILIARIS (DOG).  OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; OC EUTHERIA; CARNIVORA.
(ALIA;	0; Gaps 0;	HE SALTS IN	ALIA;

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AR POTTS J.T. JR., TRECEAR G.W., KEUTMANN H.T., NIALL H.D., SAUER R., DEFTOS L.J., DAWSON B.F., HOGAN M.L., AURBACH G.D.;

AN DEFTOS L.J., DAWSON B.F., HOGAN M.L., AURBACH G.D.;

PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).

C. :- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN COMMENT OF THE MALE PROPERTY OF THE SALTS IN COMMENT OF THE SALTS IN COMMENT OF THE SALTS IN COMMENT OF THE SALTS IN EMBL; VO0106; G85; -.

EMBL; V001024; G163641; -.

EMBL; J00024; E18349; ALT_SEQ.

REMBL; J00024; E18250; ALT_INIT.

REMBL; J00024; E18350; ALT_INIT.

REMBL; M25082; G163645; -.

REMBL; M25082; G163645; -.

REMBL; R01938; G163645; -.

REMBL; R02949; R029499.
                                                      Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative
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CONFLICT
SEQUENCE
                                                                                                                                                                 PROSITE;
HORMONE;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 32-115.
MEDLINE; 71063634.
MEDLINE; 71063634.
BREWER H.B. JR., RONAN R.;
PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
                                                                                                                                                     PROPEP
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MEDLINE; 71076162.

NIALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWSO AURBACH G.D., POTTS J.T. JR.;
HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 351:1586-1588(1970).
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MEDLINE; 74142666.

HAMILTON J.W., NIALL H.D., JACOBS J.W., KEUTMANN COHN D.V.;

PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).
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MEDLINE; 84262483.
WEAVER C.A., GORDON D.F.,
GENE 28:319-329(1984).
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SEQUENCE FROM N.A.
MEDLINE; 80056617.
MERONEMBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A.,
POTTS J.T. JR., RICH A.;
PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).
60 QDVHNFVAL 68
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1 QDVHNFVAL 9
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MEDLINE; 83105964.
WEAVER C.A., GORDON D.F., KEMPER B.;
MOL. CELL. ENDOCRINOL. 28:411-424(1982).
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MEDLINE; 82037785.
WEAVER C.A., GORDON D.F., KEMPER B.;
PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).
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106
115 AA;
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Pred. No. 3.54e-04;
0; Mismatches 0;
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RESULT 1

1D Q63473;
AC Q63473;
DT Q1-NOV-1996 (TREMBLREL. 01, CREATED)
DT Q1-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT Q1-NOV-1996 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE PARATHYROID HORMONE (FRAGMENT).

GN PTH.

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; M
C EUTHERIA; RODENTIA.

RN [1]
RA SCHMELZER H.J., GROSS G., MAYER H.;
ADV. GENE TECHNOL. 21:228-229(1984).
DR EMBL; M54875; G601933; -.
FT NON_TER 1
SEQUENCE 105 AA; 11746 MW; 6AC3163E CRC32;
  RESULT 2
ID P95793
AC P95793
DT 01-MAY-1997 (TREMBLREL 03, DT 01-MAY-1997 (TREMBLREL 03, DT 01-MAY-1997 (TREMBLREL 03, DT 01-MAY-1997 (TREMBLREL 03, DE STBA.

GN STBA.
OS SERRATIA MARCESCENS.
OG PLASMID R478.
OC PROKARYOTA; GRACILICUTES; SG PLASMID R478.
RM [1]
RP SEQUENCE FROM N.A.
RA WHELAN K.F., BEKKERING M., T
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Best Local Similarity 77.8%;
Matches 7; Conservative
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
[1]
SEQUENCE FROM N.A. WHELAN K.F., BEKKERING M., TAYLOR D.E.;
                                                                                                                                                                                                                                                                                                                                                   50 QDGHNFVSL 58
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1 QDVHNFVAL 9
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                                                                                     SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
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REMBL; US9131; G1695965; -.

REMBL; US9131; G1695965; -.

KN PLASMID.

G1695965; -.

KN PLASMID.

G1695965; -.

KN PLASMID.

G1702122 345 AA; 38433 MW; E194251E CRC32;

QUERY MATCH

G1.34; Score 52; DB 9; Length 345;

Best Local Similarity 77.84; Pred. No. 1.20e+00;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 116 ODVHLEVIL 124

Qy 1 QDVHLVAL 9

Search completed: Thu Jul 30 10:51:32 1998

Job time: 29 secs.
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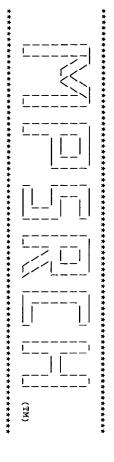
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Best Local Similarity 100.0%;
Matches 8; Conservative
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R58142;
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

on : Thu Jul 30 10:54:14 1998; MasPar time 3.34 Seconds 87.598 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Title: >US-08-817-547A-24 (1-8) from US08817547A.pep 57 1 DVHNFVAL 8

Sequence:

Scoring table: PAM 150 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 21.941; Variance 28.147; scale 0.780

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

1 2 3 3 3 3 3 3 1 1 1 1 1 1 1 1 1 1 1 1	No.
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REFERENCE #authors #submission #cross-refe REFERENCE #authors #book COMMENT Res	RESULT 2 ENTRY TITLE ALTERNATE_NAMES PDB_TITLE ORGANISM	Query Match Best Local   Matches  Db 27 DVH	#DOOK  COMMENT RECOMMENT DE  KEYWORDS FEATURE 15-25 SUMMARY	REFERENCE #submission #cross-refe REFERENCE #authors	RESULT 1 ENTRY TITLE ALTERNATE_NAMES PDB_TITLE
ren		100.0%; Score 57; DB 5; Length 34; sal Similarity 100.0%; Pred. No. 1.14e-01; 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0; DVHNFVAL 34	nn Strukturen Verschledener Parathormoniragmente in Loesung, pp.0, Bayreuth: University of Bayreuth (Thesis), 1996 Resolution: not applicable Determination: NMR hormone #region helix (right hand alpha) #length 34 #molecular-weight 4128 #checksum 5508	#formal_name Homo sapiens #common_name man A67860 Roesch, P.; Marx, U.C. Roesch, P.; Marx, U.C. submitted to the Brookhaven Protein Data Bank, June rences PDB:1ZWE TN001721 Rarx, U.C.	1ZWE #type complete parathyroid hormone (residues 4-37) - human fES HPTH(4-37) structure of human parathyroid hormone fragment 4-37, NMR 10 structures

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COMMENT

KEYWORDS

disease mutation; hormone; signal

FEATURE

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15-25

#region helix (right hand alpha)\
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#region helix (right hand alpha)\
15-25

SUMMARY

Query Match

Guery Match

Best Local Similarity 100.0%; Score 57; DB 5; Length 34;

Best Local Similarity 100.0%; Pred. No. 1.14e-01;

Matches

8; Conservative

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Db

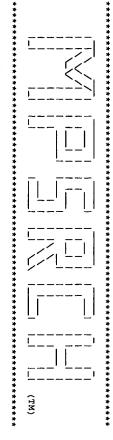
27 DVHNFVAL 34

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Search completed: Thu Jul 30 10:54:45 1998

Job time: 31 secs.
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MPsrch\_pp on: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:53:07 1998; MasPar time 2.11 Seconds 94.946 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Title: >US-08-817-547A-24 (1-8) from US08817547A.pep 57 1 DVHNFVAL 8

Sequence:

Scoring table:

PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 22.974; Variance 23.185; scale 0.991

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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8.14e-03 8.14e-03 8.14e-03 8.14e-03 2.80e+00 4.80e+00 4.80e+00 8.16e+00 8.16e+00 8.16e+00 8.16e+00 8.16e+00 8.16e+00 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.37e+01 1.3	

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24
42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	43
73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	75.4
1550	1321	1038	1004	830	790	689	541	455	316	294	284	284	212	212	208	208	208	208	207	161	2511
<b>ب</b> ــر	۳	۳	ب	۳	ب	Н	۲	Н	Н	1	Н	Ь	Н	Н	μ	<u>,</u>	Н	_	٢	<u>, ,</u>	_
GLTB_SYNY3	MDR1_CAEEL	ATNA_DROME	GCSP_CHICK	MKT1_YEAST	TNP3_HUMAN	YBP3_YEAST	YELL_DROME	HYEP_RAT	VSH5_DICDI	YHBM_ECOLI	YHBJ_ECOLI	YHBJ_KLEPN	CYPC_HUMAN	CYPC_MOUSE	CYPB_MOUSE	CYPB_HUMAN	CYPB_BOVIN	CYPB_RAT	CYPB_CHICK	YCX5_EUGGR	FAS_CHICK
FERREDOXIN-DEPENDENT G	MULTIDRUG RESISTANCE P	SODIUM/POTASSIUM-TRANS	GLYCINE DEHYDROGENASE	MKT1 PROTEIN.	TUMOR NECROSIS FACTOR,	HYPOTHETICAL 77.3 KD P	YELLOW PROTEIN.	EPOXIDE HYDROLASE (EC	VEGETATIVE SPECIFIC PR	HYPOTHETICAL 33.6 KD P	HYPOTHETICAL 32.5 KD P	HYPOTHETICAL 32.5 KD P	PEPTIDYL-PROLYL CIS-TR	HYPOTHETICAL 18.6 KD P	FATTY ACID SYNTHASE (E						
3.77e+01	3.77e+01	3.77e+01	3.77e+01	3.77e+01	3.77e+01	3.77e+01	3.77e+01	3.77e+01	3.77e+01	3.77e+01	3.77e+01	3.77e+01	3.77e+01	3.77e+01	3.77e+01	3.77e+01	3.77e+01	3.77e+01	3.77e+01	3.77e+01	2.29e+01

888	E E	Ŋ	ΡŢ	DT	2	š E	1	RES	Qy	ρb	3	O.B.	SQ	Ŧ	ΗT	Ŧ	ΚV	DR	DR	റ്റ	င္ပ	RL	RA	RA	RX	జ	ŖP	RN	ဂ္ဂ	റ്റ	လ	GN	DE	ΡŢ	ΡŢ	ΡŢ	AC	IĐ	RES
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).	(REL. 35	(REL. 01,	(REL.		TOTICO. STANUARU; FXI; LLO AA.	THE POLITY CHANDAD. DOM: 115	RESULT 2	1 DVHNEVAL 8	61 DVHNFVAL 68	Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	atch 100.0%; Score 57; DB 1; Length 115; cal Similarity 100.0%; Pred. No. 8.14e-03;	SEQUENCE 115 AA; 12957 MW; 16EDOEBC CRC32;	115	26 31	1 25 BY			; G558916;	BONE AND PREVENTING THEIR RENAL EXCRETION.	-!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN	GENE 160:241-243(1995).		ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,	MEDLINE; 95369696.		SEQUENCE FROM N.A.	[1]		EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	CANIS FAMILIARIS (DOG).		HORMONE PR	34, LAST ANNOTATIO	(REL. 34,	01-OCT-1996 (REL. 34, CREATED)	P52212;	PTHY_CANFA STANDARD; PRT; 115 AA.	RESULT 1

EUTHERIA; ARTIODACTYLA.

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DR DR DR FT FT SQ
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                                                                                                                                                                                                        SYNTHESIS OF 32-65.

MEDLINE; 71091588.

A POTTS J.T. JR., TREGEAR G.W., KEUTMANN H.T., NIALL H.D., SAU A POTTS J.T. JR., TREGEAR G.W., L., AURBACH G.D.;

A DEFTOS L.J., DANSON B.F., HOGAN M.L., AURBACH G.D.;

PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).

C -:- FUNCTION. FTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SEONE AND PREVENTING THEIR RENAL EXCRETION.

EMBL; 700106; G85; -.

EMBL; J00024; G163641; -.

EMBL; J00024; G163643; -.

EMBL; J00024; E18249; ALT_INIT.

EMBL; J00024; E18250; ALT_INIT.

EMBL; X01938; G163645; -.

EMBL; X01938; G163645; -.
                                                  Query Match
Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINE; 84262483.

WEAVER C.A., GORDON D.F., K

GENE 28:319-329(1984).

[5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE: 80056617.

KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NAT POTTS J.T. JR., RICH A.;

PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).

[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE; 82037785.
WEAVER C.A., GORDON D.F., KEMPER B.;
PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 26-115.

MEDLINE: 74142666.

HAMILTON J.W., NIALL H.D., JACOBS J.W., KEUTMANN COHN D.V.;

CON D.V.;

PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDLINE; 83105964.

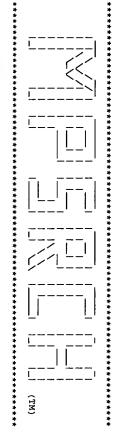
WEAVER C.A., GORDON D.F., KEMPER B.;

MOL. CELL. ENDOCRINOL. 28:411-424(1982).
                                                                                                                                  PROSITE;
HORMONE;
SIGNAL
PROPEP
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 32-115.
MEDLINE; 71063634.
BREWER H.B. JR., RONAN
PROC. NATL. ACAD. SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 32-115.

MEDLINE; 71076162.

NIALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWS AURBACH G.D., POTTS J.T. JR.;
AURBACH G.D., POTTS J.T. JR.;
AUPPE-SEYLER'S Z. PHYSIOL. CHEM. 351:1586-1588(1970).
                                                                                                        CONFLICT
SEQUENCE
                                                                                                                                                                                                   PIR;
                           61
                                                    Match 100.0%;
Local Similarity 100.0%;
Les 8; Conservative
               DVHNEVAL 68
                                                                                                                                                                                  A24949; A24949.
ITE; PS00335; PARATHYROID; 1.
  DVHNFVAL 8
                                                                                                                                                                         SIGNAL.
                                                                                                    26
32
106
115
                                                                                             25
31
115
106
12980 .
                                                                                                                                                                                                                                                                                                                                                                                                                        U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KISSIL M.S., MEAD D.A., KEMPER B.;
                                                                                                           WW;
                                                    Score 57; DB 1; L
Pred. No. 8.14e-03;
0; Mismatches 0
                                                                                                        PARATHYROID HORMONE
V -> G (IN REF. 4).
; 673EA5F2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                           67:1862-1869(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAJZOUB J.A., NATHANS J., SHARP P.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HOGAN M.L., DAWSON
                                                                               Length 115;
                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H.T.,
                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTTS J.T. JR.,
                                                                                                                                                                                                                                                                                                                                     THE SALTS IN
                                                                                                                                                                                                                                                                                                                                                                           SAUER R.,
                                                         0
                                                         Gaps
                                                         0
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Search completed: Thu Jul 30 10:53:13 1998 Job time : 6 secs.



MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Jul 30 10:53:31 1998; MasPar time 3.69 Seconds 91.336 Million cell updates/sec

Tabular output not generated.

Description:
Perfect Score:
Sequence: Title: >US-08-817-547A-24 (1-8) from US08817547A.pep 57 1 DVHNFVAL 8

Scoring table: PAM 150 Gap 15

Searched: 140542 segs, 42109429 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb15
1:sp\_fung1 2:sp\_human 3:sp\_invertebrate 4:sp\_mammal
5:sp\_mhc 6:sp\_organelle 7:sp\_phage 8:sp\_plant
9:sp\_bacteria 10:sp\_rodent 11:sp\_virus 12:sp\_vertebrate
13:sp\_unclassified

Statistics: Mean 21.944; Variance 25.449; scale 0.862

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

2098876544321 2098876544321	Result
	t Score
44444444444444444444444444444444444444	ró
33355554242486657	% Query Match
620 105 3155 2505 2505 2505 2505 2505 2505 2505 2	Length
11 11 10 10 10 10 10 10 10 10 10 10 10 1	BB
001909 963473 995793 006642 00465702 0245702 0247103 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 0221158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022158 022	Ħ
SIMILARITY TO MULTIPLE PARATHYROID HORMONE (F STBA. PUTATIVE FLAGELLA-RELA FATTY ACID SYNTHASE. FATTY ACID SYNTHASE. FATTY ACID SYNTHASE. FATTY ACID SYNTHASE. FATTY ACID SYNTHASE (E GENOME, PARTIAL SEQUEN HYPOTHETICAL 15.7 KD P. SIMILAR TO S. CEREVISI HYPOTHETICAL 49.1 KD P. DELTA3, DELTA2-ENOYL-C. ERCC2/XPD. EXASO.6 PROTEIN. KOBET.5. KOBET.5. SIMILAR TO MULTIDRUG-R. MYELOBLAST KIAAOZ79 (F FROM BASES 2775730 TO. ABC. TRANSPORTER (OLIGO CYCLOPHILIN HOMOLOG TA. ORF36L.	B
1 1 2 2 0 8 6 4 0 1 2 2 0 8 6 6 4 0 1 2 2 0 8 6 6 4 0 1 2 2 0 8 6 6 4 0 1 2 2 0 8 6 6 4 0 1 2 2 0 8 6 6 4 0 1 2 2 0 8 6 6 4 0 1 2 2 0 8 6 6 4 0 1 2 2 0 8 6 6 4 0 1 2 2 0 8 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	Pred. No.

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41	41	41	41	41	41	41	41	41	41	41	42	42	42	42	2	42	42	42	42	12	2	12	42	42
71.9	71.9	71.9	71.9	71.9	71.9	•	71.9	•	•	71.9	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7	73.7
2172	1918	1774	1584	1149	747	645	516	377	371	227	2043	1321	1037	672	568	535	485	483	477	455	404	347	284	224
ω	w	w	N	w	느	ω	ω	ω	ω	9	4	ω	w	Ь	w	œ	9	æ	ω	10	ဖ	Н	ω	Ģ
Q09515	Q93637	Q93636	014514	Q23315	Q08491	002261	018198	017273	018285	P95962	002811	Q21349	Q27766	Q01576	002437	P93479	P95169	Q40223	Q18153	P97869	Q53662	Q08726	094311	P78259
HYPOTHETICAL 236.2 KD	F29G6.3A.	F29G6.3B.	BAI 1.	ZC434.5.	CHROMOSOME XV READING	F44F1.5.	SIMILAR TO K12H4.7 AND	T27A1.2 PROTEIN.	2K1010.6.	ORF C04023.	PHOSPHATIDYLINOSITOL 4	K08E7.9.	SODIUM/POTASSIUM ATPAS	ACETYL-COA SYNTHETASE.	YELLOW.	BERBERINE BRIDGE ENZYM	NUOM (FRAGMENT).	CYCLIN.	COSMID C25E10.	MICROSOMAL EPOXIDE HYD	HYPOTHETHECAL MEMBRANE	CHROMOSOME XV READING	SIMILARITY TO EGF-LIKE	ALPHA-AMYLASE (EC 3.2.
1.33e+02	1.33e+02	1.33e+02	1.33e+02	1.33e+02	1.33e+02	1.33e+02	1.33e+02	1.33e+02	1.33e+02	1.33e+02	8.47e+01	8.47e+01	8.47e+01	8.47e+01	8.47e+01	8.47e+01	8.47e+01	8.47e+01	8.47e+01	8.47e+01	8.47e+01	8.47e+01	8.47e+01	8.47e+01

Ф	Quer: Best Matc	So	RE	RA	RC	RР	R F	RA	RC	RP :	Z	2 3	2 2	RA	RA	RΑ	RA	₽	RΑ	RΑ	RΑ	콨	RC	ŖP	Z (	3 8	2 6	2 15	DT	Dī	ΡŢ	AC	ID	RESULT
134 DVHREVIL 141	Query Match 80.7%; Score 46; DB 3; Length 620; Best Local Similarity 75.0%; Pred. No. 1.28e+01; Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	SEQUENCE 620 AA; 67475 MW; 17C581A5 CRC32;	TIED (MAY-1997) TO E	R.,	STRAIN-BRISTOL N2;	SEQUENCE FROM N.A.	SUBMITTED (MAY-1997) TO EMBL/GENBANK/DUBJ DATA BANKS.	TUNG S.;	STRAIN=BRISTOL N2;	SEQUENCE FROM N.A.		NATURE 368:32-38(1994).	THIERRY MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATEKSTON K., WATEKSTON K., WATEKSTON K.,	SONNHAMMER E., STADEN R., SULSTON J.,	PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,	, MCMURRAY	ERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,	AWKINS T., HILLIER L., JIER	Z., DURBIN R., FAVELLO A., FULTON	., BURTON J., CONNELL M., COPSEY T., CC	WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,	MEDLINE; 94150718.	STRAIN-BRISTOL N2;	SEQUENCE FROM N.A.		STRANSVEREUTIFFO BEEGGEON ATTERS. NEMATODA: SECTERNICATE REALITITAL	ALURAUTHER DE DANG	SIMILARITY TO MULTIPLE CAUHERIN-TYPE REPEATS.	(TREMBLREL. 04, LAST ANNO	04,	(TREMBLREL.	•	O01909 PRELIMINARY; PRT; 620 AA.	A7 1

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1 DVHNFVAL 8

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RESULT

ID Q63473;
AC Q63473;
DT Q1-NOV-1996 (TREMBLREL. Q1, CREATED)
DT Q1-NOV-1996 (TREMBLREL. Q1, LAST SEQUENCE UPDATE)
DT Q1-NOV-1998 (TREMBLREL. Q5, LAST ANNOTATION UPDATE)
DT Q1-JAN-1998 (TREMBLREL. Q5, LAST ANNOTATION UPDATE)
DE PARATHYROID HORMONE (FRAGMENT).
GN PTH.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MACC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-THYROID, AND PARATHYROID;
RATESUE-THYROID, AND PARATHYROID;
RATESUE-THYROID, GROSS G., MAYER H.;
ADV. GENE TECHNOL. 21:228-229(1984).
Search completed: Thu Jul 30 10:53:58 1998 Job time: 27 secs.
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                                                                                                                                                       ₽
                                                                                                                                                                                                  Query Match 78.9%; Score 45; DB 10; Length 105; Best Local Similarity 75.0%; Pred. No. 2.08e+01; Matches 6; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

TISSUE-THYROID, AND PARATHYROID;
SCHMELZER H.J., GROSS G., MAYER H.;
ADV. GENE TECHNOL. 21:228-229(1984).
EMBL; M54875; G601933; -.

NON_TER 1 1

NON_TER 1 1746 MW; 6AC3163E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTH.

RATTUS NORVEGICUS (RAT).

EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

EUTHERIA; RODENTIA.

[1]
                                                                                                 51 DGHNFVSL 58
| ||||:|
1 DVHNFVAL 8
                                                                                                                                                                                                     0;
                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                  0;
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***************************************	[TM)
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**	( TM)

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:57:17 1998; MasPar time 2.55 Seconds 42.121 Million cell upda cell updates/sec

Description: Perfect Score: Title: (1-7) from US08817547A.pep >US-08-817-547A-25

abular output not generated.

Sequence: VHNFVAL 7

Scoring table: PAM 150 Gap 15

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Listing Match first 0% 45 summaries

Database:

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 15.130; Variance 42.680; scale 0.354

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

1100 8 8 7 6 6 5 4 4 3 2 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	esult No:
55555555555555555555555555555555555555	Score
1000.00	Query Match
3000 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Length
00000000000000000000000000000000000000	BB
R58142 R58133 R58133 P30015 P30015 W251687 R23227 R23227 R23314 R23314 R233279 R233279 R233279 R233279 R233424 R233424 R233424 R233424 R233424 R233424 R233424 R233424 R233424 R233424 R233424 R233424	Ħ
[Asn21]-hPTH(1-38)-OH [His9]-hPTH(1-38)-OH [Asp19]-hPTH(1-38)-OH Human parathyroid hor Fusion protien compri Human parathyroid hor Human parathyroid hor Human parathyroid hor Bovine parathyroid ho Bovine parathyroid ho Porcine parathyroid hor Porcine parathyroid hor	Description
1.640+01 1.640+01 1.640+01 1.640+01 1.640+01 1.640+01 1.640+01 1.640+01 1.640+01 1.640+01 1.640+01 1.640+01 1.640+01 1.640+01 1.640+01 1.640+01 1.640+01 1.640+01 1.640+01	Pred. No.

밁

31 vhnfval

37

0;

Gaps

0

51 100.0 84 4 R21241 Human parathyroid hor 51 100.0 84 4 R21240 Human parathyroid hor 51 100.0 84 4 R21240 Human parathyroid hor 51 100.0 84 5 R29562 Oxidation resistant [ 51 100.0 84 5 R29562 Oxidation resistant [ 51 100.0 84 5 R29562 Oxidation resistant [ 51 100.0 84 4 R21250 Human parathyroid hor 51 100.0 84 4 R21250 Human parathyroid hor 51 100.0 84 4 R21187 Human parathyroid hor 51 100.0 84 4 R21187 Human parathyroid hor 51 100.0 84 4 R21234 Human parathyroid hor 51 100.0 84 4 R21234 Human parathyroid hor 51 100.0 84 4 R22332 Porcine parathyroid hor 51 100.0 84 4 R23332 Porcine parathyroid hor 51 100.0 84 4 R23334 Bovine parathyroid hor 51 100.0 84 4 R23336 Bovine parathyroid hor 51 100.0 84 4 R23336 Bovine parathyroid hor 51 100.0 84 4 R23363 Bovine parathyroid hor 51 100.0 84 4 R23449 Porcine parathyroid hor 51 100.0 84
0 84 4 R21241 Human parathyroid 0 84 4 R21241 Human parathyroid 0 84 4 R21240 Human parathyroid 0 84 5 R29562 Oxidation resistar 0 84 4 R21240 Human parathyroid 0 84 5 R29562 Oxidation resistar 0 84 5 R29561 Oxidation resistar 0 84 4 R21250 Human parathyroid 0 84 4 R23309 Bovine parathyroid 0 84 4 R21187 Human parathyroid 0 84 4 R21187 Human parathyroid 0 84 4 R21181 Human parathyroid 0 84 4 R21234 Human parathyroid 0 84 4 R23392 Porcine parathyroid 0 84 4 R23393 Bovine parathyroid 0 84 4 R23393 Bovine parathyroid 0 84 4 R23370 Bovine parathyroid 0 84 4 R23363 Bovine parathyroid 0 84 4 R23340 Human parathyroid 0 84 4 R23449 Bovine parathyroid
k x21101  K x21101  K x21101  K x21201  K x21241  K x21241  K x21240  K x21240  K x21240  K x21240  K x21240  K x21250  K x29562  K x21250  K x21260  K x21219  K x21219  K x21219  K x21219  K x21181  K x2181  K x21181  K x2118
k x21101  K x21101  K x21101  K x21201  K x21241  K x21241  K x21241  K x21240  K x21240  K x21240  K x21240  K x21240  K x21250  K x29562  K x29562  K x29562  K x29562  K x29562  K x29562  K x21250  K x21219  K x21219  K x21219  K x21219  K x21181  K x2181  K x21181  K x2118
oxidation resistan Human parathyroid Human parathyroid Human parathyroid Human parathyroid Oxidation resistan Oxidation resistan Oxidation resistan Oxidation resistan Oxidation resistan Human parathyroid Porcine parathyroid Human parathyroid Bovine parathyroid Human parathyroid
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HESULT IN ENGINEER ACCORDANCE SOLUTION IN ENGINEER ACCORDANCE 
Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SANO) SÂNDOZ LTD.
(BAUE/) BAUER W.
(SANO) SANDOZ PATENT GMBH.
(SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
Albert R, Bauer W, Breckenridge R, Card:
Gombert F, Gram H, Lewis I, Ramage P, (
Waelchil R, Rainer A;
WBI; 99-018352/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-JUL-1993; 014384.

15-JUL-1992; GB-015009.

18-DEC-1992; GB-026415.

23-DEC-1992; GB-026861.

23-DEC-1992; GB-026861.

28-JAN-1993; GB-001691.

28-JAN-1993; GB-001692.

14-APR-1993; GB-007673.

19-APR-1993; GB-008033.
                                                                                                                                                       hypoparathyroidism.
Sequence 38 AA;
                                                                                                                                                                                                                           New active para-thyroid hormone variants - used for treating or preventing osteoporosis etc.

Example 139; Page 40; 92pp; English.

This peptide is an example of a highly generic formula covering parathyroid hormone variants useful for treating or preventing bone conditions associated with calcium depletion/resorption, in cases where calcium fixation is required (esp. osteoporosis) or to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GB2269176-A.
02-FEB-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypoparathyroidism. Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-SEP-1994 (first entry) [Asn21]-hPTH(1-38)-OH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R58142 standard; peptide; R58142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     calcium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 parathyroid hormone; hPTH; variant; analogue;
um; depletion; fixation; resorption; osteopathy; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3
8
   Score 51; DB 9; Length 38; Pred. No. 1.64e+01; 0; Mismatches 0; Indels
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P, Schneider
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ξ
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RESULT

RESULT
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\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* (MT)

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Jul 30 10:56:41 1998; MasPar time 3.23 Seconds 79.088 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Title: >US-08-817-547A-25 (1-7) from US08817547A.pep 51 1 VHNFVAL 7

Sequence:

Scoring table: PAM 150 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 21.152; Variance 25.908; scale 0.816

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

1 2 3 3 3 4 4 4 4 4 7 7 6 6 7 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1	sult No.
7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	Score
11000.00 11000.00 11000.00 11000.00 11000.00 11000.00 11000.00 11000.00 11000.00 11000.00 11000.00 11000.00 11000.00 11000.00 11000.00	Query
34 34 34 35 35 37 37 37 37 37 37 37 37 37 37 25 25 25 25 25 25 25 25 47 25	Length
0 L 0 0 L 0 0 0 0 0 0 0 0 L L 0 L 0 0 0 0 0 0 0 0	DB
12WE 12WG 11ZWF 12WD 11ZWB 11ZWB 11ZWB 11ZWB 11ZWB 11ZWB 11ZWC 12WC 12WC 12WB 12WB 12WB 12WB 12WB 12WB 12WB 12WB	Ü
parathyroid hormone 4 parathyroid hormone 4 parathyroid hormone 6 parathyroid hormone 9 parathyroid hormone p parathyroid sommone p fatty-acid synthase ( peptidylprolyl isomer	Description
7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.97e-01 7.9	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	
41	41	41	41	41	41	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	-
80.4	80.4	80.4	80.4	80.4	80.4	82.4	82.4	82.4	82.4	82.4	82.4	82.4	82.4	82.4	82.4	82.4	82.4	82.4	2	82.4	
1520	924	864	632	599	537	672	541	316	216	212	212	208	207	183	182	182	182	182	178	105	
N	N	N	N	N	N	N	N	N	N	N	N	<b></b> -	N	N	Ų	υı	U	ഗ	ທ	N	1
G69634	S34926	S13381	S73824	S18612	S67434	S46276	A25696	S07569	A56861	A40047	A54204	CSHUB	A40516	S71547	2RMCA	2RMCG	2RMCC	2RMCE	1CYNA	I51851	
glutamate synthase (l	hypothetical protein	lipoxygenase (EC 1.13	Φ	lipoxygenase (EC 1.13	hypothetical protein	acetateCoA ligase (	yellow protein - frui	protein H5 - slime mo	peptidylprolyl isomer	Cyclophilin c complex	Cyclophilin c complex	a	Cyclophilin c complex	cyclophilin b, chain	parathyroid hormone -						
9.32e+01	9.32e+01	9.32e+01	9.32e+01	9.32e+01	9.32e+01		5.98e+01		5.98e+01	5.98e+01	5.98e+01	5.98e+01	5.98e+01	,							

1.0esung, 3), 1996 28 Gaps 0; 31 Gaps 0; 31 Structures 31 Structures 32 Structures 33, 1996
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COMMENT

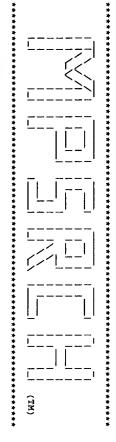
disease mutation; NAR

EXAMPLE

#region helix (right hand alpha)\
15-25  #region helix (right hand alpha)\
15-25  #region helix (right hand alpha)\
SUMMARY #region helix (right hand alpha)\
100.08; Score 51; DB 5; Length 34;
Best Local Similarity 100.08; Pred. No. 7.97e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 28 WHEVAL 34
Qy 1 VHNEVAL 7

Search completed: Thu Jul 30 10:57:00 1998
Job time: 19 secs.
```



Psrch\_pp protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:55:35 1998; MasPar time 2.08 Seconds 84.457 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-817-547A-25 (1-7) from US08817547A.pep 51 1 VHNFVAL 7

Scoring table: PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 22.139; Variance 21.222; scale 1.043

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

No.	Score	% Query Match	Length	BG	Ħ	Description	Pred. No.
-	51	100.0	115	_ ;	PTHY_CANFA	PARATHYROID HORMONE PR	8.19e-02
N	51	•	115	Н	1	HORMONE	8.19e-02
ω	51		115	Н	PTHY_PIG	HORMONE	
4	51	100.0	115	μ	PTHY_HUMAN	PARATHYROID HORMONE PR	&
IJ	49	96.1	115	Н	PTHY_RAT	HORMONE	2
σ	46	90.2	136	Н	Y441_MYCPN	HYPOTHETICAL PROTEIN M	
7	46	90.2	200	Н	YIGP_ECOLI	HYPOTHETICAL 22.3 KD P	
8	45	88.2	297	<u>,                                    </u>	YMY9_YEAST	HYPOTHETICAL 34.0 KD P	2.95e+00
9	45	88.2	687	Н	CSTA_HELPY	CARBON STARVATION PROT	2.95e+00
10	45	88.2	2504	H	FAS_HUMAN	FATTY ACID SYNTHASE (E	2.95e+00
11	45	88.2	2505	<b>ب</b>	FAS_RAT	FATTY ACID SYNTHASE (E	2.95e+00
12	44	86.3	227	μ	UBL_DROME	UBIQUITIN CARBOXYL-TER	5.18e+00
13	44	86.3	505	۳	Y4XG_RHISN	HYPOTHETICAL 55.5 KD P	
14	43	84.3	752	μ	CUL1_HUMAN	CULLIN HOMOLOG 1 (CUL-	9.02e+00
15	43	84.3	2511	Н	FAS_CHICK	FATTY ACID SYNTHASE (E	9.02e+00
16	42	82.4	161	Н	YCX5_EUGGR	HYPOTHETICAL 18.6 KD P	1.55e+01
17	42	82.4	207	Н	CYPB_CHICK	PEPTIDYL-PROLYL CIS-TR	1.55e+01
18	42	82.4	208	Н	CYPB_RAT	PEPTIDYL-PROLYL CIS-TR	
19	42		208	Н	CYPB_HUMAN	PEPTIDYL-PROLYL CIS-TR	
20	42	82.4	208	μ	CYPB_MOUSE	PEPTIDYL-PROLYL CIS-TR	<u>,</u>
21	42	•	208	Н	CYPB_BOVIN	PEPTIDYL-PROLYL CIS-TR	<u>, , , , , , , , , , , , , , , , , , , </u>
22	42	•	212	Н	CYPC_HUMAN	PEPTIDYL-PROLYL CIS-TR	1
23	42	82.4	212	ш	CYPC_MOUSE	PEPTIDYL-PROLYL CIS-TR	1.55e+01

LOCOCH LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO LNCCHPO	45	44	43	42	41	40	3 9	38	37	36	35	34	33	3 2	31	30	29	28	27	26	25	*
541 1 YELL_DROME 541 1 YELL_DROME 537 1 AREH_SCHPO 637 1 YA42_MYCPN 864 1 LOXX_SOYEN 924 1 YE53_YEAST 216 1 YE6_CREEL 274 1 CDL_SYLFL 408 1 GPT_CRIGR 570 1 EMP7_HUMAN 1 CADB_ECOLI 1 CAD	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	40	41	41	41	41	42	*
1 YELL_DROME 1 YAREH SCHPO 1 YB53_YEAST 1 YB53_YEAST 1 YB53_YEAST 1 YB53_YEAST 1 YB53_YEAST 1 GPT_CRIGR 1 CCADB_ECOLI 1 CCADB_	78.4	78.4	78.4	78.4	78.4	78.4	78.4	78.4	78.4	78.4	78.4	78.4	78.4	•	78.4	78.4	80.4	80.4	80.4	80.4	82.4	. 4
YELL_DROWE AREH_SCHPO Y242_MYCPN Y283_YEAST YEAST YEAST YEAST YEAST CRIGAT GPT_CRIGA GPT_CRIGA GPT_CRIGA GPT_HUMAN CADB_ECOLI LCK_CHICK YEAA_ECOLI UGST_SOLTU DEST_SOLTU DEST_SOLTU SECS_YEASN YEAA_ECOLI UGST_SOLTU SETS_HUMAN SECS_YEASN SECS_YEASN SECS_YEASN SECS_YEASN SECS_YEASN SECS_YEASN SECS_YEASN	847	805	805	801	783	782	607	578	507	444	431	430	408	408	274	216	924	864	632	537	541	OTO
3 000 F 420 F 42200F	Н	ب	ᆫ	Ь	ب	<b>ب</b>	Ь	μ	μ.	μ.	Н	Н	<b>js</b>	_	Н	₽	<u>,                                    </u>	<b>-</b>	_	ᆫ	,_	٢
YELLOW PROTEIN.  PROBABLE STEROL O-ACYL HYPOTHETICAL PROTEIN M SEED LIPOXYGENASE (EC HYPOTHETICAL 104.5 KD HYPOTHETICAL 23.9 KD HYPOTHETICAL 23.9 KD P-N-ACETYLGLUCOSAMIN BONE MORPHOGENETIC PRO BONE MORPHOGE	ENV_HV1W2	SEC6_YEAST	ZFX_HUMAN	ZFY_HUMAN	ZFY2_MOUSE	ZFY1_MOUSE	UGST_SOLTU	YFAA_ECOLI	LCK_CHICK	CADB_ECOLI	BMP7_HUMAN	BMP7_MOUSE	GPT_CRILO	GPT_CRIGR	CD1_SYLFL	YS86_CAEEL	YB53_YEAST	LOXX_SOYBN	Y242_MYCPN	AREH_SCHPO	YELL_DROME	TOTALLORD
	ENVELOPE POLYPROTEIN G	EXOCYST COMPLEX COMPON	FINGER	FINGER	FINGER	ZINC FINGER Y-CHROMOSO	GRANULE-BOUND GLYCOGEN	HYPOTHETICAL 64.5 KD P	PROTO-ONCOGENE TYROSIN	PROBABLE CADAVERINE/LY	MORPHOGENETIC		UDP-N-ACETYLGLUCOSAMIN	UDP-N-ACETYLGLUCOSAMIN	T-CELL SURFACE GLYCOPR		HYPOTHETICAL 104.5 KD		HYPOTHETICAL PROTEIN M	PROBABLE STEROL O-ACYL	YELLOW PROTEIN.	APPROPRIATION OFFICERS AN

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	PTH.	PARATHYROID HORMONE DR	01-NOV-1997 (REI 35 LAST ANNOTATIO	21 - THI - 1986 (REI OI)	21 - TIII 1986 (REI.	P01268:		RESULT 2	<b></b>	Db 62 VHNFVAL 68	Matches 7; Conservative 0; Mismatches 0; Indels 0; (	100.0%; Score 51; DB 1; Leng ilarity 100.0%; Pred. No. 8.19e-02;	SEQUENCE 115 AA;	CHAIN 32 115 PARATHYROII	PROPEP 26 31	SIGNAL 1 25 BY	HORMONE; SIGNAL.	PROSITE; PS00335; PARAS	EMBL; U15662; G558916;	BONE AND PREVENTING THEIR RENAL EXCRETION.	-1-		DEWILLE J.W., CAPEN C.C.;				DD GEOGRAPH BOM N A			CANIS FAMILIARIS (DOG).	PTH.	PARATHYROID HORMONE PR	01-OCT-1996 (REL. 34, LAST ANNOTATIO	01-OCT-1996 (REL. 34,	01-OCT-1996 (REL.	P52212:	TO DEBY CAMEA STANDARD: DRT: 115 AA	RESULT 1
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                                                Query Match
Best Local S
Matches
                                                                                                                                                                                                             MEDLINE; 71091588.

MEDLINE; 71091588.

POOTTS J.T. JR., TREGEAR G.W., KEUTMANN H.T., NIALL H.D., SAUER R., DEFTOS L.J., DAWSON B.F., HOGAN M.L., AURBACH G.D.;
DEFTOS L.J., DAWSON B.F., HOGAN M.L., AURBACH G.D.;
PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).

-I- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN BONE AND PREVENTING THEIR RENAL EXCRETION.

EMBL; V00106; G85; -.
EMBL; V001023; G163641; -.
EMBL; J00024; G163643; -.
EMBL; J00024; E18259; ALT_INIT.
EMBL; K01938; G163647; -.
EMBL; N01938; G163645; -.
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MEDLINE; 83105964.

WEAVER C.A., GORDON D.F., KEMPER B.;

MOL. CELL. ENDOCRINOL. 28:411-424(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE; 84262483.
MEAVER C.A., GORDON D.F.,
GENE 28:319-329(1984).
[5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 32-115.

MEDLINE; 71076162.

NIALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWS AURBACH G.D., POTTS J.T. JR.;

HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 351:1586-1588(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 26-115.
MEDLINE; 74142666.
HAMILTON J.W., NIALL H.D.,
COHN D.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE: 82037785.
WEAVER C.A., GORDON D.F.,
PROC. NATL. ACAD. SCI. U.S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., POTTS J.T. JR., RICH A.; PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EUTHERIA; ARTIODACTYLA.
[1]
SEQUENCE FROM N.A.
MEDLINE; 80056617.
                                                                                                  CHAIN
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 71063634.
BREWER H.B. JR., RONAN
PROC. NATL. ACAD. SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).
                                                                                                                                                                                        PIR; A01534; PTBO.
PIR; A24949; A24949.
                                                                                                                                                                                                                                                                                                                                                                                SYNTHESIS OF 32-65.
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 32-115.
                                                                                                                                                               HORMONE; SIGNAL.
                                                                                                                                        PROPEP
                                                                                                                                                    SIGNAL
                                                                                                                                                                            PROSITE; PS00335; PARATHYROID; 1.
                          62 VHNFVAL 68
  1 VHNFVAL 7
                                               h 100.0%;
Similarity 100.0%;
7; Conservative
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32
106
115 AA;
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31
115
P.
106
V
12980 MW;
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U.S.A. 78:4073-4077(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KISSIL M.S., MEAD D.A., KEMPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JACOBS J.W., KEUTMANN H.T.,
                                                 Score 51; DB 1; Length 115; Pred. No. 8.19e-02; 0; Mismatches 0; Indels
                                                                                                  PARATHYROID HORMONE.
V -> G (IN REF. 4).
; 673EA5F2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                          67:1862-1869(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HOGAN M.L., DAWSON B.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTTS J.T. JR.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.
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                                                     0
                                                     Gaps
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Search completed: Thu Jul 30 10:55:41 1998 Job time : 6 secs.

1 45 3 44 4 43 5 42 6 42 7 42 110 111 113 114 115 116 117 118 119 119 119 119 119 119 119	Pred. No. score gree and is de Result No. Score	<pre>pearched: Post-processing Database:</pre>	psrch_pp n on: abular ou itle: escriptic erfect se equence: coring to	Release 3
88.2 2505 10 053 88.2 2505 20 88.3 368 3 221 84.3 1221 3 023 82.4 196 3 099 82.4 196 3 099 82.4 485 9 P99 82.4 535 8 P99 82.4 555 8 P99 82.4 572 1 000 82.4 932 3 011 82.4 2408 2 099 82.4 2408 2 099 82.4 326 3 017 82.4 326 3 017 82.4 326 3 017 82.4 326 3 017 82.4 326 3 017 82.4 2408 2 099 82.4 2408 3 017 82.4 2408 3 001 82.4 2408 3 017 82.4 2408 3 017 82.4 2408 3 017 82.4 2408 3 017 82.4 2408 3 017 82.4 2408 3 017 82.4 2408 3 017 82.4 2408 3 017 82.4 2408 3 017 82.4 2408 3 017 82.4 2408 3 017 83.4 340 340 340 84.4 340 340 340 85.4 378 3 017 86.4 378 3 017 86.4 599 8 041	Mean 21.229; Variar No. is the number of resu greater than or equal to s derived by analysis of t SUMA Query Query Tre Match Length DB ID	140542 seqs, 42109 : Minimum Match 08 Listing first 45 s sptrembl5 1:sp_fungi 2:sp_ 5:sp_mhc 6:sp_or 9:sp_bacteria 10 13:sp_unclassifi	stribution righ - protein datab - protein datab - Jul 30 10:55:5 - penerated 08-817-547A-25 - 7) from USO8817 - 7) from USO8817 - 7) HNFVAL 7 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150 - 150	1 John F. COLL
063577 FATTY ACID SYNTHASE 016702 FATTY ACID SYNTHASE 021158 SIMILAR TO S. CEREVY 021344 KORET.5. 024347 PARATHYROID HORMONE 034770 CYCLOPHILIN HOMOLOG 094311 SIMILARITY TO ESF-L. 094311 NUOM (FRAGMENT). 1002437 PELLOW. 101301 ZELLOW. 101301 ZK250.6 PROTEIN. 092566 MYELOBLAST KIAAO279 084562 GENOME, PARTIAL SEQU 017775 GENOME, PARTIAL SEQU 017775 F09G3.4. 013303 ZK849.4. 0122315 ZC434.5.	riance 23.108; scale 0.919 results predicted by chance to to the score of the result bei of the total score distribution SUMMARIES  D Description	wnmaries  human 3:sp_invertebrate 4  ganelle 7:sp_phage 8:sp_p  :sp_rodent 11:sp_virus 12  ed	ts by Oxford Molecular I	
ASE. 7.93e+00 ASE (E 7.33e+01) REVISI 1.33e+01 ONE (F 3.67e+01) LOG TA 3.67e+01 ENZYM 3.67e+01 ENZYM 3.67e+01 3.67e+01 3.67e+01 3.67e+01 3.67e+01 3.67e+01 6.00e+01 6.00e+01 6.00e+01 6.00e+01 6.00e+01 6.00e+01 6.00e+01 6.00e+01 6.00e+01	to have a being printed, tion.	:sp_mammal lant :sp_vertebrate	Waterman algorithm 5 Seconds cell updates/sec	T K THE TENT OF TH

45	44	3	42	41	40	39	38	37	<b>3</b> 6	35	34	ω ω	32	ដ	30	29	28	27	26	25	24	23	22	21
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78.4	78.4	78.4	78.4			8	78.4	8	78.4	78.4	8	8	78.4	78.4	8	78.4	78.4	œ	78.4	78.4	78.4	80.4	.0	80.4
1113	862	861	852	801	747	659	635	620	601	562	488	460	400	296	256	175	115	91	91	91	90	19:8	1903	1774
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015056	Q73336	Q71819	041593	Q15558	Q20046	Q18406	യ	001909	007176	P76923	P71364	Q51510	015216	P76472	Q04315	P77949	Q33000	Q72854	Q72856	Q72852	Q72849	Q93637	P87204	Q93636
KIAA0348.	ENVELOPE POLYPROTEIN.	ENV GLYCOPROTEIN.	ENVELOPE GLYCOPROTEIN	TESTIS DETERMINING FAC	COSMID F35D2.	CODED FOR BY C. ELEGAN	Y48E1B.5.	SIMILARITY TO MULTIPLE	HYPOTHETICAL 68.6 KD P	SIMILAR TO.	GLUCONATE PERMEASE (GN	PROTEIN E1 PRECURSOR.	GLCNAC-1-P TRANSFERASE	FROM BASES 2360084 TO	HYPOTHETICAL 20.0 KD P	CYCLOPHILIN SCCYPB (EC	ORF115.	ENVELOPE GLYCOPROTEIN	ENVELOPE GLYCOPROTEIN	ENVELOPE GLYCOPROTEIN	ENVELOPE GLYCOPROTEIN	F29G6.3A.	FKSP PROTEIN INVOLVED	F29G6.3B.
9.72e+01	•	9.72e+01	9.72e+01	٠	9.72e+01	•	9.72e+01	9.72e+01	9.72e+01	•	9.72e+01	9.72e+01	9.72e+01	9.72e+01	9.72e+01	9.72e+01	9.72e+01	9.72e+01	9.72e+01	9.72e+01	9.72e+01	6.00e+01	6.00e+01	6.00e+01

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RESULT 2

ID 016702

AC 016702;

AC 016702;

DT 01-NOV-1996 (TREMBLREL. 01, CREATED)

DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)

DT 01-JAN-1998 (TREMBLREL. 01, LAST ANNOTATION UPDATE)

DE FATTY ACID SYNTHASE (EC 2.3.1.85) (FATTY-ACID SYNTHASE).

OS HOMO SAPIENS (HUMAN).
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Best Local Similarity 71.4%;
Matches 5; Conservative
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063577;
Q63577;
O1-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
FATTY ACID SYNTHAEL
RATTUS NORVECICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE; 92141210.

SMITH S., NAGGERT J., WILLIAMS-AHLF B., AMY C.M.;

PROC. NATL. ACAD. SCI. U.S.A. 89:1105-1108(1992).

EMBL; M84761; G204099; -.

PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.

PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.

TRANSFERASE.

SEQUENCE 2505 AA; 272663 MW; 5151416A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                             550 VHSFVSL 556
||:||:|
1 VHNFVAL 7
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MEDLINE; 89240686.
AMY C.M., WITKOWSKI A., NAGGERT J., WILLIAMS B., RANDHAWA Z.,
SMITH S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROC. NATL. ACAD. SCI. U.S.A. 86:3114-3118(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 45; DB 10; Length 2505; Pred. No. 7.93e+00; 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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OC EUTHERIA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; OC EUTHERIA; PRIMATES.

RN [1]

RN [1]

RP SEQUENCE FROM N.A.

RA HENNIGAR R.A., JENNER K.H., HEINE H.S., KAYLER A.E., WOOD F.D.,

RA KUHAJDA F.P., PASTERNACK G.R.;

RL SUBMITTED (AUG-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.

CC -!- CATALYTIC ACTIVITY: ACETYL-COA + N MALONYL-COA + 2N NADP(+).

CC LONG-CHAIN FATTY ACLD + (N+1) COA + N CO(2) + 2N NADP(+).

DR EMBL; U29344; G915392; -.

DR PROSITE; PSO00012; PHOSPHOPANTETHEINE; 1.

DR PROSITE; PSO0006; B_KETOACYL_SYNTHASE; 1.

PROSITE; PSO0066; B_KETOACYL_SYNTHASE; 1.

SQ SEQUENCE 2509 AA; 273089 MW; D1E74B76 CRC32;

SQ SEQUENCE 2509 AA; 273089 MW; D1E74B76 CRC32;

Guery Match

Best Local Similarity 71.4%; Pred. No. 7.93e+00;

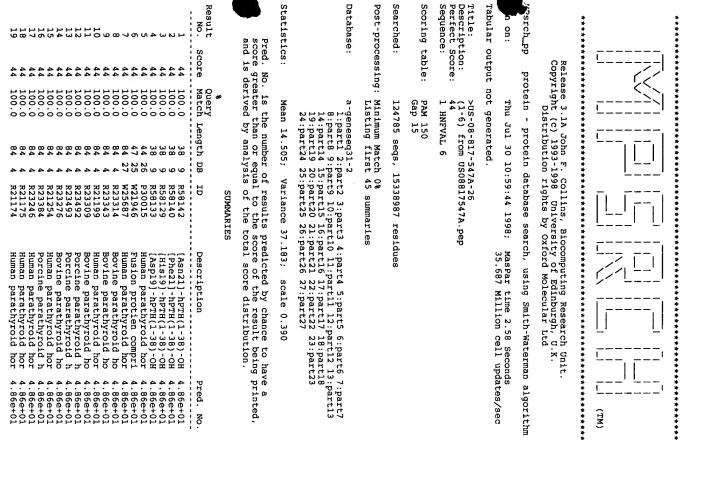
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

1 VHNFVAL 7

Search completed: Thu Jul 30 10:56:24 1998

Job time: 26 secs.
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45	44	43	42	41	40	39	38	37	36	35	34	<b>ω</b>	32	31	30	29	28	27	26	25	24	23	22	21	20	
44	44	44	44	44	44	44	44	44	44	44	44	44	44	44	44	44	44	44	44	44	44	44	44	44	44	
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R23449	121	R21210	336	ഗ	4	7	ω	vo	123	R21234	œ	N	œ	R21219	o	*	R29561	o		24	R21241	956	116	R23383	R23424	
Porcine parathyroid h	Human parathyroid hor	ש	Bovine parathyroid ho	Porcine parathyroid h	Human parathyroid hor	Bovine parathyroid ho	Porcine parathyroid h	Porcine parathyroid h	Human parathyroid hor				Human parathyroid hor	parathyroid		Human parathyroid hor	Oxidation resistant P	tan	id	Human parathyroid hor	Human parathyroid hor	Oxidation resistant P	5	Porcine parathyroid h	Porcine parathyroid h	
4.86e+01		4.86e+01				4.86e+01			4.86e+01	-	4.86e+01		4.86e+01				4.86e+01		&	<u>.</u>	4.86e+01				4.86e+01	

### ALIGNMENTS

20-SEP-1994 R58142 standard; R58142;

(first entry)

peptide;

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SOCCO
 멍
                      Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                            12-JUL-1993;
15-JUL-1992;
18-DEC-1992;
23-DEC-1992;
23-DEC-1992;
23-DEC-1992;
28-JAN-1993;
14-APR-1993;
14-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                          [Asn21]-hPTH(1-38)-OH.
Human parathyroid hormone; hPTH; variant;
calcium; depletion; fixation; resorption;
hypoparathyroidism.
                                                                                          New active para-thyroid hormone variants - used for treating or preventing osteoporosis etc.

Example 139; Page 40; 92pp; English.

This peptide is an example of a highly generic formula covering parathyroid hormone variants useful for treating or preventing bond conditions associated with calcium depletion/resorption, in cases where calcium fixation is required (esp. osteoporosis) or to treat
                                                                                                                                                                             Albert R, Bauer W, Breckenridge R, Cardinaux Gombert F, Gram H, Lewis I, Ramage P, Schnei Waelchli R, Rainer A;
WPI: 94-018352/03.
                                                                     hypoparathyroidism.
Sequence 38 AA;
                                                                                                                                                                                                                              (SANO)
                                                                                                                                                                                                                                                      (SANO)
                                                                                                                                                                                                                                                                                                                                                                                                   GB2269176-A.
32 hnfval 37
                                                                                                                                                                                                                              SANDOZ PATENT GMBH.
SANDOZ-ERFINDUNGEN VERW GES MBH.
                                                                                                                                                                                                                                                                    SANDOZ
                                                                                                                                                                                                                                                        BAUER W.
                                                                                                                                                                                                                                                                             014384.

GB-015009.

GB-026415.

GB-026859.

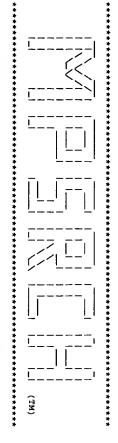
GB-026861.

GB-001691.

GB-001697.

GB-007673.

GB-008033.
                                                                                                                                                                                                                                                                  LTD.
                      Score 44; DB 9; I
Pred. No. 4.86e+01;
0; Mismatches C
                                                                                                                                                                                                     dinaux F;
Schneider
                                                                                                                                                                                                                                                                                                                                                                                                                                   analogue;
osteopathy; osteoporosis;
                         0
                                            Length 38;
                         Indels
                         0
                                                                                                                      bone
                         Gaps
                         0
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MPsrch\_pp on: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:59:09 1998; MasPar time 3.02 Seconds
72.657 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-817-547A-26 (1-6) from US08817547A.pep 44 1 HNEVAL 6

Scoring table: PAM 150 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 20.121; Variance 22.615; scale 0.890

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

22210887654321 22210887654321	No.
44444444444444444444444444444444444444	Score
9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	Query Match 1
34 34 35 35 36 37 37 37 37 37 37 37 37 37 37 37 37 37	Length I
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12WE 12WG 12WG 12WG 12WG 11ZWD 11ZWD 11ZWC 174402 PTPG PTPG PTPG PTPG PTPG PTPG PTPG PTP	Ħ
parathyroid hormone ( parathyroid hormone 4 parathyroid hormone 4 parathyroid hormone ( parathyroid hormone poretin protein IUDP-N-acetylglucosami UDP-N-acetylglucosami Osteogenic protein I osteogenic protein - Tscher protein - Tsroil protein - Tsroil protein - Tsroil protein hypothetical protein hypothetical protein	Description
6.34e+00 6.34e+00 6.34e+00 6.34e+00 6.34e+00 6.34e+00 6.34e+00 6.34e+00 6.34e+00 1.77e+01 1.77e+01 1.77e+01 1.76e+01 4.76e+01 4.76e+01 4.76e+01 4.76e+01 4.76e+01 4.76e+01 4.76e+01 4.76e+01 4.76e+01 4.76e+01 4.76e+01 4.76e+01 4.76e+01 4.76e+01 4.76e+01 4.76e+01 4.76e+01	Pred. No.

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A57788	E69121	240040	200000	20202	A42363	G69287	S04110	S67660	JN0878	S72497	S68161	A56163	S43297	140811	86569¤	S33956	S39966	JC5638	C65188	S73520	A60776
fatty-acid synthase (	Conserved hypothetical	hypothetical protein	transredulatory prote		peptidase T - Salmone		integrase - Streptomy	hypothetical protein	100K protein - fowl a	oligopeptide transpor	oligopeptide transpor	peptide transport pro	oligopeptide transpor	uroporphyrinogen-III	maturation of the out	ubiquitin thiolestera	hypothetical protein	pH-sensing regulatory	hypothetical 22.3 kD	MG441 homolog E09_orf	230k bullous pemphigo
1.24e+02	1 246+02	1 2/0+02	1.246+02	1 240+02	1.24e+02	1.24e+02	1.24e+02	7.71e+01	7.71e+01	7.71e+01	7.71e+01	7.71e+01	7.71e+01	7.71e+01	7.71e+01	7.71e+01	7.71e+01	7.71e+01	7.71e+01	7.71e+01	4.76e+01

#authors Marx U.C. #authors Marx U.C. #book in Strukturen Verschiedener Parathormonfragmente in Loesung, #book pp.0, Bayreuth: University of Bayreuth (Thesis), 1996 COMMENT Resolution: not applicable	rs ssion referen	ALTERNATE_NAMES n-Succinyl-hpth(4-37)  PDB_TITLE Succinyl human parathyroid hormone 4-37, NMR, 10 structures  ORGANISM #formal_name synthetic  REFERENCE A57743	RESULT 2  IZWG #type complete  TITLE parathyroid hormone 4 37 mutant N-TERMINAL SUCCINYLATED -  Synthetic	Db 29 HNFVAL 34        Qy 1 HNFVAL 6	Query Match 100.0%; Score 44; DB 5; Length 34; Best Local Similarity 100.0%; Pred. No. 6.34e+00; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	15-25 #region helix (right hand alpha) SUMMARY #length 34 #molecular-weight 4128 #checksum 5508	COMMENT Resolution: Dp.0, Hayreutn : University of Hayreutn (Thesis), 1996 COMMENT Determination: NMR KEYWORDS hormone FEATURE	_	ion eferen	#formal_name Homo A67860	IZWE #type complete TITLE parathyroid hormone (residues 4-37) - human ALTERNATE_NAMES HPTH(4-37) PDB_TITLE structures  #type complete PDB_TITLE structures	RESULT 1
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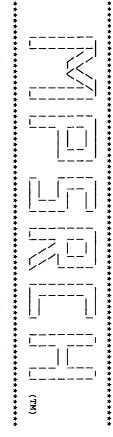
```
COMMENT Determination: NMR
KEYWORDS disease mutation; hormone; signal
FEATURE 2-9
15-25 #region helix (right hand alpha)\
SUMMARY #length 34 #molecular-weight 4128 #checksum 5508

Query Match 100.0%; Score 44; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 6.34e+00;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 29 HNFVAL 4
QY 1 HNFVAL 6

Search completed: Thu Jul 30 10:59:26 1998

Job time: 17 secs.
```



MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Thu Jul 30 10:57:48 1998; MasPar time 2.03 Seconds 74.131 Million cell updates/sec

0n:

Title:
Description:
Perfect Score:
Sequence: >US-08-817-547A-26 (1-6) from US08817547A.pep 44 1 HNFVAL 6

Scoring table: PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 21.045; Variance 18.682; scale 1.127

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Length DB ID  115   PTHY_CANFA 115   PTHY_BOVIN 115   PTHY_PIG 115   PTHY_PIG 115   PTHY_RAT 115   PTHY_RAT 115   PTHY_RAT 115   PTHY_RAT 121   PTHY_RAT 131   PTHY_RAT 140   GPT_CRIGR 140   GPT_CRIGR 141   GPT_MOUSE 1431   BMP7_HUMAN 1507   LCK_CHICK 1578   YEAA_ECOLI 1578   PETI_RAT 1578   PETI_RAT 1578   PETI_RAT 1579   L110_ADEGX	NO.
Length DB ID  115   PTHY_CANFA 115   PTHY_BOVIN 115   PTHY_PIG 115   PTHY_PIG 115   PTHY_RAT 115   PTHY_RAT 115   PTHY_RAT 115   PTHY_RAT 121   PTHY_RAT 131   PTHY_RAT 140   GPT_CRIGR 140   GPT_CRIGR 141   GPT_MOUSE 1431   BMP7_HUMAN 1507   LCK_CHICK 1578   YEAA_ECOLI 1578   PETI_RAT 1578   PETI_RAT 1578   PETI_RAT 1579   L110_ADEGX	Score
DB ID  PTHY_CANFA  PTHY_BOVIN  PTHY_BOVIN  PTHY_RAT  VELL_DROME  GPT_CRIGA  GPT_CRIGA  GPT_CRIGA  GPT_MOUSE  BMP7_MOUSE  BMP7_MOUSE  BMP7_HUMAN  LCK_CHICK  VEAA_ECOLI  VEAA_E	
PTHY_CANFA PTHY_BOVIN PTHY_BOVIN PTHY_HUMAN PTHY_RAT YELL_DROME GPT_CRIGA GPT_CRIGA GPT_CRIGA GPT_MOUSE BMP7_HUMAN LCK_CHICK YFAA_ECOLI YEAS_YEAST CGEE_BACSU Y441_MYCPN Y1GP_ECOLI UBL_DROME HEM4_CLOJO PET1_RABIT PET1_HUMAN PET1_RABIT DET1_RABIT DET1_RABIT	
	ID
Description  PARATHYROID HORMONE PR PARATHYROID TRANSPORT OLIGOPEPTIDE TRANSPORT OLIGOPEPTIDE TRANSPORT OLIGOPEPTIDE TRANSPORT OLIGOPEPTIDE TRANSPORT OLIGOPEPTIDE TRANSPORT OLIGOPEPTIDE TRANSPORT	Description PARATHYROID HORMONE
Pred. No. 1.12e+00 R 1.12e+00 R 1.12e+00 R 3.84e+00 N 1.26e+01 N 1.26e+01 D 2.23e+01 D 2.23e+01 D 2.23e+01 D 2.23e+01 D 2.23e+01 D 2.23e+01	Pre

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
38	38	38	38	38	38	38	ა 8	ယ 8	3 8	38	38	38	38	38 8	38 8	38	38	38	38	38	39
86.4	86.4	86.4	86.4	86.4	86.4	86.4	86.4	86.4	86.4	86.4	86.4	86.4	86.4	86.4	86.4	86.4	86.4	86.4	•	86.4	88.6
2505	2504	790	687	591	587	582	560	560	541	536	499	499	409	408	388	297	289	259	249	249	984
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FAS_RAT	FAS_HUMAN	TNP3_HUMAN	CSTA_HELPY	LAC1_CRYPA	TATR_NPVBM	TATR_NPVAC	TATR_NPVOP	TATR_NPVCF	DET1_ARATH	YB36_YEAST	GUN1_BACSU	GUN2_BACSU	PEPT_SALTY	PEPT_ECOLI	INTR_STRAM	YMY9_YEAST	ROB_ECOLI	UDP_HAEIN	UL07_HSV6Z	UL07_HSV6U	L100_ADEG1
FATTY ACID SYNTHASE (E	FATTY ACID SYNTHASE (E	TUMOR NECROSIS FACTOR,	CARBON STARVATION PROT	LACCASE PRECURSOR (EC	TRANS-ACTIVATING TRANS	TRANS-ACTIVATING TRANS	TRANS-ACTIVATING TRANS	TRANS-ACTIVATING TRANS	LIGHT-MEDIATED DEVELOP	HYPOTHETICAL 60.5 KD P	ENDOGLUCANASE PRECURSO	ENDOGLUCANASE PRECURSO	PEPTIDASE T (EC 3.4.11	PEPTIDASE T (EC 3.4.11	INTEGRASE.	HYPOTHETICAL 34.0 KD P	RIGHT ORIGIN-BINDING P	URIDINE PHOSPHORYLASE	PROTEIN U75.	PROTEIN U75.	LATE 100 KD PROTEIN.
3.91e+01		3.91e+01		3.91e+01	3.91e+01			3.91e+01	3.91e+01	3.91e+01		3.91e+01	3.91e+01	3.91e+01	•						

000	S E T	r r	Ac	RESULT	ΔĀ		DЬ	Ma Be	ğ	) H	Ή	FΤ	KW	DR	DR	გ	ც	ŖĽ	RA :	R.A	RX	გ:	R P	RN	38	38	2 2	E	DI	ď	ğ	AC	ij	RESULT
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE) PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH). PTH.	(REL. 01, REL. 01,		LT 2 PTHY_BOVIN STANDARD; PRT; 115 AA.	1 HNEVAL 6	=======================================	63 HNEVAL 68	Query Match 100.0%; Score 44; DB 1; Length 115; Best Local Similarity 100.0%; Pred. No. 1.12e+00; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	SEQUENCE IIO AA; IZ90/ MW; IOEDUEBC CRC3Z;	115 32 LIS PARATHYROLD	P 26 31	25 BY	SIGNAL.		5662; G558916;	BONE AND PREVENTING THEIR RENAL EXCRETION.	-!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN	GENE 160:241-243(1995).		ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,	MEDLINE: 95369696.		SEQUENCE FROM N.A.		CHONDRESS, TEXTEDIATES, IDIAN, OPEN,	ETIKABYONDA, METABADA CHORDATA, VERTERRATA, TETRABODDA, MAMMATITA.		PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).		(REL. 34,	(REL.	[2;	PTHY CANFA STANDARD: PRT: 115 AA.	LT 1

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                                                                                                                                                                                              DR DR DR DR FT FT SQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches
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EMBL; J00023; G163641; --
EMBL; J00024; G163643; --
EMBL; J00024; E18249; ALT_SEQ.
EMBL; J00024; E18250; ALT_INIT.
EMBL; J00024; E18250; ALT_INIT.
EMBL; M01938; G163645; --
PIR; A01534; PTBO
                                                                                                                                                                                           CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                            HORMONE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE; 84262483.
WEAVER C.A., GORDON D.F., F
GENE 28:319-329(1984).
[5]
                                                                                                                                                                                                                                                                        PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYNTHESIS OF 32-65.

MEDLINE; 71091588.

POTTS J.T. JR., TREGEAR G.W., KEUTMANN H.T., NIALL H.D., SAUER R.,

DETTOS L.J., DANSON B.F., HOGAN M.L., AURBACH G.D.;

PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).

-!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN

BONE AND PREVENTING THEIR RENAL EXCRETION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 32-115.

MEDLINE; 71063634.

MEDLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 26-115.

MEDLINE; 74142666.

HAMILTON J.W., NIALL H.D., JACOBS J.W., KEUTMAN COHN D.V.;

PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 32-115.

MEDLINE; 71076162.

MIALL H.D., KEOTMANN H.T., SAUER R., HOGAN M.L., DAWS:
AURBACH G.D., POTTS J.T. JR.;
HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 351:1586-1588(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

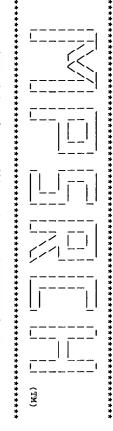
MEDLINE; 80056617.

KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A.,

POTTS J.T. JR., RICH A.;

PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).
                                                                                        y Match 100.0%;
Local Similarity 100.0%;
hes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE; 83105964.
MEAVER C.A., GORDON D.F., KEMPER B.;
MOL. CELL. ENDOCRINOL. 28:411-424(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE; 82037785.
MEAVER C.A., GORDON D.F., KEMPER B.;
PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).
                         63 HNEVAL 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EUTHERIA; ARTIODACTYLA.
[1]
1 HNFVAL 6
                                                                                                                                                                                                                                                                                                                     A01534; PTBO.
A24949; A24949.
NITE; PS00335; PARATHYROID;
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26
32
106
115 AA;
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31
115
P
106
V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JACOBS J.W., KEUTMANN H.T.,
                                                                                 Score 44; DB 1; Ler
Pred. No. 1.12e+00;
0; Mismatches 0;
                                                                                                                                                                               PARATHYROID HORMONE.
V -> G (IN REF. 4).
; 673EA5F2 CRC32;
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                                                                                                                                 Length 115;
                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEMPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTTS J.T. JR.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B.;
                                                                                 0;
                                                                                 Gaps
                                                                                 0
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Search completed: Thu Jul 30 10:57:54 1998 Job time : 6 secs.



MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 10:58:11 1998; MasPar time 3.65 Seconds 69.158 Million cell updates/sec

Tabular output not generated

Description: Perfect Score: Sequence: >US-08-817-547A-26 (1-6) from US08817547A.pep 44 1 HNEVAL 6

Title:

Scoring table:

PAM 150 Gap 15

Searched: 140542 seqs, 42109429 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb15
1:sp\_fung1 2:sp\_human 3:sp\_invertebrate 4:sp\_mamma1
5:sp\_mhc 6:sp\_organelle 7:sp\_phage 8:sp\_plant
9:sp\_bacter1a 10:sp\_rodent 11:sp\_virus 12:sp\_vertebrate
13:sp\_unclassified

Statistics: Mean 20.282; Variance 20.253; scale 1.001

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	42	95.5	105	10	Q63473	PARATHYROID HORMONE (F	1.01e+01
2	42	95.5	568	ω	002437	YELLOW.	1.01e+01
ω	42	95.5	2408	N	Q92566	MYELOBLAST KIAA0279 (F	1.01e+01
4	41	93.2	1149	ω	Q23315	ZC434.5.	1.76e+01
ر د	41	93.2	1774	ω	Q93636	F29G6.3B.	1.76e+01
o	41		1918	ω	Q93637	F29G6.3A.	1.76e+01
7	40	90.9	296	ø	P76472	FROM BASES 2360084 TO	3.04e+01
80	40	90.9	400	N	015216	GLCNAC-1-P TRANSFERASE	3.04e+01
9	40	90.9	562	9	P76923	SIMILAR TO.	3.04e+01
10	40	90.9	635	ω	018199	Y48E1B.5.	3.04e+01
11	40	90.9	747	ω	Q20046	COSMID F35D2.	3.04e+01
12	39	88.6	154	ω	Q16894	BAHAMA HEMOLYMPH POLYP	5.18e+01
13	39	88.6	208	N	014496	PH-SENSING REGULATORY	5.18e+01
14	39	88.6	208	9	033707	PUTATIVE EPIMERASE.	5.18e+01
15	39	88.6	212	ø	Q54198	DNA SEQUENCE FOR ORF'S	5.18e+01
16	39	88.6	554	w	Q09995	PUTATIVE POLY(A) POLYM	5.18e+01
17	39	88.6	635	Ц	013781	HYPOTHETICAL 71.4 KD P	5.18e+01
18	39	88.6	726	ဖ	032971	ABC-TYPE TRANSPORTER.	5.18e+01
19	39	88.6	805	ω	Q19305	SIMILAR TO F-SPONDIN.	5.18e+01
20	39	88.6	885	<u>بـر</u>	Q07533	CHROMOSOME IV READING	5.18e+01

6.4 119 11 083954 6.4 232 3 020262 6.4 380 9 028847 6.4 380 9 028847 6.4 397 9 029939 6.4 499 9 045532 6.4 562 9 058311 6.4 562 9 058311 6.4 562 10 086702 6.4 604 6 035126 6.4 711 9 027928 6.4 102166 6.4 11226 1 000750 6.4 1226 1 000750 6.4 1634 2 000750 6.4 2505 10 063577 6.4 1634 2 000750 6.4 2505 10 063577 6.4 1634 2 000750 6.4 2505 10 063577 6.4 1634 2 001750 6.4 2505 10 063577 6.4 1634 2 001750 6.4 2505 10 063577 6.4 1634 2 001750 6.4 2505 10 063577 6.4 1634 2 001750 6.4 2505 10 063577 6.4 1634 2 001750 6.4 2505 10 063577 6.4 1634 2 001750 6.4 2505 10 063577 6.4 1034 2 001750 6.4 2505 10 063577 6.4 1034 2 001750 6.4 2505 10 063577 6.4 1034 2 001750 6.4 2505 10 063577 6.4 1034 2 001750 6.4 2505 10 063577 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001750 6.4 1034 2 001					41																				
.4 119 11 083954 CCCLUSION DERIVED .4 232 3 020262 .4 380 9 028847 PHOSPHONOPYRUVATE .4 387 9 02939 HYPOTHETICAL 46.5 .4 499 9 045532 CELLULASE4 499 9 045532 HYPOTHETICAL PROTI .4 582 11 086702 HYPOTHETICAL PROTI .4 604 6 035126 CYTOCHROME C OXID .4 604 1 012166 YOR3227W FROM CHR .4 711 9 027928 CYTOCHROME C OXID .4 1026 1 006836 SIMILARITY TO TIP .4 1226 1 006836 SIMILARITY TO TIP .4 1534 2 000750 PHOSPHOINOSITIDE: .4 2505 10 063577 FATTY ACID SYNTHAN .4 2509 Q 016702 WHITE (FRACKENT)4 2509 Q 016702 WHITE (FRACKENT)4 2509 Q 016702 WHITE (FRACKENT)5 40 11 083024 WHITE (FRACKENT)1 480 9 73500 PYRIDINE NUCLEOTII .1 1083 102489 GLYCOPROTEIN B PRI .1 1083 3 024858 PYRIDINE NUCLEOTII .1 1083 3 024858 PYRIDINE NUCLEOTII .1 1083 3 024858 PYRIDINE NUCLEOTII .1 1410 11 083018 POLYPROTEIN (18 (FRACKENT)).																									
3 020262 3 020262 3 020262 3 020262 3 020262 4 CODED FOR BY C. BY 9 028847 PHOSPHONOPYRUVATE 9 02939 HYPOTHETICAL 46.5 9 045532 CELULIASE 0 025831 HYPOTHETICAL PROTI 1 086702 1 12-1 0 0235126 CYTOCHROME C OXID 1 012166 YOR3227W FROM CHR 1 0206836 YOR3227W FROM CHR 1 0206836 YOR3227W FROM CHR 1 0206836 SIMILARITY TO TIP 2 000750 PHOSPHOLNOSITIDE: 1 026577 FATTY ACID SYNTHA 2 016702 FATTY ACID SYNTHA 2 016702 FATTY ACID SYNTHA 2 016702 PATTY ACID SYNTHA 3 002409 WHITE (FRAGMENT). 1 026357 PARIDINE NUCLEOTII 1 026387 ENVELOPE GLYCOPROTEIN 1 026018 GLYCOPROTEIN B PRI 1 037453 PYRIDINE NUCLEOTII 1 083018 POLYPROTEIN 1B (FILL 1 08503) POL POLYPROTEIN 1B (FILL 1 08503)	84.1	84.1	84.1	84.1	84.1			84.1	•	•	•				•	•	•	•	•	•	•	•			86.4
Q83954 Q83954 Q83954 Q83956 Q83961 Q83961 Q83961 Q83939 Q83961 Q83939 Q8	1411	1410	1083	904	902	891	885	540	513	480	243	2509	2505	1634	1226	711	604	604	582	562	499	397	380	232	FTT
COUDSTON DERIVED CODED FOR BY C. EI PHOSPHONOPYRUVATE PHOSPHONOPYRUVATE HYPOTHETICAL 46.5 CELLULASE. HYPOTHETICAL PROTI IE-1. CYTOCHROME C OXID YOR3227W FROM CHR OLIGOSACCHARYL TRU SIMILARITY TO TIPE PHOSPHOIOSITIDE : FATTY ACID SYNTHAM WHITE (FRAGMENT). FOURDE GLYCOPROTI MC131L. EQUILME ARTERITIS Y ENVELOPE GLYCOPROT GB GLYCOPROTEIN B PRI POLYPROTEIN 1B (FI POLYPROTEIN (1)	11	11	ω	느	11	11	11	11	11	9	w	N	10	N	Н	ø	_	σ	11	9	9	9	9	w	F
FOR BY C. BI HONOPYRUVATE HASTICAL 46.5 LASTICAL 46.5 LASTICAL PROTI HETICAL PROTI HETICAL PROTI HROME C OXID 27W FROM CHR SACCHARYL TR ARITY TO TIBL HONOSITIDE: ACID SYNTHA	Q06503	Q83018	Q24858	037453	Q69095	266018	Q69387	Q83024	Q98297	P73500	002409	Q16702	Q63577	000750	Q06836	027928	Q12166	Q35126	Q86702	Q58311	Q45532	029939	028847	Q20262	Q83954
	POLYPROTEIN	18	PYRIDINE NUCLEOTIDETRA	Ħ	Ħ	GB GLYCOPROTEIN.	ENVELOPE GLYCOPROTEIN.	EQUINE ARTERITIS VIRUS	MC131L.			ACID SYNTHASE	ACID SYNTHASE	PHOSPHOINOSITIDE 3-KIN	SIMILARITY TO TIPA.	OLIGOSACCHARYL TRANSFE	YOR3227W FROM CHROMOSO	C OXIDASE	IE-1.	PROTEIN	CELLULASE.			BY C.	

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RESULT RE
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Best Local Similarity 83.3%;
Matches 5; Conservative
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TISSUE-THYROID, AND PARATHYROID;
SCHWELZER H.J., GROSS G., MAYER H.;
SCHWELZER H.J., GROSS G., MAYER H.;
ADV. GENE TECHNOL. 21:228-229(1984).
EMBL, M54875; G601933; -.
NON TER
SEQUENCE 105 AA; 11746 MW; 6AC3163
SEQUENCE FROM N.A.
MUNTE A., AGUADE M., SUBMITTED (JUN-1997)
                                                                                                                                                                                                                                                                                                               02437
002437
002437;
01-JUL-1997
01-JUL-1997
01-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O63473 PRELIMINARY; PRT; 105 AA.
Q63473;
Q1-NOV-1996 (TREMBLREL. 01, CREATED)
Q1-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
Q1-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
PARATHYROID HORMONE (FRAGMENT).
                                                                                                                                                                        YELLOW.
DROSOPHILA SUBOBSCURA (FRUIT FLY).
EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                  YELLOW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUTHERIA; RODENTIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105 AA; 11746 MW; 6AC3163E CRC32;
                                                                                                                                                                                                                                                                                                               (TREMBLREL. 04, CREATED)
(TREMBLREL. 04, LAST SEQUENCE UPDATE)
(TREMBLREL. 04, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                    SEGARRA C.;
TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 42; DB 10; Le
Pred. No. 1.01e+01;
1; Mismatches 0;
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RA SAGARRAC:
RL SUBMITTED (JUN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
RESUBATTED (JUN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR EMBL; V13909; E324295; -.
DR EMBL; V13909; E324295; -.
DR ELYBASE; FB900015179; Dewbly.
SOUTH STATE STATE
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Release	<u></u>
3.1A	'' <b>;</b>
John F.	
Collins,	
Release 3.1A John F. Collins, Biocomputing Research Unit.	
Researc	[]
h Unit.	'
:	(ME)

MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm n on: Thu Jul 30 11:02:08 1998; MasPar time 2.54 Seconds

h on: Thu Jul 30 11:02:08 1998; MasPar time 2.54 Seconds 30.164 Million cell updates/sec

Title: >US-08-817-547A-27
Description: (1-5) from US08817547A.pep
Perfect Score: 35

Sequence: 1 NFVAL 5

Scoring table: PAM 150 Gap 15

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq31-2

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 13.768; Variance 32.782; scale 0.420

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

																			Result	
19	8	17	9	15	14	13	2	11	5	9	8	7	σ	Ŋ	4	ω	2	1		
35	35	35	35	35	35	35	35	35	35	35	35	35	35	35	ა 5	35	35	35	Score	
100.	100.	100.	100.	100.	100.	100.	100.	100.	100.0	100.	100.	100.	100.0	100.0	100.0	100.0	100.0	100.0	Query Match	æ
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	y h Length	
84	84	84	84	84	84	84	84	84	84	84	84	84	47	44	<u>ა</u>	38	38	38	gth	
4	4	4	4	4	4	4	4	4	4	4	4	27	25	26	9	g	ဖ	9	BB	
R23500	R23501	R23332	R21179	R21254	R21255	R23435	R23396	R23309	R21199	R23227	R23524	W25687	W21946	P30015	R58133	R58129	R58126	R58019	Ħ	
Porcine parathyroid h	Porcine parathyroid h	Bovine parathyroid ho	Human parathyroid hor	Human parathyroid hor	Human parathyroid hor	Porcine parathyroid h	Porcine parathyroid h	Bovine parathyroid ho	Human parathyroid hor	Human parathyroid hor	Human parathyroid hor	Human parathyroid hor	Fusion protien compri	Human parathyroid hor	[Asp19]-hPTH(1-38)-OH	[H1s19]-hPTH(1-38)-OH	[Ala19]-hPTH(1-38)-OH	N-alpha-methyl[Ala1]	Description	
3.36e+02	3.36e+02	Pred. No																		

Query Match

100.0%;

Score 35;

DB 9;

Length 38;

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
35	35	35	35	35	35	35	35	35	35	<u>3</u> 5	<u>3</u> 5	35	35	35	35	<u>3</u> 5	35	35	35	<u>ა</u>	<u>သ</u> ပာ	35	35 5	35	ŭ.
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1161	σ	u	G	$\vdash$	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84
14	25	14	25	13	ហ	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	υ	ر.	25	4	4
on	on	o	o	w	R29563	_	R21210	~	$\rightarrow$	-	œ	w	R23392	w	O	~	R23353	$\mathbf{r}$	R23346	347	σ	956	942	2116	۲
e alpha-d	e beta 2 :	Mouse alpha-d subunit	Mouse beta 2 integrin	Human prepro-PTH	Oxidation resistant P	Ċ.	Human parathyroid hor	a	Ω		Porcine parathyroid h	Porcine parathyroid h	ò	Bovine parathyroid ho	Bovine parathyroid ho	parathyroid		Human parathyroid hor	Bovine parathyroid ho	Q.	Oxidation resistant P	ř	Human parathyroid hor	arathyroid	
.36e+0	.36e+0	.36e+0	.36e+0	.36e+0	w	.36e+0	3.36e+02	.36e+0	.36e+0	.36e+0	.36e+0	.36e+0	. 36	.36e+0	.36e+0	.36e+0	ყ	س	36	36	. 36	. 36	. 36	. 36	. Joetu

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RESULT

RESULT

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AC RESULT

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TO - SEP-1994 (first entry)

DE N-alpha-methyl[Ala1] parathyroid hormone(1-38).

EXEMINATION TO A CONTROL RESULT OF THE RESULT OF THE
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RESULT
AC RESULT
Search completed: Thu Jul 30 11:02:23 1998 Job time: 15 secs.
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12-UUL-1993; GB-015009.

112-UUL-1992; GB-026015.

18-DEC-1992; GB-026415.

PR 23-DEC-1992; GB-026859.

PR 23-DEC-1992; GB-001691.

PR 23-DEC-1992; GB-001691.

PR 14-APR-1993; GB-001691.

PR 14-APR-1993; GB-001691.

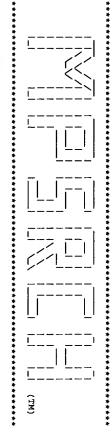
PR 14-APR-1993; GB-001692.

PR 14-APR-1993; GB-001692.

PR 14-APR-1993; GB-0008033.

PA (SANO) SANDOZ PATENT GMBH.

PA (SANO) SANDOZ PATENT 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
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                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 5; Conservative
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Human parathyroid hormone; hPTH; variant; analogue; calcium; depletion; fixation; resorption; osteopathy; osteoporosis; hypoparathyroidism.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JT 2
R58126 standard; peptide; 38
R58126;
                                                                                                                                                                             33 nfval 37
|||||
1 NFVAL 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33 nfval 37
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1 NFVAL 5
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0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                               Score 35; DB 9; Len Pred. No. 3.36e+02; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 38;
                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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MPsrch\_pp in on: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 11:01:26 1998; MasPar time 3.08 Seconds 59.234 Million cell updates/sec

Title: Tabular output not generated.

Description: Perfect Score: >US-08-817-547A-27 (1-5) from US08817547A.pep 35 1 NEVAL 5

Sequence:

Scoring table: PAM 150 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 19.157; Variance 19.754; scale 0.970

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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A44483	A46423	I84547	S28277	S73757	S48411	A64775	S70900	B40901	S64842	S74401	C64127	C33586	в26981	JQ1602	JT0321	S73498	G69417	A56861	S75497	A54204	A40047
1	transcription factor	mdl protein - Escheri		hypothetical protein	SEC6 protein - yeast	mdlB protein - Escher	aarD protein - Provid	equine arteritis viru	probable membrane pro	hypothetical protein	ADP-heptose synthase	C4-dicarboxylate tran	C4-dicarboxylate tran	replication protein B	photosystem II protei	MG456 homolog K05_orf	conserved hypothetica	peptidylprolyl isomer	hypothetical protein	peptidylprolyl isomer	peptidylprolyl isomer
4.83e+02	1.85e+02	1.85e+02	1.85e+02	1.85e+02	1.85e+02	1.85e+02	1.85e+02	1.85e+02	1.85e+02	1.85e+02	1.85e+02	1.85e+02	1.85e+02	1.85e+02	1.85e+02	1.85e+02	1.85e+02	1.85e+02	1.85e+02	1.85e+02	1.85e+02

#authors Marx, U.C. #book in Strukturen Verschiedener Parathormonfragmente in Loesung,	rs ssion -referen	ALTERNATE_NAMES n-succinyl-hpth(4-37)  PDB_TITLE succinyl human parathyroid hormone 4-37, NMR, 10 structures  ORGANISM #formal_name synthetic  REFERENCE A67743	RESULT 2  ENTRY 1ZWG #type complete  TITLE parathyroid hormone 4 37 mutant N-TERMINAL SUCCINYLATED -	Db 30 NEVAL 34       : Qy 1 NEVAL 5	Query Match 100.0%; Score 35; DB 5; Length 34; Best Local Similarity 100.0%; Pred. No. 1.85e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	3-6 #region helix (right hand alpha)\ 14-27 #region helix (right hand alpha) SUMMARY #length 34 #molecular-weight 4128 #checksum 5508		#authors Marx, U.C. #book in Strukturen Verschiedener Parathormonfragmente in Loesung, #book pp.0, Bayreuth : University of Bayreuth (Thesis), 1996	ion eferen	ORGANISM #IOTMAI_name Synthetic  REFERENCE A67742 #authors Roesch, P.; Marx, U.C.	E_NAMES n-acetyl-hptl E structure of NMR, 10 st	IZWF #type complete TITLE parathyroid hormone 4 37 mutant N-TERMINAL ACETYLATED - synthetic	
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp n on: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 11:00:15 1998; MasPar time 2.01 Seconds 62.409 Million cell updates/sec

Title: Tabular output not generated. >US-08-817-547A-27 (1-5) from US08817547A.pep 35

Sequence: Description: Perfect Score: 1 NEVAL 5

Scoring table: PAM 150 Gap 15

Searched: 69111 segs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 20.019; Variance 16.358; scale 1.224

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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(IN) CALCIUM-REGULATING HORMONES, TALMADGE R.V., OWEN M., PARSONS J.A., EDS., PP.9-14, EXCERPTA MEDICA FOUNDATION, AMSTERDAM, (1975).		POTTS J.T. JR.; BIOCHEMISTRY 17:5723-5729(1978).	KEUTMANN H.T., SAUER M.M., HENDY G.N., O'RIORDAN J.L.H.,		O'RIORDAN J.L.H., AURBACH G.D., POTTS J.T. JR.; PROC. NATL. ACAD. SCI. U.S.A. 71:384-388(1974).	R.T., JACOBS J.W., KEUTM	SEQUENCE OF 32-68.	JACOBS J.W., KEMPER B., NIALL H.D., HABENER J.F., POTTS J.T. JR.; NATURE 249:155-157(1974).		Ş	SCI. U.S.A. 80:2127-2131(1983)	VASICEK T.J., MCCEVITT B.E., FREEMAN M.W., FENNICK B.J., HENDY G.N., POTTS J.T. JR., RICH A., KRONENBERG H.M.;			PROC. NATL. ACAD. SCI. U.S.A. 78:7365-7369(1981).	NE; 82150870.	SEQUENCE FROM N.A.	PRIMATES.	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;		HORMONE PR	13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)	1986 (REL. 01, CREAT	PTHY_HUMAN STANDARD; PRT; 115 AA. P01270:	LT 1

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Query Match
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MEDLINE: 75059220.

TREGEAR G.W., VAN RIETSCHOTEN J., GREEN E., NIALL H.D.,
KEUTMANN H.T., PARSONS J.A., O'RIORDAN J.L.H., POTTS J.T.
HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 355:415-421(1974).
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MEDLINE: 73227467.

ANDREATTA R.H., HARTMANN A., JOEHL A.,

RINKER B., RITTEL W., SIEBER P.;

RINKER B., RITTEL W., SIEBER P.;

RING CHIM. ACTA 56:470-473(1973).
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BIOCHEMISTRY 14:1842-1847(1975).
[8]
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KLAUS W., DIECKMAI
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BARDEN J.A., CUTHBERTSON R.M.;
EUR. J. BIOCHEM. 215:315-321(1993).
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                                                                                                                                                                                                                                                                                                          ARNOLD A., HORST S.A., GARDELLA T.J., BABA H., LEVINE M.A., KRONENBERG H.M.;
KRONENBERG H.M.;
J. CLIN. INVEST. 86:1084-1087(1990).
J. FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS
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MEDLINE; 91009811
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12-MAR-97.
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N -> D (IN REF. 5).
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                                             MEDLINE; 71091588.

A POTTS J.T. JR., TREGEAR G.W., KEUTMANN H.T., NIALL H.D., SAUER R., A POTTS J.T. JR., TREGEAR G.W., L., AURBACH G.D.;

A POTTS J.T. JR., TREGEAR G.W., L., AURBACH G.D.;

A PROC. NATL ACAD. SCI. U.S.A. 68:63-67(1971).

LI PROC. NATL ACAD. SCI. U.S.A. 68:63-67(1971).

C -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN C. EMBL; V00106; G65; -.

EMBL; V00106; G65; -.

REMBL; J00024; G163641; -.

REMBL; J00024; G163643; -.

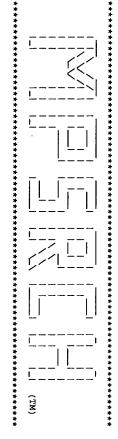
REMBL; J00024; E18250; ALT_INIT.

REMBL; J00024; E18250; ALT_INIT.

REMBL; MC1938; G163647; -.

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P01268;
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MEDLINE;
WEAVER C.
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MEDLINE; 71063634.
BREWER H.B. JR., RON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 26-115.
MEDLINE; 74142666.
HAMILTON J.W., NIALL H.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 84262483.
WEAVER C.A., GORDON D.F.,
GENE 28:319-329(1984).
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WEAVER C.A., GORDON D.:
MOL. CELL. ENDOCRINOL.
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PROC. NATL. ACAD.
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MEDLINE; 71076162.
NIALL H.D., KEUTMANN H.T.,
AURBACH G.D., POTTS J.T. J
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82037785.
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      PS00335;
SIGNAL.
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METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OF 32-65.
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(REL. 01, LAST SEQUENCE UPDATE)
(REL. 35, LAST ANNOTATION UPDATE)
HORMONE PRECURSOR (PARATHYRIN) (P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GORDON D.F., KEMPER B.;
NDOCRINOL. 28:411-424(1982)
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ACAD. SCI. U.S.A. 78:4073-4077(1981).
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                                       PARATHYROID;
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Psrch\_pp protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 11:00:41 1998; MasPar time 3.58 Seconds 58.840 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-817-547A-27 (1-5) from US08817547A.pep 35 1 NEVAL 5

Scoring table: PAM 150 Gap 15

Searched: 140542 seqs, 42109429 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: sptrembl5

1:sp\_fungi 2:sp\_human 3:sp\_invertebrate 4:sp\_mammal 5:sp\_mhc 6:sp\_organelle 7:sp\_phage 8:sp\_plant 9:sp\_bacteria 10:sp\_rodent 11:sp\_virus 12:sp\_vertebrate 13:sp\_unclassified

Statistics: Mean 19.234; Variance 18.297; scale 1.051

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

1 0 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result No.
	Score
100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0	Query
140 291 342 342 347 476 478 478 533 538 593 593 611 1361 1416 1411 1411	Length
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028710 P73988 028925 048046 045962 045962 045962 045962 04597950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 087950 0879	븅
HYPOTHETICAL 15.7 KD P HYPOTHETICAL 23.8 KD P CONSERVED HYPOTHETICAL ADP-HEPTOSE SYNTHASE. REPB. AUTOTHETICAL 57.1 KD P TO4F8.2. HYPOTHETICAL 57.1 KD P CHROMOSOME XII READING EQUINE ARTERITIS VIRUS AARD. FROM BASES 464774 TO 4 ZK287.2. MULTIDRUG RESISTANCE-L F11_ORF879 PROTEIN. HYPOTHETICAL 151.1 KD POLYPROTEIN (CONTA PARATHYROID HORMONE (F HYPOTHETICAL 16.2 KD P	Description
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21
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Ħ	KIAA0289 (FRAGMENT).	ASTROTACTIN (NEURONAL	GLYCOPROTEIN B.	GLYCOPROTEIN B.	HOAR.	NADH DEHYDROGENASE SUB	HIGH AFFINITY SULPHATE	5-AMINOIMIDAZOLE-4-CAR	NEURAL SRC INTERACTING	LIM DOMAIN BINDING PRO	MATRIX PROTEIN.	HYPOTHETICAL 37.4 KD P	YCF4 PROTEIN.	CYTOCHROME C OXIDASE P	CYCLOPHILIN HOMOLOG TA	CYTOCHROME OXIDASE II								
	4.35e+02		4.35e+02	4.35e+02	4.35e+02				4.35e+02	4.35e+02	4.35e+02	4.35e+02	4.35e+02	4.35e+02	4.35e+02	4.35e+02	4.35e+02	4.35e+02	4.35e+02	4.35e+02	4.35e+02		•	4.35e+02

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RESULT
1 P73988;
AC P73988;
DT 01-FEB-1997 (TREMBLREL. 02, CREATED)
DT 01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
DT 01-FEB-1997 (TREMBLREL. 02, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 23.8 KD PROTEIN.
OS SYNECHOCYSTIS SP.
OC EUBACTERIA; CYANOBACTERIA; CHROOCOCCALES; SYNECHOCYSTIS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PCC6803;
RL SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
PM [2]
Search completed: Thu Jul 30 11:01:07 1998 Job time: 26 secs.
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                                                                                                                 В
                                                                                                                                                 Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 5; Conservative
                                                                                                                                                                                                                  SEQUENCE FROM N.A.

STRAIN-PCC6803;

KAMEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,

MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,

HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K.,

OKUMURA S., SHIMPO S., TAKEUCHI C., WADA T., WATANABE A.,

YAMADA M., YASUDA M., TABATA S.;

DNA RES. 3:109-136(1996).

EMBL; D9091; G1653142; -.

HYPOTHETICAL PROTEIN.

SEQUENCE 215 AA; 23768 MW; 329FA3F6 CRC32;
                                                                                             128 NFVAL 132
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1 NFVAL 5
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                                                                                                                                               Score 35; DB 9; Length 215; Pred. No. 1.56e+02; O; Mismatches 0; Indels
                                                                                                                                                                                       Length 215;
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

n on: Thu Jul 30 11:04:35 1998; MasPar time 2.73 Seconds 72.991 Million cell updates/sec Tabular output not generated.

Title: >US-08-817-547A-28
Description: (1-13) from US08817547A.pep
Perfect Score: 95
Sequence: 1 LRKKLQDVHNFVA 13

Scoring table: PAM 150 Gap 15

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part5 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part14 25:part25 26:part26 27:part27

Statistics: Mean 18.865; Variance 63.388; scale 0.298

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Re

No.	Score	Query	Length	BB	Ħ	Description	Pred. No.
ъ	95	100.0		ø	R58173	[Indole-3-carboxylic	6.12e-03
ນ	95	100.0	36	9	R58052	[L8,A17,Q18,A19]-hPTH	6.12e-03
ω	95	100.0		9	R55820	[L8,D10,K11,Q18]-hPTH	6.12e-03
4	95	100.0		φ	R58037	[Ser14]-hPTH(1-38)-OH	6.12e-03
ហ	95	100.0		10	R54234	PTH N-terminal.	٠
6	95	100.0		9	R58141	[Leu21]-hPTH(1-38)-OH	6.12e-03
7	95	100.0		26	P30015	Human parathyroid hor	6.12e-03
œ	95	100.0		25	W21946	Fusion protien compri	6.12e-03
φ	95	100.0		27	W25687	o1d	6.12e-03
10	95	100.0	84	4	R21213	Human parathyroid hor	6.12e-03
11	95	100.0	84	4	R21212	Human parathyroid hor	6.12e-03
12	95		84	4	R21256	Human parathyroid hor	
13	95	100.0	84	4	R23522	Human parathyroid hor	6.12e-03
14	95	100.0	84	4	R23359	Bovine parathyroid ho	•
15	95		84	4	R23360	Bovine parathyroid ho	
16	95	100.0	84	4	R23489	Porcine parathyroid h	6.12e-03
17	95	100.0	84	4	R23488	Porcine parathyroid h	
18	95	100.0	84	4	R21247	Human parathyroid hor	٠
19	95	100.0	84	4	R23247	Human parathyroid hor	6.12e-03

95 100.0 84 4 R21177 Human parathyroid hor 95 100.0 84 4 R23528 Human parathyroid hor 95 100.0 84 4 R23528 Human parathyroid hor 95 100.0 84 4 R23529 Human parathyroid hor 95 100.0 84 4 R233365 Bovine parathyroid hor 95 100.0 84 4 R23276 Bovine parathyroid hor 95 100.0 84 4 R23276 Bovine parathyroid hor 95 100.0 84 4 R23276 Bovine parathyroid hor 95 100.0 84 4 R23278 Human parathyroid hor 95 100.0 84 4 R23238 Human parathyroid hor 95 100.0 84 4 R23238 Human parathyroid hor 95 100.0 84 4 R23238 Bovine parathyroid hor 95 100.0 84 4 R23278 Bovine parathyroid hor 95 100.0 84 4 R23278 Bovine parathyroid hor 95 100.0 84 4 R23237 Bovine parathyroid hor 95 100.0 84 4 R23237 Bovine parathyroid hor 95 100.0 84 4 R23352 Bovine parathyroid hor 95 100.0 84 4 R23359 Porcine parathyroid hor 95 100.0 84 4 R23359 Porcine parathyroid hor 95 100.0 84 4 R23359 Bovine parathyroid hor 95 100.0 84 4 R23359 Bovin
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ID RSBIT3 standard; peptide; 36 AA.

AC RSB173; standard; peptide; 36 AA.

AC RSB173; standard; peptide; 36 AA.

BT 20-SEP-1994 (first entry)

DE [Indole-3-carboxylic acid1]-hPTH(1-36)-NH2.

KW Human parathyroid hormone; hPTH; variant; analogue;

KW dalcium; depletion; fixation; resorption; osteopathy; osteoporosis;

KW hypoparathyroidism.

S Synthetic.

Location/Qualifiers

FT modified_site 1, label- other

FT modified_site 1, label- other

FT modified_site 3, label- other

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RESULT
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Search completed: Thu Jul 30 11:04:57 1998 Job time: 22 secs.
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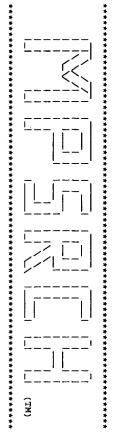
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

n on: Thu Jul 30 11:03:49 1998; MasPar time 3.36 Seconds 141.457 Million cell updates/sec

Tabular output not generated.

Description:
Perfect Score:
Sequence: Title: >US-08-817-547A-28 (1-13) from US08817547A.pep 95 1 LRKKLQDVHNFVA 13

Scoring table: PAM 150 Gap 15

Searched: 120441 segs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 26.057; Variance 41.730; scale 0.624

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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ULT 1 12ME #type complete LE parathyroid hormone (residues 4-37) - human ERNATE_NAMES HPTH(4-37)  _TITLE	COMMENT Res	#book	#authors	REFERENCE	#cross-refe	#submission	#authors	REFERENCE	ORGANISM	PDB_TITLE	ALTERNATE_NAMES	TITLE	ENTRK	RESULT 2	Qy 1 LRKF	Db 21 LRKF	Query Match Best Local S Matches	SUMMARY	15-25	FEATURE	מ	COMMENT Res	#book	#authors	REFERENCE	addination and the second	#submission	#authors	REFERENCE	CECANICA	PDB_TITLE	ALTERNATE NAMES	ENTRY	RESULT 1
			Marx, U.C.	TN003319	rences PDB:1ZWG	submitted to the Brookhaven Protein Data Bank, June	Roesch, P.; Marx, U.C.	A67743		succinyl human parathyroid hormone 4-37, NMR, 10	n-succinyl-hpth(4-37)	4 3/ mutant N-TERMINAL	#type complete				Score 95; DB 5; Length 34; Pred. No. 1.21e-06; 0; Mismatches 0; Indels 0; Gaps	+checksum	<pre>#region helix (right hand alpha)</pre>		hormone	olution: not applicable ermination: NMR	ren Verschiedener Parathormonfragmente in	Marx, U.C.	TN001721		submitted to the Brookhaven Protein Data Bank, June	Roesch, P.: Marx, U.C.	T_Hame Bollo sapiens *Common_Hame	110110 cast oss # commos samo	structure of human parathyroid hormone fragment 4-37, NMR	HPTH(4-37)	thype con	

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COMMENT ACTIONS disease mutation; hormone; signal

FRATURE

1-9
15-25
15-25

#region helix (right hand alpha)\
SUMMARY

SUMMARY

#length 34 #molecular-weight 4128 #checksum 5508

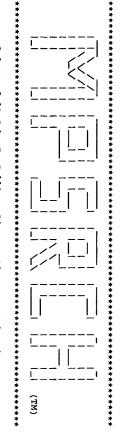
Query Match
Best Local Similarity 100.0%; Score 95; DB 5; Length 34;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 21 LRKKLODVHNFVA 33

Qy 1 LRKKLODVHNFVA 13

Search completed: Thu Jul 30 11:04:18 1998

Job time: 29 secs.
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. n on: Thu Jul 30 11:02:41 1998; MasPar time 2.34 Seconds 139.385 Million cell updates/sec

Title: >US-08-817-547A-28 (1-13) from US08817547A.pep 95 1 LRKKLQDVHNFVA 13

Description: Perfect Score: Sequence:

Scoring table: PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 27.347; Variance 34.537; scale 0.792

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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VP3 CORE PROTEIN.	PARAMYOSIN, LONG FORM.	HYPOTHETICAL 69.2 KD P	UREASE ALPHA SUBUNIT (	GALACTOSE-1-PHOSPHATE	CITRATE-PROTON SYMPORT	CITRATE-PROTON SYMPORT	HYPOTHETICAL PROTEIN I	FILENSIN (LENS FIBER C	DYSTROPHIN.	DNA POLYMERASE ALPHA (	MULTIDRUG RESISTANCE P	HYPOTHETICAL PROTEIN M	SPORE-SPECIFIC PROTEIN	HYPOTHETICAL PROTEIN M	CITRATE LYASE ALPHA CH	HNRNP ARGININE N-METHY	DNA-DIRECTED RNA POLYM	DNA-DIRECTED RNA POLYM	KINESIN HEAVY CHAIN.	HPR1 PROTEIN.	SERYL-TRNA SYNTHETASE
	•	2.20e+01	2.20e+01	2.20e+01	2.20e+01		2.20e+01	2.20e+01	1.45e+01	1.45e+01	1.45e+01	1.45e+01	1.45e+01	1.45e+01	1.45e+01	1.45e+01	1.45e+01	1.45e+01	9.54e+00	9.54e+00	9.54e+00

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DR DR DR SON
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RA POTIS J.T. JR., TREGEAR G.W., KEUTMANN H.T., NIALL H.D., SAUER R., POTIS J.T. JR., TREGEAR G.W., KEUTMANN H.T., NIALL H.D., SAUER R., ADETOS L.J., DAWSON B.F., HOGAN M.L., AURBACH G.D.;

RA DEFTOS L.J., DAWSON B.F., HOGAN M.L., AURBACH G.D.;

RPOC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).

C. BONE AND PREVENTING THEIR CALCIUM LEVEL BY DISSOLVING THE SALTS IN C. BMBL; Y00106; G85; -.

EMBL; Y00106; G85; -.

EMBL; J00024; G163643; -.

EMBL; J00024; G163643; -.

EMBL; J00024; E18249; ALT_SEQ.

EMBL; J00024; E18249; ALT_SEQ.

EMBL; MJ038; G163647; -.

REMBL; MJ038; G163645; -.
                                              Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 13; Conservative
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MEDLINE; 71063634.
BREWER H.B. JR., RONI
PROC. NATL. ACAD. SCI
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MEDLINE; 82037785.
MEDLINE; 82037785.
MEDAVER C.A., GORDON D.F., KEMPER B.;
PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).
[3]
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MEDLLINE; 80056617.

KRONENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A.,

POTTS J.T. JR., RICH A.;

PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 26-115.

MEDLINE; 74142666.

HAMILTON J.W., NIALL H.D., JACOBS J.W., KEUTMANN H.T.,
COHN D.V.;
PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE; 84262483.
WEAVER C.A., GORDON D.F.,
GENE 28:319-329(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE; 83105964.
WEAVER C.A., GORDON D.F., KEMPER B.;
MOL. CELL. ENDOCRINOL. 28:411-424(1982).
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MEDLINE; 71076102.

NIALL H.D., KEUTMANN H.T., SA

AURBACH G.D., POTTS J.T. JR.;

HOPPE-SEYLER'S Z. PHYSIOL. CH
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  LRKKLQDVHNFVA 13
               LRKKLQDVHNEVA 67
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115 AA;
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CI.
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31
115 P
106 V
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                                                   Pred.
                                                                         score 95;
                                                                                                  PARATHYROID HORMONE.
V -> G (IN REF. 4).
; 673EA5F2 CRC32;
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                                                     Mismatches
                                                               95; DB 1; I
No. 6.50e-09;
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                                                                            Length 115;
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Search completed: Thu Jul 30 11:02:48 1998 Job time : 7 secs.

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RESULT 1

1D 063473;
AC 063473;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE PARATHYROID HORMONE (FRAGMENT).

GN PTH.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; M
C EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RN SCHMELZER H.J., GROSS G., MAYER H.;
ADV. GENE TECHNOL. 21:228-229(1984).
DR EMBL; M54875; G601933; -.
FT NON_TER 1
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SEQUENCE 105 AA; 11746 MW; 6AC3163E CRC32;
         RESULT

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Best Local Similarity 84.6%;
Matches 11; Conservative
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Q08358;
Q08358;
Q08358;
Q1-NOV-1996 (TREMBLREL. 01, CREATED)
Q1-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
Q1-FEB-1997 (TREMBLREL. 02, LAST ANNOTATION UPDATE)
POLYPROTEIN PP220.
QCP2475L.
AFRICAN SWINE FEVER VIRUS (STRAIN BA71V) (ASFV).
VIRIDAE; DS-DNA NONENVELOPED VIRUSES; IRIDOVIRIDAE.
Q11
SEQUENCE FROM N.A.
MEDLINE; 93327788.
SIMON-MATEO C., ANDRES G., VINUELA E.;
EMBO J. 12:2977-2987(1993).
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RATTUS NORVEGICUS (RAT).

EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

EUTHERIA; RODENTIA.
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Pred. No. 7.94e-06;
1; Mismatches 1; Indels
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RN [2]

RA YANGER.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,

RA YANGER.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,

RA YANGER.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,

RA YANGER.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,

RA YANGER.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,

RA YANGER.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,

RA YANGER.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,

RA YANGER.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,

RA YANGER.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,

RA YANGER.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,

RA YANGER.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,

RA YANGER.J., RODRIGUEZ J., NOGAL M.L., YUSTE L., ENRIQUEZ C.,

RA YANGER.J., RODRIGUEZ J., NOGAL M.L., YUSTE L., ENRIQUEZ C.,

RA YANGER.J., RODRIGUEZ J., NOGAL M.L., YUSTE L., ENRIQUEZ C.,

RA YANGER.J., NOGAL M.L., YUSTE L., ENRIQUEZ C.,

RA RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,

RA RODRIGUEZ J., NOGAL M.L., YUSTE L., ENRIQUEZ C.,

RA RODRIGUEZ J., NOGAL M.L., YUSTE L., ENRIQUEZ C.,

RA RODRIGUEZ J.F., VINUELA E.;

RA RODRIGUEZ
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

n on: Thu Jul 30 11:07:12 1998; MasPar time 2.78 Seconds 66.125 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Title: >US-08-817-547A-29 (1-12) from US08817547A.pep 91 1 LRKKLQDVHNFV 12

Sequence:

Scoring table: PAM 150 Gap 15

Searched: 124785 segs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 18.683; Variance 61.585; scale 0.303

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Query Match	Length	₽B	Ħ	Description	Pred.	ŏ
<u>,</u>	91	100.0	36	إٰ ڡ	R58214	[Ala19]-hPTH(1-36)-NH	1.17e-02	22
2	91	100.0	36	و	R58213	[D-Ser17]-hPTH(1-36)-	1.17e-02	2
ω	91	•	36	9	R58286	[D-Leu24]-hPTH(1-36)-	1.17e-02	ဥ
4	91	٠	36	9	R58052	[L8,A17,Q18,A19]-hPTH	1.17e-02	2
U	91	100.0	44	26	P30015	Human parathyroid hor	1.17e-02	ဥ
6	91	100.0	47	25	W21946	Fusion protien compri	1.17e-02	2
7	91	100.0	84	27	W25687	Human parathyroid hor	1.17e-02	ဂ္ဂ
80	91	100.0	84	4	R23545	Bovine parathyroid ho	1.17e-02	2
9	91	100.0	84	4	R23354	Bovine parathyroid ho	1.17e-02	2
10	91	100.0	84	4	R23520	Bovine parathyroid ho	1.17e-02	2
11	91	100.0	84	4	R23463	Porcine parathyroid h	1.17e-02	2
12	91	100.0	84	4	R23350	Bovine parathyroid ho	1.17e-02	2
13	91	100.0	84	4	R23522	Human parathyroid hor	1.17e-02	2
14	91	100.0	84	4	R21242	Human parathyroid hor	1.17e-02	ಬ
15	91	100.0	84	4	R23273	Bovine parathyroid ho	1.17e-02	2
16	91	100.0	84	4	R23230	Human parathyroid hor	1.17e-02	2
17	91	100.0	84	4	R21247	Human parathyroid hor	1.17e-02	2
18	91	100.0	84	4	R23247	Human parathyroid hor	1.17e-02	2
19	91	100.0	84	5	R29561	Oxidation resistant P	1.17e-02	02

Query Match 100.0%; Best Local Similarity 100.0%;

Score 91; DB 9; Length 36; Pred. No. 1.17e-02;

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of prepro	Protein including hum	Human parathyroid hor	Human parathyroid hor		Human parathyroid hor			Bovine parathyroid ho	Human parathyroid hor	Human parathyroid hor	Bovine parathyroid ho	Human parathyroid hor					ne parathyroi	Human parathyroid hor		Human parathyroid hor	Bovine parathyroid ho	Bovine parathyroid ho	Porcine parathyroid h	Bovine parathyroid ho	Oxidation resistant [
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Search completed: Thu Jul 30 11:07:36 1998 Job time : 24 secs.
                                                                                                                                                                                                                                                                                                       PR 13-TUL-1992; GB-015009.
PR 18-DEC-1992; GB-026415.
PR 23-DEC-1992; GB-026861.
PR 28-JAN-1993; GB-001691.
PR 28-JAN-1993; GB-001692.
PR 14-APR-1993; GB-001692.
PR 14-APR-1993; GB-001692.
PR 14-APR-1993; GB-008033.
PA (SANO) SANDOZ PATENT GMBH.
PA (SANO) SANDOZ GRETIODOR GMBH.
PA (SANO) SANDOZ GRETIODOR GMBH.
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Best Local Similarity 100.0%;
Matches 12; Conservative
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R58213;
20-SEP-1994 (first entry)
[D-Ser17]-hPTH(1-36)-NH2.
Human parathyroid hormone; hPTH; variant; an calcium; depletion; fixation; resorption; os Synthetic.
                                                                                     24 lrkklqdvhnfv 35
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1 LRKKLQDVHNFV 12
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                                                                                                                                                                   Score 91; DB 9;
Pred. No. 1.17e-
0; Mismatches
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1.17e-02;
0;
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osteopathy; osteoporosis;
                                                                                                                                                                                                         Length 36;
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(MT)

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MPsrch\_pp n on: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 11:06:37 1998; MasPar time 3.31 Seconds 132.368 Million cell updates/sec

Tabular output not generated.

Title: Description: Perfect Score: Sequence: >US-08-817-547A-29 (1-12) from US08817547A.pep 91 1 LRKKLQDVHNFV 12

Scoring table: PAM 150 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 25.786; Variance 40.708; scale 0.633

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

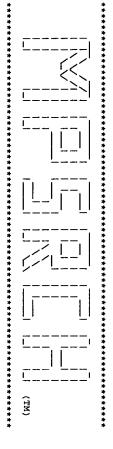
#### SUMMARIES

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<b>4</b> 5	44	43	42	41	40	39	38	37	36	35	34	သ	32	31	30	29	28	27	26	25	24
53	53	53	54	54	54	54	54	54	54	54	54	54	54	54	54	54	55	55	55	55	55
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S62851	C64043	S45890	S51866	1SERB	1SESB	S38948	1SESA	1SETA	1SRYB	1SRYA	1SETB	S51402	S59264	I40594	S03242	S53076	S28098	A42401	S59436	S43492	C64864
MG397 homolog D02_orf	citrate (pro-3S)-lyas	ODP1 protein - yeast	HPR1 protein - yeast	seryl-tRNA synthetase	Seryl-trna synthetase	serinetRNA ligase (	Seryl-trna synthetase	probable membrane pro	hypothetical protein	DNA-directed DNA poly	hypothetical protein	probable membrane pro	ste6 protein - fissio	macrophage elastase (	ote	surface antigen - hep	hypothetical protein				
4.29e+01	4.29e+01	4.29e+0	2.99e+01	2.99e+01	2.99e+01	2.99e+01	2.99e+01	2.99e+01	2.99e+01	2.99e+01	2.99e+01	2.99e+01	2.99e+01	2.99e+01	2.99e+01	2.99e+01	2.08e+0	2.08e+01	2.08e+0	2.08e+01	2.08e+0

TITLE parathyroid hormone 4 37 mutant N-TERMINAL SUCCINYLATED - Synthetic  ALTERNATE_NAMES n-succinyl-hpth(4-37) PDB_TITLE succinyl-hpth(4-37) PDB_TITLE suc	#length 34 #molecular-weight 4128 #checksum 5508  Match 100.0%; Score 91; DB 5; Length 34; ocal Similarity 100.0%; Pred. No. 4.58e-06; s 12; Conservative 0; Mismatches 0; Indels 0; Gaps 1 LRKKLQDVHNFV 32	human le fragment 4-37, NMR le man le man sata Bank, June 1996 sata Bank, June 1996 ata Bank, June 1996
ATED - ructures 1996 Loesung,	ps 0;	, NMR 10 1996 Loesung,

Search completed: Thu Jul 30 11:06:55 1998 Job time : 18 secs. ş COMMENT KEYWORDS FEATURE 2-9 15-25 SUMMARY Db Query Match
100.0%; Score 91; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.58e-66;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 21 LRKKLQDVHNFV 32 |||||||||||| 1 LRKKLQDVHNFV 12 Determination: NMR
disease mutation; hormone; signal #region helix (right hand alpha)\
#region helix (right hand alpha)
#length 34 #molecular-weight 4128 #checksum 5508 0;



MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

n on: Thu Jul 30 11:06:12 1998; MasPar time 2.30 Seconds 130.665 Million cell updates/sec

Tabular output not generated.

Title: Description: Perfect Score: Sequence: >US-08-817-547A-29 (1-12) from US08817547A.pep 91 1 LRKKLQDVHNFV 12

Scoring table: PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 27.047; Variance 34.136; scale 0.792

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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50000000000000000000000000000000000000	Score
100.0 100.0 100.0 65.9 63.7 63.7 62.6 60.4 60.4 60.4 60.4 60.4 60.4 60.4 60	% Query Match
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PARATHYROID HORMONE PR PARATHYROID HORMONE PR PARATHYROID HORMONE PR PARATHYROID HORMONE PR PARATHYROID HORMONE PR CITRATE-PROTON SYMPORT GLUCOSE-1-PHOSPHATE AD MYC I PROTO-ONCOGENE P PROTEIN PHOSPHATASE 2C HYPOTHETICAL PROTEIN M PARATHYROID HORMONE PR HYPOTHETICAL 18.0 KD P PROTESIN E (HEMOLYSIN MACROPHAGE METALLOELAS STE6 PROTEIN. UBIQUITIN-ACTIVATING E VERY HYPOTHETICAL 11.7 DNA POTHETICAL 11.7 DNA POTHETICAL 21.7 DNA POTHETICAL 21.7 DNA POTHETICAL 21.7 ENTY HYPOTHETICAL 21.7 DNA POTHETICAL 11.6 EP SERYL-TRAA SYNTHETASE HPR1 PROTEIN.	Description
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45	44	43	42	41	40	39	38	37	36	35	34	<b>ω</b>	32	31	30	29	28	27	26	25	24
51	51	51	51	51	51	51	51	52	52	52	52	52	52	52	52	53	53	53	53	53	53
56.0	56.0	56.0	56.0	56.0	56.0	56.0	56.0	57.1	57.1	57.1	7.	57.1	57.1	57.1	7.	œ.	58.2	œ	œ	8	58.2
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APC_HUMAN	RRPL_RDV	ADB2_YEAST	HIS8_LACLA	SYNK_ARATH	RPOC_PROHO	YD89_METJA	YIM5_BPPH1	MYSP_DROME	RPOC_CYAPA	YO4E_MYCTU	URE1_STAXY	GAL7_STRMU	CIT1_SALTY	CIT1_ECOLI	SFAS_CHLEU	DPOA_TRYBB	YSW1_YEAST	Y397_MYCPN	CILA_HAEIN	HMT1_YEAST	PRRA_RAT
ADENOMATOUS POLYPOSIS	RNA-DIRECTED RNA POLYM	PROBABLE BETA-ADAPTIN	HISTIDINOL-PHOSPHATE A	SYNTAXIN-RELATED PROTE	DNA-DIRECTED RNA POLYM	HYPOTHETICAL PROTEIN M	HYPOTHETICAL IMMUNITY	PARAMYOSIN, LONG FORM.	DNA-DIRECTED RNA POLYM	HYPOTHETICAL 69.2 KD P	UREASE ALPHA SUBUNIT (	GALACTOSE-1-PHOSPHATE	CITRATE-PROTON SYMPORT	CITRATE-PROTON SYMPORT	SF-ASSEMBLIN.	DNA POLYMERASE ALPHA (	SPORE-SPECIFIC PROTEIN	HYPOTHETICAL PROTEIN M	CITRATE LYASE ALPHA CH	HNRNP ARGININE N-METHY	PLACENTAL PROLACTIN-LI
2.79e+01	2.79e+01	2.79e+01	2.79e+01	2.79e+01	2.79e+01	2.79e+01	2.79e+01	1.85e+01	1.85e+01	1.85e+01	1.85e+01	1.85e+01	1.85e+01	1.85e+01	1.85e+01	1.22e+01	1.22e+01	1.22e+01	1.22e+01	1.22e+01	1.22e+01

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MEDLINE; 71063634.	HOPPE-SEYLER'S 2. PHYSIOL. CHEM. 351:1586-1588(1970).	NIALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWSON B.F.,		ì	PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).	NIGHT H.D., ORCODO O.W., REGIRANN M.L., FOLLO O.L.	TW NITHIN TACORS TW KENTMANN H.T.	•••	GENE 28:319-329(1984).	WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;	MEDLINE; 84262483.	[4] SEQUENCE FROM N.A.	Ē		MEDLINE; 83105964.	UENCE		U.S.A. 78:40	WEDVER C.A., GORDON D.F., KEMPER B.;	SEQUENCE FROM N.A.		NATL ACAD	JR. RICH A.:	KRONENBERG H M. MCDEVITT B.E. MAIZOUB J.A. NATHANS J. SHARP P.A.			ARTIODACTYLA.	FUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:		PARATHYROLD HORMONE PRECURSOR (PARATHYRIN) (PIH).	(REL. 35, LAST AN	(REL. 01,	21-JUL-1986 (REL. 01, CREATED)	PO1268:	1 CHANDADD. DDH. 115

SYNTHESIS OF 32-65. MEDLINE; 71091588.

1 3 3 3 3 3 3 4 4 4 4 3 7 6 6 7 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result Score	Statistics	Database:	Post-proce	Scoring ta	Title: Descriptic Perfect Sc Sequence:	n on:	<u>}</u>	
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7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	derived b	. ea ⊦	sptr 1:: 5:: 9::	r 3	PAM 15 Gap 15 140542	>US-1 (1-1: 91 1 LR	Thu ,ut not ge	Release 3.1A Copyright (c	
105 2475 2075 3207 3320 3320 3320 3320 3320 3320 3445 445 445 445 445 445 445 2742 2815 342	han or equaby analysis	sp_unc 25.804	rembl5 sp_fung: sp_mhc ( sp_bacte		150 15 142 segs	S-08-817-547 -12) from US LRKKLQDVHNFV	u Jul 30 1 generated.	John 199 ribut	
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	tesulcs the tof the t SUMMARIE	ariance 3	sp_human _organell _10:sp_rc	e 5 summarie	2109429 res.	47A-29 US08817547A.pı FV 12	05:15 1998;	ollins, E 8 Univer ights by	
ARATHYROID HORMONE FOLLYPOTEIN PP220. RF36L.	predicted by challe to ha score of the result being total score distribution.  ES  Description	scale 0.764	3:sp_invertebrate 4:sp_ma .e 7:sp_phage 8:sp_plant pdent 11:sp_virus 12:sp_ve	ss	idues	pep	MasPar time 3.96 S 127.714 Million ce	computing Research ty of Edinburgh, U. ford Molecular Ltd	
F 1.73e 3.90e 1.07ee 1.07ee 1.07ee 2.05ee 2.05ee 4.1.69ee 4.1.69ee 5.4.20e 6.4.20e 6.4.20e 6.4.20e 6.4.20e 6.4.20e 9.91ee 6.4.20e 9.91ee	printed,		.vertebrate				0,0		

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51 51	51	51	51	52	52	52	52	52	52	52	52	52	52	52	52	53	53	53	53	53	54	54	54
56.0					•		•	•		•	•					58.2	•	•	•	•	•	•	•
1630 2829	1354	509	360	1972	1938	1371	1312	957	929	621	602	485	279	160	90	2401	1744	398	373	232	962	735	400
12 12	ω	N	9	10	10	ω	N	9	9	10	9	ω	10	ø	ω	w	w	œ	ω	o	9	w	ω
Q90724 P70039	Q23669	Q13977	034130	008638	008639	001777	Q92878	028565	032491	Q63339	P94876	016873	Q63338	Q44535	P91244	Q26216	Q22516	004471	Q17639	P95776	P95235	Q17750	Q26648
MYOMESIN. ADENOMATOUS POLYPOSIS	ZK930.1.	MAJOR YO PARANEOPLASTI	HISC.	MYOSIN.	MYOSIN.	SIMILAR TO PROTEIN-TYR	RAD50.	O	PUTATIVE N6-ADEININE S	MYOSIN HEAVY CHAIN 21	OLIGOPEPTIDASE.	Cl3A2.5 PROTEIN.	MYOSIN HEAVY CHAIN (AA	ORF 3.	COSMID F11G11.	RHOPTRY PROTEIN (FRAGM	T14G8.1 (FRAGMENT).	SIMILAR TO SACCHAROMYC	C04G6.2 PROTEIN.	DNA FOR DTDP-RHAMNOSE	HYPOTHETICAL 104.6 KD	C06G3.9 PROTEIN.	TEKTIN B1.
	3.51e+01			2.32e+01		2.32e+01	2.32e+01	2.32e+01	2.32e+01		2.32e+01	2.32e+01		2.32e+01		1.52e+01	1.52e+01	1.52e+01	1.52e+01			9.91e+00	

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RESULT 2
1D 008358;
AC 008358;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-FEB-1997 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-FEB-1997 (TREMBLREL. 02, LAST ANNOTATION UPDATE)
DE POLYPROTEIN PP220.
GN CP2475L.
OS AFRICAN SWINE FEVER VIRUS (STRAIN BA71V) (ASFV).
OC VIRIDAE; DS-DNA NONENVELOPED VIRUSES; IRIDOVIRIDAE.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93327788.
RA SIMON-MATEO C., ANDRES G., VINUELA E.;
EMBO J. 12:2977-2987(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT RE
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Best Local Similarity 91.7%;
Matches 11; Conservative
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RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE-THYROID, AND PARATHYROID;
TISSUE-THYROID, AND PARATHYROID;
SCHMELZER H.J., GROSS G., MAYER H.;
ADV. GENE TECHNOL. 21:228-229(1984).
EMBL; M54875; G601933; -.
SEQUENCE 105 AA; 11746 MW; 6AC3163E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CT 1
063473 PRELIMINARY; PRT; 105 AA.
063473; OFFICE OFFIC
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1 LRKKLQDVHNFV 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 105;
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Parch completed: Thu Jul 30 11:05:54 1998
                                                                                                                                  RN [2]

RP COMPLETE GENOME.

RA YANEZ R.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,

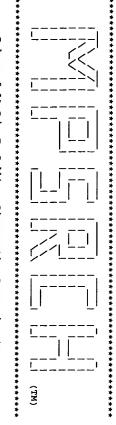
RA CONCIGUEZ J.E., VINUELA E.;

RL VIROLOGY 208:249-278(1995).

CC -1- FUNCTION: POLYPROTEIN PP220 IS THE PRECURSOR OF THE MAJOR VIRION DR EMBL; Z2777; G394799; -24 AND P14 OF AFRICAN SWINE FEVER VIRUS.

DR EMBL; U18466; G780461; -.

SQ SEQUENCE 2475 AA; 281479 MW; 6F4E3COA CRC32;
                                                                                                                                                                                    Query Match 72.5%; Score 66; DB 11; Length 2475; Best Local Similarity 75.0%; Pred. No. 3.90e-02; Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps
                                                                                            0,
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MPsrch\_pp n on: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 11:10:20 1998;

Tabular output not generated. MasPar time 2.67 Seconds 63.142 Million cell updates/sec

Sequence: Description: Perfect Score: >US-08-817-547A-30 (1-11) from US08817547A.pep 84 1 LRKKLQDVHNF 11

Title:

Scoring table: PAM 150 Gap 15

Searched: 124785 segs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq31-2
l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 18.206; Variance 59.063; scale 0.308

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Re

NO.	Score 84 84	Match 100.0	Match Length	26 26	ID R62432 W17957	Description Accelerator peptide b Human parathyroid hor
U 4 IU	0 00 00	100.0	334 44	222	W17958 W17959	human parathyroid Human parathyroid
σ, (	84	100.0	34.	7	R34363	
7	84	100.0	36	9	R58182	[Nva8]-hPTH(1-36)
œ	84	100.0	36	9	R58184	[Tyr18]-hPTH(1-36)-NF
9	84	100.0	36	9	R58179	[Leul]-hPTH(1-36)-NH2
10	84	100.0	36	ø	R58069	7.
11	84	100.0	36	9	R58285	[Ala23]-hPTH(1-
12	84	100.0	36	9	R58074	[L8, Y18] - hPTH(
13	84	100.0	44	26	P30015	Human parathyroid
14	84	100.0	84	27	W25687	Human parathyroid
15	84	100.0	84	4	R23523	Human parathyroid
16	84	100.0	84	4	R23447	Porcine parathyroid h
17	84	100.0	84	4	R23253	Bovine parathyroid
18	84	100.0	84	9	R49695	Sequence of variant
19	84	100.0	84	4	R23444	Porcine parathyroid

84 100.0 84 4 R21221 Human parathyroid hor 84 100.0 84 4 R21201 Human parathyroid hor 84 100.0 84 4 R21201 Human parathyroid hor 84 100.0 84 4 R21203 Human parathyroid hor 84 100.0 84 4 R21203 Human parathyroid hor 84 100.0 84 4 R21202 Human parathyroid hor 84 100.0 84 4 R23376 Bovine parathyroid hor 84 100.0 84 4 R23365 Bovine parathyroid hor 84 100.0 84 4 R23365 Bovine parathyroid hor 84 100.0 84 4 R23354 Bovine parathyroid hor 84 100.0 84 4 R23354 Bovine parathyroid hor 84 100.0 84 4 R23237 Human parathyroid hor 84 100.0 84 4 R23331 Bovine parathyroid hor 84 100.0 84 4 R23331 Bovine parathyroid hor 84 100.0 84 4 R23338 Bovine parath
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4 R21221 4 R23483 4 R21201 4 R21201 4 R21201 4 R21200 4 R21203 4 Human parathyroid 4 R21203 4 Human parathyroid 4 R21203 4 Human parathyroid 4 R21203 6 Human parathyroid 4 R23376 6 Bovine parathyroid 6 R23354 6 Bovine parathyroid 7 R23355 7 Bovine parathyroid 7 R23355 8 Bovine parathyroid 8 R21206 8 Human parathyroid 8 R21207 8 Human parathyroid 8 R21207 8 Human parathyroid 8 R21207 8 Human parathyroid 8 R23331 8 Human parathyroid 8 R23331 8 Bovine parathyroid 8 R23310 8 Bovine parathyroid 8 R23311 8 Bovine parathyroid 8 R23310 8 Bovine parathyroid 8 R23380 8 Bovine parathyroid 8 R23380 8 Bovine parathyroid 8 R23381 8 Bovine parathyroid 9 R23381 8 Bovine parathyroid 9 R23381 9 Bovine parathyroid 9 R23381 9 Bovine parathyroid 9 R23381 9 P304888888888888888888888888888888888888
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RESULT
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                                                                                                                                                                                           Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 11; Conservative
LT 2
W17957;
W17957;
29-JUL-1997 (first entry)
Human parathyroid hormone analogue [A1b3]hPTH(1-34)NH2.
                                                                                                                                                                                                                                                              Disclosure; Page 3; 7pp; Japanese.

The sequences in R62425-36 are peptide fragments of an accelerator protein which contain at least two basic anino acids. The accelerator also comprises a cell growth factor. The accelerator may be used to accelerate the growth of periodontal tissue regeneration. The accelerator is applied by opening the gingiva, treating the tissue destroyed by periodontitis and applying the accelerator in the periodontal pocket. The accelerator reduces the down growth of the epithelium and accelerates fibre adhesion and regenerates cement. Sequence 34 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Accelerator for regenerating periodontal tissue - comprises peptide having 3-34 aminoacid residues having connected basic aminoacid residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-UUL-1995 (first entry)
Accelerator peptide basic region peptide, P-8.
Accelerator; basic amino acid; cell growth factor; growth; gingiva;
periodontal tissue; regeneration; periodontitis; periodontal pocket;
down growth; epithelium; fibre adhesion; cement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R62432 standard; peptide; R62432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 95-157631/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-FEB-1993; 045998.
10-FEB-1993; JP-045998.
(SUNZ.) SUNSTAR CHEM IND CO LID.
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                                                                                                                           1 LRKKLQDVHNF 11
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                                                                                                                                                                                             Score 84; DB 26;
Pred. No. 4.45e-02;
0; Mismatches (
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Pi Dong 7x;

Pi Dong 7x;

Pi Dong 7x;

New variants of human parathyroid hormone 1-34 peptide - which provide the variants of human parathyroid hormone 1-34 peptide - which provide the provide sequence is a specific example of a human parathyroid contain 11; page -; 33pp; English.

CC The present sequence is a specific example of a human parathyroid confide amino acid residues at positions 3, 12, 16, 17, 19 and 34 confide amino acid residues at positions 3, 12, 16, 17, 19 and 34 confide aminoisobutyric acid (Aib). In this example the Ser residue at position 3 of the wild-type has been substituted by Aib. The hPTH confidence of treatment of osteoporosis and bone fracture, optionally in conjunction with anti-resorptive therapy (bisphosphonates and conjunction with anti-resorptive ther
                                                                                                                                                                                                                            Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09702834-A1.
30-JAN-1997.
03-JUL-1995; U11292.
13-JUL-1995; US-001105.
06-SEP-1995; US-003305.
29-MAR-1996; US-626186.
(BIOM-) BIOMEASURE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Osteoporosis; agonist; PTH; human; anti-resorptive therapy; bone fracture.
Homo sapiens.
Synthetic.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified_site
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                                                                                                            24 lrkklqdvhnf 34
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1 LRKKLQDVHNF 11
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34
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                              30 11:10:35 1998
                                                                                                                                                                                                                            Score 84; DB 22;
Pred. No. 4.45e-02;
0; Mismatches (
                                                                                                                                                                                                                                                                                   Length 34;
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# # # #	
(TM)	

MPsrch\_pp in on: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 11:09:33 1998; MasPar time 3.26 Seconds 123.270 Million cell updates/sec

Tabular output not generated.

Title: Description: Perfect Score: Sequence: >US-08-817-547A-30 (1-11) from US08817547A.pep

1 LRKKLQDVHNF 11

Scoring table: PAM 150 Gap 15

Searched: 120441 segs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 25.053; Variance 38.928; scale 0.644

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

1 3 3 4 4 4 4 4 7 7 7 7 11 11 11 11 11 11 11 11 11 11 1	sult No.
00000000000000000000000000000000000000	Score
100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0	Query Match
34 34 34 34 34 35 36 37 37 37 37 37 37 37 37 37 37 37 37 37	Length
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	BG
12WG 11WH 11WH 12WA 11ZWA 11ZWA 11ZWA 11ZWA 11ZWA 11ZWA 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PPH 11PP	ID
parathyroid hormone 4 cyclic parathyroid hormone 4 cyclic parathyroid hormone 6 parathyroid hormone ( parathyroid hormone p hypothetical protein hypothetical protein hypothetical protein nacrophage elastase ( DNA-directed DNA poly	Description
4.83e-05 4.83e-05 4.83e-05 4.83e-05 4.83e-05 4.83e-05 4.83e-05 4.83e-05 4.83e-05 4.83e-05 4.83e-05 1.66e-03 1.75e-01 1.25e+01 1.25e+01 1.25e+01 1.25e+01	Pred. No.

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60.7	60.7	61.9	61.9	61.9	61.9	63.1	63.1	63.1	•	63.1				64.3				64.3		64.3	
431	360	957	879	878	571	569	500	348	227	102	752	421	421	421	421	421	421	421	421	342	189
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ZTEC3	B45734	C69463	S22028	S20486	S38485	S62851	C64043	S45890	A24911	S53076	S51866	1SERB	1SESB	1SESA	1SETB	1SETA	1SRYB	1SRYA	S38948	S51402	S59264
citrate utilization d	HisC - Lactococcus la	type I restriction-mo	paramyosin, standard	- fr	urease (EC 3.5.1.5) 6	MG397 homolog D02_orf	citrate (pro-3S)-lyas	ODP1 protein - yeast	prolactin-like prote1	probable membrane pro	HPR1 protein - yeast	seryl-tRNA synthetase	-trna	Seryl-trna synthetase	RNA ligas	$\mathbf{r}$	nypothetical protein				
5.53e+01	5.53e+01	3.84e+01	3.84e+01	•		2.66e+01	•	2.66e+01	2.66e+01	2.66e+01	1.83e+01	1.83e+01	1.83e+01	1.83e+01	1.83e+01	1.83e+01	1.83e+01	1.83e+01	1.83e+01	1.83e+01	1.83e+01

#authors #submission #cross-refere REFERENCE #authors #authors	ALTERNATE_NAMES PDB_TITLE ORGANISM	RESULT 2 ENTRY	Db 21 LRKKLQDVHNF           Qy 1 LRKKLQDVHNF	Query Match Best Local Simi Matches 11;	2-9 15-25 SUMMARY	ω	#authors #book	#submission #cross-refere REFERENCE	ALTERNATE_NAMES PDB_TITLE ORGANISM REFERENCE	RESULT 1 ENTRY TITLE
#AUTHORS ROSECH, P.; Marx, U.C. #AUTHORS ROSECH, P.; Marx, U.C. #SUDMISSION SUDMITTED to the Brookhaven Protein Data Bank, June 1996 #SCROSS-references PDB:12WF ERENCE TN003318 #BAUTHORS MARX, U.C. #BAUTHORS MARX, U.C. #BOOK in Strukturen Verschiedener Parathormonfragmente in Loesung,	hetic yl-hpth(4-37) ure of n-terminal acetyla 10 structures l_name synthetic	12WF #type complete parathyroid hormone 4 37 mutant N-TERMINAL ACETYLATED -	DVHNF 31	100. larity 100. Conservati	<pre>#region helix (right hand alpha)\ #region helix (right hand alpha) #length 34 #molecular-weight 4128 #checksum 5508</pre>	pp.0, Bayreuth : University of Bayreuth (Thesia), 1996 Resolution: not applicable Determination: NMR disease mutation; hormone; signal	C. turen Verschiedener Parathormonfragmente in	#SUDDISSION SUBDITIED to the Brookhaven Protein Data Bank, June 1996 #CTOSS-TEFERCES PDB:12WG ERENCE TN003319	nyl-hpth(4 L human pa _name synt	12WG #type complete parathyroid hormone 4 37 mutant N-TERMINAL SUCCINYLATED - synthetic

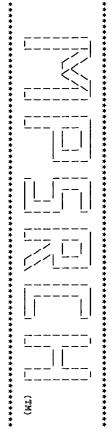
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COMMENT COMMENT Resolution: not applicable
COMMENT Determination: NMR
KEYWORDS HAPPHICABLE

S-6 #region helix (right hand alpha)
14-27 #length 34 #molecular-weight 4128 #checksum 5508

Query Match 100.0%; Score 84; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.83e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 21 LRKKLODVHNF 31
1 | | | | | | | | | | | |
Qy 1 LRKKLODVHNF 11

Search completed: Thu Jul 30 11:10:03 1998
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(Psrch\_pp n on: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 11:07:53 1998; MasPar time 2.18 Seconds 126.596 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-817-547A-30 (1-11) from US08817547A.pep 84 1 LRKKLQDVHNF 11

Scoring table: PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 26.284; Variance 32.770; scale 0.802

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

222 23	שמש	sult No.
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	888	Score
100.00 100.00 67.94 65.56 65.56 65.56 64.33 64.33 64.33 61.96 61.96 61.96	100.0	% Query Match
115 115 115 1144 144 162 119 119 119 162 305 218 175 227 752 227 752 227 227 227 227 257 267 278 279 279 279 279 279 279 279 279 279 279	115	Length
	إمومون	BB
PHY_RATE PHY_RATE CIT1_KLEPN GIG2_ARATH PTHY_CHICK Y4XD_RHISN HIYE_ECOLI COGM_MOUSE YNOO_YEAST DP3E_BUCAP SYS_THETH YM88_YEAST HORL_YEAST HAT1_YEAST HAT1_YEAST PRRA_RAT PRRA_RAT PRRA_RAT TATAT HAT1_YEAST PRRA_RAT YAST PRRA_RAT TATAT YAGE_MYCTU WYSP_DROME	PTHY_BOVIN PTHY_CANFA	Ħ
HORMONE HORMON	PARATHYROID HORMONE PR PARATHYROID HORMONE PR PARATHYROID HORMONE DR	Description
		Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
49	50	50	50	50	50	50	50	50	50	50	50	51	51	51	51	51	51	51	51	51	51
										59.5			60.7	60.7	60.7	60.7	60.7	60.7		60.7	0
455	4725	1314	1257	610	610	609	586	525	510	437	281	2843	1444	434	431	419	360	317	310	133	111
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YHCL_ECOLI	DYHC_DICDI	SS22_YEAST	RBB1_HUMAN	LKHA_HUMAN	LKHA_MOUSE	LKHA_RAT	YM61_CAEEL	Y107_METJA	CILA_ECOLI	FOLC_HAEIN	P2C1_YEAST	APC_HUMAN	RRPL_RDV	CIT1_SALTY	CIT1_ECOLI	MYC1_XENLA	HIS8_LACLA	MSHR_BOVIN	SYNK_ARATH	YIM5_BPPH1	ARPP_BOVIN
HYPOTHETICAL 48.8 KD P	DYNEIN HEAVY CHAIN, CY	SERINE/THREONINE PROTE	RETINOBLASTOMA BINDING	LEUKOTRIENE A-4 HYDROL	LEUKOTRIENE A-4 HYDROL	LEUKOTRIENE A-4 HYDROL	HYPOTHETICAL 65.8 KD P	HYPOTHETICAL PROTEIN M	CITRATE LYASE ALPHA CH	FOLYLPOLYGLUTAMATE SYN	PROTEIN PHOSPHATASE 2C	ADENOMATOUS POLYPOSIS	RNA-DIRECTED RNA POLYM	CITRATE-PROTON SYMPORT	CITRATE-PROTON SYMPORT	MYC I PROTO-ONCOGENE P	HISTIDINOL-PHOSPHATE A	MELANOCYTE STIMULATING	SYNTAXIN-RELATED PROTE	HYPOTHETICAL IMMUNITY	CAMP-REGULATED PHOSPHO
3.87e+01	2.56e+01	2.56e+01								2.56e+01	2.56e+01	1.68e+01	1.68e+01	1.68e+01	1.68e+01	1.68e+01	1.68e+01	1.68e+01	1.68e+01	1.68e+01	1.68e+01

RA R	RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	R R R R R R R R R R R R R R R R R R R	RESULT PAC PO DT 2 DT
UENCE LLL H. BACH PE-SE UENCE	CARES ESES	SEQUENCE FRO MEDLINE; 820 WEAVER C.A., PROC. NATL. [3] SEQUENCE FRO MEDLINE; 831 WEAVER C.A., MOL. CELL. E	EUKARYOTA; N EUTHERIA; AF [1] SEQUENCE FRO MEDLINE; 800 KRONENBERG; FOTTS J.T. C PROC. NATL.	1 01268; 01268; 1-JUL-1986 1-JUL-1986 1-JUL-1997 1-NOV-1997 1-NOV-1997
-115. 162. UTMANN H.T., UTMANN J.T. JR POTTS J.T. JR Z. PHYSIOL. -115.	N.A. 483. ORDON D.F., K 9(1984). -115. -115. 666. NIALL H.D., AD. SCI. U.S.	M N.A. 37785. GORDON D.F ACAD. SCI. M N.A. 05964. GORDON D.F	OTA; METAZOA; CHORDATA; OTA; METAZOA; CHORDATA; (IA; ARTIODACTYLA. (CE FROM N.A. (E); 80056617. (B); 80056617. (B); 80056617. (B); 80056617. (B); 80056617. (B); 80056617. (B); 80056617. (B); 80056617. (B); 80056617. (B); 80056617.	DARD; 1, CREA 1, LAST 5, LAST 5 PRECUR;
SAUER R., HOGAN M.L., DAWSON B.F., (,) CHEM. 351:1586-1588(1970).	KISSIL M.S., MEAD D.A., KEMPER B.; JACOBS J.W., KEUTMANN H.T., POTTS J.T. JR.,	U.S.A. 78:4073-4077(1981).  U.S.A. 78:4073-4077(1981).	N; VERTEBRATA; TETRAPODA; MAMMALIA; E., MAJZOUB J.A., NATHANS J., SHARP P.A., N. 76:4981-4985(1979).	PRT; 115 AA. IED) SEQUENCE UPDATE) ANNOTATION UPDATE) SOR (PARATHYRIN) (PTH).

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SO SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
ID PT
AC PS
DT 01
DT 01
DT 01
DT 01
DT 02
CC ECC
CC
                                                                                    Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
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Best Local s
Matches 1
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K MEDLINE; 71091588.

A POTTS J.T. JR., TREGEAR G.W., KEUTMANN H.T., NIALL H.D., SAU DETTOS L.J., DAWSON B.F., HOGAN M.L., AURBACH G.D.;

A DETTOS L.J., DAWSON B.F., HOGAN M.L., AURBACH G.D.;

C PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).

C PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).

C BOME AND PREVENTING THEIR RENAL EXCRETION.

R EMBL; U00026; G85; -.

R EMBL; J00023; G163641; -.

R EMBL; J00024; E18249; ALT_SEQ.

R EMBL; J00024; E18249; ALT_SEQ.

R EMBL; J00024; E18250; ALT_INIT.

REMBL; M01938; G163647; -.

REMBL; M01938; G163645; -.

REMBL; M25082; G163645; -.

REMBL; M25082; G163645; -.
                                                                                                                                                                                           SIGNAL
PROPEP
CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                   MISSUE-PARATHYROID;

MEDLINE; 95369696.

ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,

DEWILLE J.W., CAPEN C.C.;

GENE 160:241-243(1995).

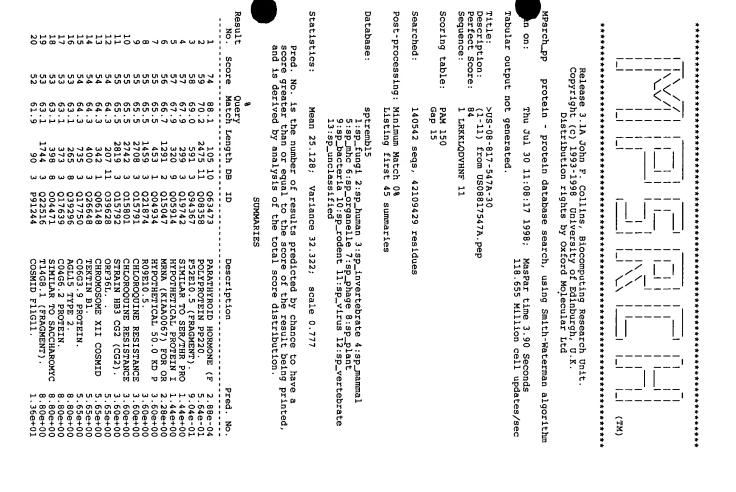
-1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS

BONE AND PREVENTING THEIR RENAL EXCRETION.

EMBL; U15662; G558916; -.
                                                                                                                                                                                                                                                                             PROSITE; PS00335; PARATHYROID; 1. HORMONE; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CANIS FAMILIARIS (DOG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTHY_CANFA STANDARD; PRT; 115 AA.
P52212;
01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
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PROPEP
CHAIN
CONFLICT
SEQUENCE
                              55 LRKKLQDVHNF 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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PIR; A24949; A24949.
PROSITE; PS00335; PARATHYROID; 1.
1 LRKKLQDVHNF 11
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Local Similarity 100.0%;
nes 11; Conservative
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26
32
115 AA;
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32
106
115 AA;
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                                                                                                                                                                                   25 B
31 B
115 P
; 12957 MW;
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. SCI. U.S.A. 67:1862-1869(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25
31
115 PARATHYROID HORMONE.
106 V -> G (IN REF. 4).
12980 MW; 673EA5F2 CRC32;
                                                                               Score 84; DB 1; Ler
Pred. No. 9.02e-07;
0; Mismatches 0;
                                                                                                                                                                         BY SIMILARITY.
BY SIMILARITY.
PARATHYROID HORMONE.
16ED0EBC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 84; DB 1; Length 115;
Pred. No. 9.02e-07;
0; Mismatches 0; Indels
                                                                                                                             Length 115;
                                                                                  Indels
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                                                                       Gaps
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Search completed: Thu Jul 30 11:08:00 1998 Job time : 7 secs.



RESULT 1 ID Q63473		45	44	43	42	41	40	39	38	37	36	35	34	33 33	32	31	30	29	28	27	26	25	24	23	22	21	
173		51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	52	52	52	52	52	52	
P		60.7	60.7	60.7	60.7	•	60.7	•	•	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	61.9	61.9	61.9	61.9	1-4	61.9	
PRELIMINARY;				2842									330	317	317	257	242	242	231	110	1312	957	929	602	485	160	
ARY		10	N	10	12	N	12	1	9	w	w	9	12	4	4	œ	œ	œ	9	4	N	Q	φ	Q	ω	9	
; PRT;	ALIGNMENTS	Q61315	Q15163	P70478	P70039	Q15162	Q90724	Q98631	P73340	Q24250	017076	034130	Q91794	P79328	019037	Q40700	P93468	Q40970	Q55290	P79322	Q92878	028565	032491	P94876	87	Q44535	
105 AA.	TS	ADENOMATOSIS POLYPOSIS	POLYPOSIS LOCUS-ENCODE	APC PROTEIN.	ADENOMATOUS POLYPOSIS	POLYPOSIS LOCUS-ENCODE	MYOMESIN.	RNA-DEPENDENT RNA POLY	CHROMOSOME SEGREGATION	TARTAN PROTEIN PRECURS	C38C3.3 PROTEIN.	HISC.	MYC PROTEIN (FRAGMENT)	MELANOCYTE STIMULATING	MC1-R PROTEIN.	BOX PROTEIN.	MADS-BOX FAMILY TRANSC	PUTATIVE MADS-BOX FAMI	ORF10.	CAMP-REGULATED PHOSPHO	RAD50.	TYPE I RESTRICTION-MOD	PUTATIVE N6-ADEININE S	OLIGOPEPTIDASE.	Cl3A2.5 PROTEIN.	ORF 3.	
		2.10e+01	٠	2.10e+01	٠	٠	•	2.10e+01	٠	٠		2.10e+01	2.10e+01			•		2.10e+01	•		•	1.36e+01		1.36e+01	1.36e+01	1.36e+01	

#### Š 밁 Query Match Best Local Matches Q63473; 01-NOV-1996 01-NOV-1996 01-JAN-1998 PARATHYROID MON\_TER SEQUENCE FROM N.A. TISSUE-THYROID, AND PARATHYROID; SCHWELZER H.J., GROSS G., MAYER ADV. GENE TECHNOL. 21:228-229(19 EMBL, M54875; G601933; -. RATTUS NORVEGICUS (RAT). EUKARYOTA; METAZOA; CHOR SEQUENCE EUTHERIA; 45 LRKKLQDGHNF 55 Match 88.1%; Local Similarity 90.9%; دبو LRKKLQDVHNF 10; RODENTIA. 105 AA; 11746 MW; (TREMBLREL. 01, CREATED) (TREMBLREL. 01, LAST SEQ (TREMBLREL. 05, LAST ANN HORMONE (FRAGMENT). Conservative 11 SS G., MAYER H.; 21:228-229(1984). CHORDATA; VERTEBRATA; Score 74; DB 10; Pred. No. 2.88e-04; 0; Mismatches 1 6AC3163E CRC32; SEQUENCE UPDATE) ANNOTATION UPDATE) TETRAPODA; MAMMALIA; Length 105; Indels 0 Gaps

RESULT
AC QOLD
DT QOLD

CP2475L. AFRICAN

SWINE FEVER

PP220.

SWINE FEVER VIRUS (STRAIN BA71V) (ASFV).
DS-DNA NONENVELOPED VIRUSES; IRIDOVIRIDAE

VIRIDAE;

SEQUENCE FROM N.A.
MEDLINE; 93327788.
SIMON-MATEO C., ANDRES G.,
EMBO J. 12:2977-2987(1993).

VINUELA

DIT 2
Q08358;
Q08358;
01-NOV-1996
01-NOV-1996
01-FEB-1997
POLYPROTEIN 1

(TREMBLREL.)
(TREMBLREL.)

01, CREATED)
01, LAST SEQUENCE UPDATE)
02, LAST ANNOTATION UPDATE)

PRELIMINARY;

PRT;

2475 B

0

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RN [2]

RP COMPLETE GENOME.

RA YANGE R.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,

RA YANGE R.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,

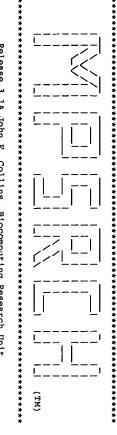
RA RODRIGUEZ J.F., VINUELA E.;

RA RODRIGUEZ C.,

RA RODRIGUEZ C., ENRIQUEZ C.,

RA RODRIGUEZ J.F., VINUELA E., ENRIQUEZ C.,

RA RODRIGUEZ J.F., VINUELA E.,
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MPsrch\_pp m on: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 11:12:42 1998; MasPar time 2.67 Seconds 57.535 Million cell updates/sec

Tabular output not generated.

Description: Title: >US-08-817-547A-31 (1-10) from US08817547A.pep 73

Sequence: Perfect Score: 1 LRKKLQDVHN 10

Scoring table: PAM 150 Gap 15

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match Listing first 400 summaries

Database: a-geneseq31-2

i:parti 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 17.167; Variance 59.785; scale 0.287

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	73	73	73	73	13 73 100	73	73	73	73							_	_	No. Score Ma
200	0.0 36	)0.0 36	0.0 35	0.0 35	0.0 35	0.0 34	0.0 34	0.0 34	.0	0.0 34	.0		.0	.0	0.0 34	.00.0 34	)0.0 33	Match Length
0 0	9	9	14	14	14	22	22	22	_		7	-	13	-	-	26	18	BG
R58026	R58057	R58243	R74527	R74413	R74442	W17962	W20003	W20002	R41582	R34345	R34352	R34353	R69037	R45528	R45508	R62432	R88841	Ħ
N-alpha-methyl[Ala1]	[L8,D10,A16,Q18]-hPTH	Propargyl-[Al]-hPTH(1	Human parathyroid hor	Parathyroid hormone p	Parathyroid hormone p	Human PTH analogue [C	Cyclised [Nle 8,18, T	Cyclised rat parathyr	[Arg15,16,17]hPTH (1-	Bovine parathyroid ho	Bovine parathyroid ho	Human parathyroid hor	PTH analogue with amp	Parathyroid hormone/p	Parathyroid hormone/p	Accelerator peptide b	Human parathyroid hor	Description
8.53e-01	8.53e-01	8.53e-01	8.53e-01	8.53e-01	8.53e-01	8.53e-01	8.53e-01	8.53e-01	8.53e-01	8.53e-01	8.53e-01	8.53e-01	8.53e-01	8.53e-01	8.53e-01	8.53e-01	8.53e-01	Pred. No.

ij RESULT

T 2 R62432 standard; peptide; 34 AA.

73 100.0 38 9 R58061 [Ilel]-hPPH(1-38)-OH 73 100.0 38 9 R580291 [Tys1]-hPPH(1-38)-OH 73 100.0 38 9 R580291 [Tys1]-hPPH(1-38)-OH 73 100.0 38 9 R58028 [Thr1]-hPPH(1-38)-OH 73 100.0 84 27 W25687 Human parathyroid hor 73 100.0 84 4 R23521 Human parathyroid hor 73 100.0 84 4 R23521 Human parathyroid hor 73 100.0 84 4 R23521 Human parathyroid hor 73 100.0 84 4 R23242 Human parathyroid hor 73 100.0 84 4 R23346 Bovine parathyroid hor 73 100.0 84 4 R23336 Bovine parathyroid hor 73 100.0 84 4 R23336 Bovine parathyroid hor 73 100.0 84 4 R23529 Human parathyroid hor 73 100.0 84 4 R23529 Human parathyroid hor 73 100.0 84 4 R23529 Human parathyroid hor 73 100.0 84 4 R23536 Human parathyroid hor 73 100.0 84 4 R2356 Human parathyroid hor 73 100.0 84 6 R30857 Cys35 hPTH mutein. 73 100.0 84 4 R21241 Human parathyroid hor 73 100.0 84 4 R21241 Human parathyroid hor 73 100.0 84 4 R23474 Porcine parathyroid hor 73 100.0 84 4 R23474 Porcine parathyroid hor 73 100.0 84 4 R23474 Porcine parathyroid hor 74 100.0 84 4 R23474 Porcine parathyroid hor 75 100.0 84 4 R23474 Porcine parathyroid hor 85 100 100 100 100 100 100 100 100 100 10	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	
0 38 9 R58061 [Ile]5]-hPH(1-38) 0 38 9 R58091 [Cys13]-hPH(1-38) 0 38 9 R58092 [Thr]]-hPH(1-38) 0 38 9 R58124 [Lys19]-hPH(1-38) 0 44 26 P30015 Human parathyroid 0 44 27 W25687 Human parathyroid 0 84 4 R23521 Bovine parathyroid 0 84 4 R23523 Porcine parathyroid 0 84 4 R23453 Porcine parathyroid 0 84 4 R23242 Human parathyroid 0 84 4 R23243 Bovine parathyroid 0 84 4 R23346 Bovine parathyroid 0 84 4 R23346 Bovine parathyroid 0 84 4 R23336 Bovine parathyroid 0 84 4 R23316 Bovine parathyroid 0 84 4 R23529 Human parathyroid 0 84 4 R23521 Human parathyroid 0 84 4 R23251 Human parathyroid 0 84 4 R23251 Bovine parathyroid 0 84 4 R23251 Bovine parathyroid 0 84 6 R30856 Cys35 hPH mutein 0 84 6 R30856 Cys35 hPH mutein 0 84 4 R21241 Human parathyroid 0 84 4 R21241 Human parathyroid 0 84 4 R21240 Porcine parathyroid 0 84 4 R23474 Porcine parathyroid	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	ì
9 R58061 [TIE15] hpHH[1-38] 9 R58091 [Cys13]-hpHH[1-38] 9 R580928 [Thr1] hpHH[1-38] 9 R58028 [Lys19]-hpHH[1-38] 10 R58028 [Lys19]-hpHH[1-38] 11 R58028 [Lys19]-hpHH[1-38] 12 R58028 [Lys19]-hpHH[1-38] 13 R58028 [Lys19]-hpHH[1-38] 14 R58028 [Lys19]-hpHH[1-38] 15 R58028 [Lys19]-hpHH[1-38] 16 R58028 [Lys19]-hpHH[1-38] 17 R58028 [Lys19]-hpHH[1-38] 18 R58028 [Lys19]-hpHH[1-	•		٠		٠			٠		•	•		•	•	•	•	•		•			٠	•	•	٠	٠
R58061 [ILE15]-hpHH(1-38) R58069 [Cys13]-hpHH(1-38) R58028 [Thr1]-hpHH(1-38) R58028 [Thr1]-hpHH(1-38) R58028 [Lys19]-hpHH(1-38) R58028 [Lys19]-hpHH(	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84	84							
[11e15]-hrH(1-38) [Cys13]-hrH(1-38) [Thr]-hrH(1-38) [Thr]-hrH(1-38) [Lys19]-hrH(1-38) [Lys19]-hrH(1-38	4	4	4	4	O	σ	4	4	4	4	4	4	4	4	4	4	4	4	4	27	26	9	9	9	ø	,
S  -hpTH(1-38)   -hpTH(1-38)   -hpTH(1-38)   -hpTH(1-38)   -parathyroid   parathyroid   parathyroid	347	347	12	13	085	085	R23368	R21256	R23251	R21198	R21217	R23529	R23336	R23346	R23241	R23242	R23453	R23521	R21244	œ	مبو	812	$\sim$	w	908	0
		parathyroid	parathyroid ho	n parathyroid ho	Ų.	w	parathyroid	19]-hPTH(1-38)	1]-hPTH(1-38)-	13]-hPTH(1-38)-C	5]-hPTH(1-38)-	E ( + 00 ) 0														

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RESULT RE
ş
                                                                                 밁
                                                                                                                                                      Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                     New human parathyroid hormone analogues - which have increased adenyly! cyclase activating activity, used for treating osteoporosi Claim 2; Page -; 21pp; English.

R88829-R88841 are human parathyroid hormone (hPTH) analogues. The analogues increase G-protein coupled adenyly! cyclase (cAMPase) activity and reduce protein kinase C (PKC) activity. The analogues can reverse the loss of bone and increase bone mass and density without undesirable effects. They are useful for the treatment of osteoporosis and other bone related disorders and disorders involving bone cell calcium regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human parathyroid hormone analogue, [Leu27]-hPTH(1-33)-NH2. Parathyroid hormone; PTH; analogue; osteoporosis; bone cell calcium regulation; reduced PKC activity; protein kinase C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R88841 standard; peptide; R88841; 07-OCT-1996 (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 96-151754/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-JUN-1994; 126299.
20-JUN-1994; CA-126299.
(WILL/) WILLICK G E.
Neugebauer W, Sung WL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CA2126299-A.
21-DEC-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    increased adenylyl cyclase activity; Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified_site
                                                                             24 lrkklqdvhn 33
    μ
    LRKKLQDVHN 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "amidated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Surewicz W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33 AA.
                                                                                                                                                      Score 73; DB 18; Le
Pred. No. 8.53e-01;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cAMPase; bone loss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Whitfield JF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for treating osteoporosis
                                                                                                                                                                                                                                Length 33;
                                                                                                                                                              Indels
                                                                                                                                                              0;
                                                                                                                                                          Gaps
                                                                                                                                                              0
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AC R62432;
DT 31-JUL1995 (first entry)
DE Accelerator peptide basic region peptide, p-8.

RW Accelerator; basic amino acid; cell growth factor; growth; gingiva; periodontal tissue; regeneration; periodontitis; periodontal pocket; Synthetic.

Synthetic.
PN J06234653-A.
PD 23-ANG-1994.
PF 10-FEB-1993; 045998.
PN (SUNZ) SUNSTAR CHEM IND CO LTD.
PR Accelerator for regenerating periodontal tissue - comprises PR (SUNZ) SUNSTAR CHEM IND CO LTD.
PR Accelerator for regenerating periodontal tissue onnected basic PR peptide having 3-34 aminoacid residues having connected basic PR aminoacid residues in R62425-36 are peptide fragments of an accelerator for regeneration at least two basic amino acids. The accelerator accelerator accelerator to be periodontal tissue regeneration. The accelerator accelerator accelerator is applied by opening the gingiva, treating the tissue periodontal pocket. The accelerator regeneration in the accelerator regenerator in the accelerator and applying the accelerator in the periodontal pocket. The accelerator reduces the down growth of the generator periodontal pocket. The accelerator reduces the down growth of the sequence 34 AA;

Ouery Match 100.0%; Score 73; DB 26; Length 34;

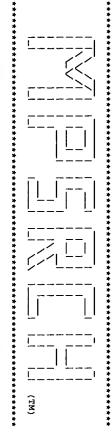
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 Irkklqdvhn 33

Ouery Match 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 11 IRKKLODVHN 10

Search completed: Thu Jul 30 11:13:00 1998
```



MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

n on: Thu Jul 30 11:12:07 1998; MasPar time 3.23 Seconds 113.195 Million cell updates/sec

Tabular output not generated.

Description:
Perfect Score:
Sequence: Title: >US-08-817-547A-31 (1-10) from US08817547A.pep 73-

1 LRKKLQDVHN 10

Scoring table: PAM 150 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nr13d

Statistics: Mean 23.845; Variance 36.931; scale 0.646

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

sult	Score	% Query Match	Length DB		Ð	Description	Pred. No.
_	73	100.0	34	Çī j	1ZWG	parathyroid hormone 4	.82e-
N	73	100.0	34	G	1ZWF		2.82e-03
w	73	٠		5	1HTH	cyclic parathyroid ho	٠
4	73	100.0		Çī	12WE		
υ	73	•		G	12WA	parathyroid hormone (	.82e-
σ	73	100.0		Ç,	1ZWD		.82e
7	73	•		٠,	1ZWB	parathyroid hormone (	2.82e-03
ထ	73	100.0		G	1HPH	parathyroid hormone f	2.82e-03
Q	73	٠		v	1ZWC	parathyroid hormone (	2.82e-03
10	73	100.0	115	μ,	PTPG	parathyroid hormone p	
11	73	100.0		μ.	PTBO	parathyroid hormone p	2.82e-03
12	73	100.0		Ν	JC4202	hormone	
13	73	100.0		_	PTHU	parathyroid hormone p	
14	73	100.0		N	A05091	hormone	
15	63	86.3		N	I51851	hormone	.30e-
16	55	75.3		N	A34937	parathyroid hormone p	6.14e+00
17	54	74.0		N	S38948	A ligase	•
18	54	74.0	421	u	1SRYA	Seryl-trna synthetase	9.09e+00
19	54			u	1SRYB		9.09e+00
20	54	74.0		S	1SETA		9.09e+00
21	54	74.0		5	1SETB	-trna	9.09e+00
22	54	74.0	421	u	1SESA	-trna	9.09e+00
23	54	74.0	421	G	1SESB	-trna	9.09e+00

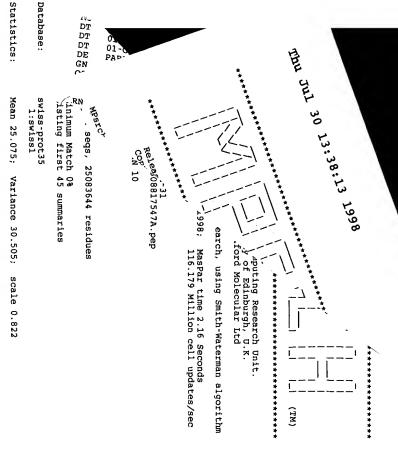
45	44	43	42	41	40	39	38	37	36	ω 5	34	ω	32	31	30	29	28	27	26	25	24
49	49	49	49	50	50	50	50	50	50	50	50	51	51	51	51	52	52	52	53	53	54
67.1	67.1				68.5	•				•		•	•		•	•	71.2	٠			
899	630	444	215	4725	1972	1938	621	586	437	412	360	1200	571	317	257	2475	879	878	569	348	421
N	N	N	N	-4	ν	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	σ
S51341	C64302	S09681	S35640	A44357	JC5420	JC5421	S10450	S44850	C64113	S07537	B45734	S77524	S38485	S45708	S53306	S35307	S22028	S20486	S62851	S45890	1SERB
probable membrane pro	hypothetical protein	citrate transport pro	hypothetical protein	dynein heavy chain, c	smooth muscle myosin	smooth muscle myosin	myosin heavy chain -	K12H4.1 protein - Cae	tetrahydrofolylpolygl	myosin heavy chain, c	HisC - Lactococcus la	chromosome segregatio	urease (EC 3.5.1.5) 6	MSH receptor - bovine		polyprotein pp220 pre	paramyosin, standard	paramyosin - fruit fl	MG397 homolog D02_orf	ODP1 protein - yeast	seryl-tRNA synthetase
6.04e+01	6.04e+01	6.04e+01	6.04e+01	4.17e+01	4.17e+01	4.17e+01	4.17e+01	4.17e+01	4.17e+01	4.17e+01	4.17e+01	2.87e+01	2.87e+01	2.87e+01	2.87e+01	1.97e+01	1.97e+01	1.97e+01	1.34e+01	1.34e+01	9.09e+00

RESULT 2 ENTRY 12WF TITLE parathyroid synthetic ALTERNATE_NAMES necetyl-byt PDB_TITLE structure of ORGANISM #formal_name REFERENCE #authors Roesch, P.; #submission submitted to #cross-references PDB:1ZWF REFERENCE TN00318 #authors Marx, U.C. #book in Strukture	Query Match Best Local Similar: Matches 10; Cor Db 21 LRKKLQDVHN            Qy 1 LRKKLQDVHN	RESULT 1  ENTRY   1ZWG # TITLE synthetic synthetic synthetic succinyl-hum organism # 67743 # 67743 # authors # no strukture COMMENT COMMENT RESUNCAL # RESOLUTION: NATE COMMENT Determination: NATE RESUNCAL # authors #
12WF #type complete parathyroid hormone 4 37 mutant N-TERMINAL ACETYLATED - synthetic n-acetyl-hpth(4-37) structure of n-terminal acetylated human parathyroid hormone, NMR, 10 structures #formal_name synthetic A67742 ROESCH, P.; Marx, U.C. submitted to the Brookhaven Protein Data Bank, June 1996 nces PDB:1ZWF TM003318 Marx, U.C. In Strukturen Verschiedener Parathormonfragmente in Loesung, In Strukturen Verschiedener Parathormonfragmente in Loesung,	Query Match 100.0%; Score 73; DB 5; Length 34; Best Local Similarity 100.0%; Pred. No. 2.82e-03; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 21 LRKKLQDVHN 30           1 LRKKLQDVHN 10	12WG #type complete parathyroid hormone 4 37 mutant N-TERMINAL SUCCINYLATED - synthetic succinyl-hpth(4-37) succinyl human parathyroid hormone 4-37, NMR, 10 structures #formal_name synthetic A67743 P.; Marx, U.C. 10n submitted to the Brookhaven Protein Data Bank, June 1996 eferences PDB:12WG FN003319 Marx, U.C. 1n Strukturen verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth: University of Bayreuth (Thesis), 1996 Resolution: Not applicable Determination: NMR disease mutation; hormone; signal #region helix (right hand alpha)

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Search completed: Thu Jul 30 11:12:24 1998 time : 17 secs.
                                                                                                                                                                                                COMMENT
COMMENT
KEYWORDS
FEATURE
3-6
14-27
SUMMARY
                                                                                                        Query Match
100.0%; Score 73; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.82e-03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps
                                                               21 LRKKLQDVHN 30
|||||||||
1 LRKKLQDVHN 10
                                                                                                                                                                                                                                 Resolution: not applicable
Determination: NMR
disease mutation; hormone; signal
                                                                                                                                                                      #region helix (right hand alpha)\
#region helix (right hand alpha)
#length 34 #molecular-weight 4128 #checksum 5508
                                                                                                            0;
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Qy

В



Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	S S	21	20	19	18	17	16	15	14	13	12	Ľ	10	9	œ	7	σ	ហ	4	ω	2	سر	NO.	Bult	•
	49	49	49	49	50	50	50	50	51	51	51	52	52	53	53	54	55	73	73	73	73	73	Score		
•	2	٠	67.1	•	68.5					69.9	•	•	71.2	72.6	72.6	74.0	75.3	100.0	100.0		100.0	100.0	Match		#P
) i	154	630	444	209	4725	586	437	360	571	317	310	879	621	569	348	421	119	115	115	115	115	115	Length		
4 د	_	⊢	Н	دسو	Н	_	Н	۲	<b></b>	دسو	µ.	_	H	<b>_</b>	Н	Н	ب	_	<u> </u>	ب	<u>, , , , , , , , , , , , , , , , , , , </u>	_	BB		
* + 1 * 1 00 * +	V17K SSV1	Y019_METJA	CIT1_KLEPN	VS10_ROTBS	DYHC_DICDI	YM61_CAEEL	FOLC_HAEIN	HIS8_LACLA	URE1_STAXY	MSHR_BOVIN	SYNK_ARATH	MYSP_DROME	YO4E_MYCTU	Y397_MYCPN	HMT1_YEAST	SYS_THETH	PTHY_CHICK	PTHY_HUMAN	PTHY_RAT	PTHY_PIG	PTHY_CANFA	PTHY_BOVIN	ID		SUMMAKIES
1		HYPOTHETICAL PROTEIN M	CITRATE-PROTON SYMPORT	MINOR OUTER CAPSID PRO	DYNEIN HEAVY CHAIN, CY	HYPOTHETICAL 65.8 KD P	FOLYLPOLYGLUTAMATE SYN	HISTIDINOL-PHOSPHATE A	UREASE ALPHA SUBUNIT (	MELANOCYTE STIMULATING	SYNTAXIN-RELATED PROTE	PARAMYOSIN, LONG FORM.	HYPOTHETICAL 69.2 KD P	HYPOTHETICAL PROTEIN M	HNRNP ARGININE N-METHY	SERYL-TRNA SYNTHETASE	PARATHYROID HORMONE PR	PARATHYROID HORMONE PR	Description						
	2.56e+01	1.66e+01	1.66e+01	1.66e+01	1.07e+01	1.07e+01	1.07e+01	1.07e+01	6.80e+00	6.80e+00	6.80e+00	4.31e+00	4.31e+00	2.72e+00	2.72e+00	1.70e+00	1.06e+00	8.74e-05	8.74e-05	8.74e-05	8.74e-05		Pred. No.		

44	43	41	40	39	38	37	36	35	34	ω ω	32	3	30	29	28	27	26	25	24
46	4 4 0 0	4.0	46	46	46	47	47	47	47	47	47	47	48	48	48	48	48	48	48
63.0 63.0	63.0	63.0	63.0	63.0	63.0	64.4	64.4	64.4	64.4	64.4	64.4	64.4	65.8	65.8	65.8	65.8	65.8	65.8	65.8
637 1679	590	457	380	326	297	1225	1036	911	752	189	112	100	2663	1126	926	920	857	669	419
11		ــو د	_	Н	ш	μ	ш	ы	۳	μ	Ь	ب	Ь	μ.	Ь	_ر	Ь	ш	ᆫ
YIO9_YEAST	YM63_YEAST	EMB8_PICGL	CAPM_STAAU	YIE1_YEAST	YUBO_CAEEL	SMC1_YEAST	YAN2_SCHPO	STE6_SCHPO	HPR1_YEAST	YNOO_YEAST	YI91_SHIDY	YI91_ECOLI	CENE_HUMAN	RPOB_SULAC	PQQL_HAEIN	YML1_YEAST	MEDB_GIALA	YMS2_YEAST	PEXA_PICPA
PTS SYSTEM, MANNITOL-S HYPOTHETICAL 195.1 KD	HYPOTHETICAL 67.7 KD P	EMBRYOGENESIS A	CAPM PROTEIN.	36.7 KD PROTEIN IN CBR	HYPOTHETICAL 33.2 KD P	CHROMOSOME SEGREGATION	HYPOTHETICAL 117.4 KD	STE6 PROTEIN.	HPR1 PROTEIN.	VERY HYPOTHETICAL 21.7	INSERTION ELEMENT IS91	INSERTION ELEMENT IS91	CENTROMERIC PROTEIN E	DNA-DIRECTED RNA POLYM	PROBABLE ZINC PROTEASE	HYPOTHETICAL 104.8 KD	MEDIAN BODY PROTEIN.	HYPOTHETICAL 76.2 KD P	PEROXISOME ASSEMBLY PR
5.97e+01 5.97e+01	5.97e+01	5.97e+01	5.97e+01	5.97e+01	5.97e+01	3.93e+01	3.93e+01	3.93e+01	3.93e+01	3.93e+01	3.93e+01	3.93e+01	2.56e+01	2.56e+01	2.56e+01	2.56e+01	2.56e+01	2.56e+01	2.56e+01

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SEQUENCE OF 26-115.

MEDILNE; 74142666.

HAMILTON J.W., NIALL H.D., JACOBS J.W., KEUTMANN H.T.,

COHN D.V.;
                                                                                                                                                                                                                                                                      MEDLINE; 83105964.
MEDLINE; 83105964.
WEAVER C.A., GORDON D.F., KEMPER B.;
WEAVER C.A., FINDOCRINOL. 28:411-424(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE; 8005661.

KRONDENBERG H.M., MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A.,

POTTS J.T. JR., RICH A.;

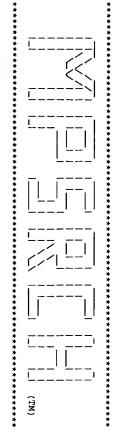
PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTH.
BOS TAURUS (BOVINE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTHY_BOVIN STANDARD; PRT; 115 AA. P01268; P1268; P120L-1986 (REL. 01, CREATED) P120L-1986 (REL. 01, LAST SEQUENCE UPDATE) P1-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
SEQUENCE OF 32-115. MEDLINE; 71063634.
                                       SEQUENCE OF 32-115.

MEDLINE; 71076162.

NIALL H.D., KEUTMANN H.T., SA

AURBACH G.D., POTTS J.T. JR.;

HOPPE-SEYLER'S Z. PHYSIOL. CH
                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE: 84262483.
WEAVER C.A. GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;
GENE 28:319-329(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EUTHERIA; ARTIODACTYLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
                                                                                                                             PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).
                                                                                                                                                                                                                                                                                                                                                   WEAVER C.A., GORDON D.F., KEMPER B.;
PROC. NATL. ACAD. SCI. U.S.A. 78:4073-4077(1981).
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE; 82037785.
                                           CHEM. 351:1586-1588(1970).
                                                                     SAUER R., HOGAN M.L., DAWSON B.F.,
                                                                                                                                                        POTTS J.T. JR.,
```



MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

bular output not generated. 01: Thu Jul 30 09:57:51 1998; MasPar time 6.04 Seconds 25.396 Million cell updates/sec

Title:
Description:
Perfect Score: >US-08-817-547A-1 (1-10) from US08817547A.pep 68

Sequence: 1 SVSEIQLMHN 10

Scoring table: PAM 150 Gap 15

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 16.093; Variance 66.058; scale 0.244

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

sult No.	Score	% Query Match	Length	DB	Ħ	Description	Pred. No
_	68	100.0	34	22	W17954	Human parathyroid hor	6.37e+00
2	68	100.0	34	22	9	n parathyroid	
ω	68		34	22	W17950	n PTH analoque	6.37e+00
4	89		34	22	W20006	۴.	6.37e+00
ر ت	68	100.0	34	7	R34366	Human parathyroid hor	٠
6	68	٠	34	7	R34362	Human parathyroid hor	6.37e+00
7	68	•	34	20	W14310	Cyclic parathyroid ho	6.37e+00
8	68		34	20	W14309	Cyclic parathyroid ho	6.37e+00
9	83	•	34	22	W17947	מ	6.37e+00
10	68	100.0	34	7	R34365		6.37e+00
11	68		34	7	R34364	Human parathyroid hor	6.37e+00
12	68		34	7	R34356		6.37e+00
13	68		34	9	R58228	ω	6.37e+00
 <b>4</b> .	68		36	9	R58301	[NMeAla36]-hPTH(1-36)	
J.	83		36	9	R58298	[NMeVal35]-hPTH(1-36)	6.37e+00
16	68	100.0	36	o	R58276	[Met(02)18]-hPTH(1-36	6.37e+00
17	68	٠	36	ø	R58275	[Ala16]-hPTH(1-36)-NH	6.37e+00
18	68	•	36	· φ	R58242	sopropy1)13]-	
19	68	100.0	36	9	R58191	[Ala34]-hPTH(1-36)-NH	6.37e+00

Query Match
Best Local Similarity 100.0%;

Score 68; DB 22; Length 34; Pred. No. 6.37e+00;

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
68	68	68	68	68	68	68	68	68	83	8	68	68	68	83	68	83	68	83	83	68	6 8	68	68	68	68
8	100.0	00.			•		100.0	٠	٠	•	•	•			8	00.	00.	8	8	100.0	•	00.	8	100.0	00.
229	84	84	84	47	44	38	ა 8	38	38	38	37	37	36	36	36	36	36	36	36	36	36	36	36	36	36
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R47971	R23790	W29420	W25687	W21946	P30015	R58109	R58097	R58077	R58105	R58131	Æ24778	R58244	R58274	R39450	R58249	R58288	R58287	R58234	R58198	R58264	R58260	R58284	R58290	R58289	m
Sequence of a full-le	Parathyroid hormone g	Human parathyroid hor	Human parathyroid hor	Fusion protien compri	Human parathyroid hor	4]-hPTH(1-38)	w	]-hPTH(1-38)	4]-hPTH(1-38	[Gly19]-hPTH(1-38)-OH	hPTH(1-37)-amide/ethy	٠.	]-hpTH(1-36)-N	1-(hPTH 3-3	) HTTdd - []	(1-36)-	]-hpTH(1-36)-	-hPTH(1-36	3]-hPTH	hPTH(1-3	2]-hPTH(1-	23	1 - 3	[Ala25]-hPTH(1-36)-NH	[D-Met18]-hPTH(1-36)-
•	6.37e+00	6.37e+00	٠.	ω	6.37e+00	٠.		w		6.37e+00		<u>ښ</u>		6.37e+00		6.37e+00		6.37e+00	6.37e+00	ښ.	:	٠.,	:	6.37e+00	6.37e+00

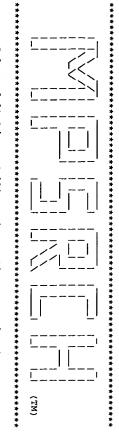
88888	ននន	ဂ္ဂ	88	នួន	38	PS	Η H	d d H	DR	דק	PΑ	PR	PR	PR	'n,	PD	PN	ΗŢ	ΗŢ	ΗT	FΤ	ΉH	သ	လ္ထ	KW	Χ¥	Į.	g ?	3 8	RESULT
N.B. The present sequence does not appear in the specification. It corresponds to the known hPTH 1-34 fragment with the modifications as stated in the claim.  Sequence 34 AA;	medicine for treatment of osteoporosis and bone fracture, optionally in conjunction with anti-resorptive therapy (bisphosphonates and calcitonin).	alogues stimulate bone growth and so are useful in	is alpha-aminoisobutyric acid (Aib). In this example the Glu residue at position 19 of the wild-type has been substituted by Aib. The hPTH	12, 16, 1	a specific example of a human parathy	e -; 33pp; English.	bone fracture		WPI; 97-118819/11.				06-SEP-1995; US-003305.		03-JUL-1996; U11292.	30-JAN-1997.		/note= "In amide form"		/label= Aib	ified_site	Key Location/Qualifiers	Synthetic.	Homo sapiens.			₹	29-JUL-1997 (first entry)	bediedata, peperae,	1 1705/ standard: pontido: 3/

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                                                                                                                                                                                     Search completed: Thu Jul 30 09:58:02 1998 Job time: 11 secs.
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                                                                                         밁
                                                                                                                                                                            PI Dong ZX;

PR WPI: 97-18819/11.

PR New variants of human parathyroid hormone 1-34 peptide - which PT New variants of human parathyroid hormone fracture stimulate bone growth and are used for treatment of osteoporosis and property bone fracture property from fragment 1-34 in which at least one confunction and residues at positions 3, 12, 16, 17, 19 and 34 confunction and fragment 1-34 in which at least one confunction and fragment fragment 1-34 in which at least one confunction and fragment fragment 1-34 in which at least one confunction and of the wild-type has been substituted by Aib. The hPTH canalogues stimulate bone growth and so are useful in human or veterinary confunction with anti-resorptive therapy (bisphosphonates and conjunction with anti-resorptive therapy (bisphosphonates and conjunction).

CC N.B. The present sequence does not appear in the specification. It corresponds to the known hPTH 1-34 fragment with the modifications case stated in the claim.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                    uery Match 100.0%;
est Local Similarity 100.0%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JAN-1997.
03-JUL-1996; U11292.
13-JUL-1995; US-001105.
06-SEP-1995; US-003305.
29-MAR-1996; US-626186.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JUL-1997 (first entry)
Human parathyroid hormone analogue [Aib34]hPTH(1-34)NH2.
Osteoporosis; agonist; PTH; human; anti-resorptive therapy;
bone fracture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LT 2
W17955 standard; peptide; 34
W17955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9702834-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BIOM-) BIOMEASURE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Н
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                                                           1 svseiqlmhn 10
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1 SVSEIQLMHN 10
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34
/label- Aib
/note- "In amide form"
                                                                                                                       Score 68; DB 22; Le
Pred. No. 6.37e+00;
0; Mismatches 0;
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                                                                                                                                                    Length 34;
                                                                                                                            Indels
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                                                                                                                            0;
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                                                                                                                          Gaps
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                                                                                                                            0;
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

n on: Thu Jul 30 09:57:07 1998; MasPar time 3.27 Seconds 111.690 Million cell updates/secondar output not generated.

Title: >US-08-817-547A-1
Description: (1-10) from US08817547A.pep
Perfect Score: 68
Sequence: 1 SYSEIQLMHN 10

Scoring table: PAM 150 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 22.419; Variance 28.455; scale 0.788

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

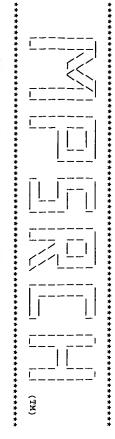
23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	œ	7	6	s	4	ω	N	_	sult	
46	46	47	47	48	48	50	53	53	53	57	57	59	59	61	63	64	64	66	68	68	68	68	Score	
67.6	67.6	69.1						•	•		83.8	•	•	•	•	•	94.1	97.1	100.0	•	100.0		Query	•
843	445	176	108	1015	448	383	34	34	34	35	34	115	37	115	119	105	36	115	115	115	37	34	Length	
Ν	N	N	N	N	N	N	u	σ	տ	ű	U	μ	ر.	N	N	N	Ŋ	N	ب	ш	ហ	G	BB	
A40970	B40970	S27192	S23204	S55474	S76701	B42377	12WF	12WG	1ZWE	12WD	1HTH	PTBO	1ZWC	JC4202	A34937	I51851	1ZWB	A05091	PTPG	PTHU	1HPH	12WA	ID	
1 - human (f	2 - human (f		retinol-binding prote	Human giant larvae ho	hypothetical protein	acetylornithine deace	parathyroid hormone 4	parathyroid hormone 4	parathyroid hormone (	parathyroid hormone (	rt	roid hormone	parathyroid hormone (	lhormone		hormone	hormone	parathyroid hormone p	hormone	hormone	parathyroid hormone f	parathyroid hormone (	Description	
2.76e+01	. 2	-		1.12e+01	1.12e+01				.07€	.48e-	1.486	ر.	.34€	.89e-	. 60e	ω,	3.87e-03	. 326	4.43e-04	4.436	4.4	4.4	Pred. No.	

45	44	43	42	41	40	39	38 8	37	36	35	34	33	32	31	30	29	28	27	26	25	24
44	44	44	44	44	44	44	45	45	45	45	45	45	45	45	45	45	45	45	46	46	46
64.7	64.7	64.7	64.7	64.7	64.7	64.7	66.2	66.2	66.2	66.2	66.2	66.2	66.2	66.2	66.2	66.2	66.2	66.2	67.6	67.6	6/.6
610	557	553	542	508	490	338	494	444	405	393	324	209	177	177	177	176	175	152	2163	1371	1034
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A49082	TLBPT3	TLBPF7	S56651	A43713	S71776	JGECT	S64386	PC4436	E64995	GIMSM	GIMS	PTHU3L	JC4201	PTHU2L	A30012	S10202	JN0103	S14236	S50675	S77521	535/58
calcium-dependent pro	tail fiber protein -	tail fiber protein -	probable calcium-depe	calcium-dependent pro	calcium-dependent pro	-	pre-mRNA splicing pro	monoclonal antibody 1	hypothetical protein	gamma-1	Ig gamma-1 chain C re	parathyroid hormone-r	parathyroid hormone-r	parathyroid hormone-r	parathyroid hormone-1	parathyroid hormone-r	н	Ig gamma-1 chain C re	pre-mRNA splicing hel	O	mgil protein - mouse
6.57e+01	6.57e+01	6.57e+01	6.57e+01		6.57e+01	6.57e+01	4.27e+01	4.27e+01	4.27e+01	4.27e+01	4.27e+01	4.27e+01	4.27e+01	4.27e+01	4.27e+01	4.27e+01	4.27e+01	4.27e+01	2.76e+01	2.76e+01	2./be+01

RESULT 2  ENTRY  IHPH #type complete parathyroid hormone fragment 1 37 (hpth(1-37)) (NMR, 10  Structures) - synthetic  ORGANISM #formal_name synthetic  REFERENCE A65802	19-30 #Tegion helix (right hand alpha) SUMMARY #length 34 #molecular-weight 4118 #checksum 5629 Query Match 100.0%; Score 68; DB 5; Length 34; Best Local Similarity 100.0%; Pred. No. 4.43e-04; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Db 1 SVSEIQLMHN 10	sapiens #com J.C. cookhaven Pro cookhaven Pr	RESULT 1  ENTRY 12WA #type complete TITLE parathyroid hormone (residues 1-34) - human ALTERNATE_NAMES HPTH(1-34)  PDB_TITLE structure of human parathyroid hormone fragment 1-34, NMR 10
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17-28
SUMMARY
                                                                                                         gg
                                                                                                                                                                                                                                                                                                                                      100.0%; Score 68; DB 5; Length 37; Query Match 100.0%; Pred. No. 4.43e-04; Indels 0; Gaps 0; Best Local Similarity 100.0%; Pred. No. 4.4se-04; Indels 0; Gaps 0; Matches 10; Conservative 0; Mismatches 0; Indels 0; Mismatches 0;
#region helix (right hand alpha)
#length 37 #molecular-weight 4401 #checksum 3791
```

search completed: Thu Jul 30 09:57:31 1998 Job time : 24 secs.



MPsrch\_pp n on: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 09:55:44 1998; MasPar time 2.16 Seconds 116.271 Million cell updates/sec

bular output not generated.

Description: Perfect Score: Title: >US-08-817-547A-1 (1-10) from US08817547A.pep 68 1 SVSEIQLMHN 10

Sequence:

Scoring table:

PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 23.348; Variance 23.508; scale 0.993

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

3 66 100.0 113 3 66 97.1 115 4 63 92.6 119 5 61 89.7 115 6 59 88.8 115 7 50 73.5 369 7 7 73.5 383	No. Score Match Length
1115 1119 1119 1115 1115 1115 1115 1115	h DB
PTHY PIG PTHY CANFA PTHY CANFA PTHY CONGL PTHY BOVIN PROB CORGL ARGE ECOLI RETI ONCMY Y413 ARATH BRRZ YEAST PTHR CHICK PTHR CHICK PTHR CANFA PTHR CANFA PTHR CANFA PTHR HAD PTHR HAD PTHR HAD PTHR HAD PTHR HAD PTHR HAD PTHR HAD	ID
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3.53e-05 3.53e-05 3.57e-04 3.25e-03 3.25e-03 6.99e-01 3.65e+00 3.65e+00 3.65e+00 1.05e+01 1.05e+01 1.05e+01 1.05e+01 1.05e+01 1.05e+01 1.05e+01 1.05e+01 1.05e+01 1.05e+01	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	<u>3</u>	30	29	28	27	26	25	24
42	42	42	42	43	43	43	43	43	43	43	43	43	43	43	44	44	44	44	44	44	44
61.8	61.8	61.8	61.8	63.2	63.2	63.2	63.2	63.2	63.2	63.2	63.2	63.2	63.2	63.2	64.7	64.7	64.7	64.7	64.7	64.7	64.7
2345	1967	551	312	1436	1136	1134	1069	870	842	651	537	444	295	103	610	557	553	542	534	508	338
ш	Н	Ь	Н	Н	Н	Ь	ш	ш	Ь	Ц	ш	۳	ш	μ	μ	μ	Н	Н	ب	$\vdash$	ᆫ
COAC_RAT	YG50_YEAST	Y275_HAEIN	Y085_MYCPN	WC11_BOVIN	TIE1_BOVIN	TIE1_MOUSE	ENTK_MOUSE	COPG_CAEEL	AMPN_LACDL	YHJK_ECOLI	AREH_SCHPO	PGL2_ARATH	LPLC_BACSU	YF17_HAEIN	CDP1_ARATH	VTFP_BPT3	VTFP_BPT7	CDP3_ORYSA	CDP1_ORYSA	CDPK_SOYBN	CYSP_ECOLI
ACETYL-COA CARBOXYLASE	PUTATIVE RNA HELICASE	HYPOTHETICAL PROTEIN H	HYPOTHETICAL PROTEIN M	ANTIGEN WC1.1.	TYROSINE-PROTEIN KINAS	TYROSINE-PROTEIN KINAS	ENTEROPEPTIDASE (EC 3.	PROBABLE COATOMER GAMM	AMINOPEPTIDASE N (EC 3	HYPOTHETICAL 73.1 KD P	PROBABLE STEROL O-ACYL	EXOPOLYGALACTURONASE C	LPLC PROTEIN.	HYPOTHETICAL PROTEIN H	CALCIUM-DEPENDENT PROT	TAIL FIBER PROTEIN.	TAIL FIBER PROTEIN.	CALCIUM-DEPENDENT PROT	CALCIUM-DEPENDENT PROT	CALCIUM-DEPENDENT PROT	THIOSULFATE-BINDING PR
4.76e+01	4.76e+01	4.76e+01	4.76e+01	2.91e+01	2.91e+01	2.91e+01	2.91e+01		2.91e+01	2.91e+01	2.91e+01	2.91e+01	2.91e+01	2.91e+01	1.76e+01	1.76e+01	1.76e+01	1.76e+01	1.76e+01	1.76e+01	1.76e+01

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(IN) CALCIUM-REGULATING HORMONES, TALMADGE K.V., OWEN M., PARSONS J.A., EDS., PP.9-14, EXCERPTA MEDICA FOUNDATION, AMSTERDAM, (1975). [7]	J.T. JR.;	SEQUENCE OF 75-100.	EMIST	DOTTE IT ID:	855.	UENCE		ACAD SCT H S A 7	R.T., JACOBS J		UENCE		NATURE 249:155-157(1974).	# 17	SEQUENCE OF 26-37.		A. 80:2127	VASICER T.J., MCCEVITT B.E., EREEMAN M.W., FENNICK B.J., HENDY G.N., POTTS J.T. JR., RICH A., KRONENBERG H.M.;	; 83109834.			NATL. ACAD. SCI. U.S.A. 78:7365-7369(1981).	N., KRONENBERG H.M.,	821508	SECULENCE EROM N. A.	ECTHERIA; PRIMATES:	ĭ.	HOMO SAPIENS (HUMAN).		HORMONE PRECURE	35, LAST ANNOTATIO	REL 05	(REL.	BOTOTON GIONNAM, FAI, III FAI.	

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Thu Jul 30 13:37:52 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYNTHESIS OF 32-65.

SYNTHESIS OF 32-65.

MEDILINE: 75059220.

TREGEAR G.W., VAN RIETSCHOTEN J., GREEN E., NIALL H.D.,
TREGEAR G.W., VAN RIETSCHOTEN J.,
TREGEAR G.W., VAN RIETSCHOTEN J.,
TREGEAR G.W., VAN RIETSCHOTEN J.,
KEUTMANN H.T., PARSONS J.A.,
KEUTMANN H.T., PARSONS J.A.,
KEUTMANN H.T., PARSIOL. CHEM. 355:415-421(1974).
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AUDILINE: 73227467.

ANDREATURA R.H., HARTWANN A., JOEHL A.,

ANDREATURA R.H., SIEBER P.;

RINIKER B., RITTEL W., SIEBER P.;

RINIKER B., RITTEL W.,

RINIKER B., RINIKER B.,

RINIKER B., R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WARLANT ARG-18.

VARIANT ARG-18.

ARNOLD A. HORST S.A., GARDELLA T.J., BABA H., LEVINE M.A., ORDER S.A., ORDER S.A., ORDER S.A., CLIM. INVEST. REJECTION.

REAL J. CLIM. INVEST. 86:1084-1087(1990).

CC C. INVEST. 86:1084-1087(1990).

CC C. INVEST. 86:1084-1087(1990).

CC C. INVEST. 86:1084-1087(1990).

CC C. INVEST. BELEVATES CALCIUM LEVEL BY DISSOLVING THE SALIES OF FAMILIAL ISOLATED

CC C. INVEST. BELEVATES CALCIUM.

CC C. INVEST. STANLAR ARE A CAUSE OF FAMILIAL ISOLATED

CC C. INVEST. SALIES OF FAMILI
                                                                                                                                        STRUCTURE BY NMR OF 32-65.
STRUCTURE; 91299748.
MEDLINE; 91299748.
T. WRAY V., SCHOMBURG D., WINGENDER E.,
KLAUS W., DIECKMANN T., WRAY V.,
BIOCHEMISTRY 30:6936-6942(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRUCTURE BY NMR OF 32-65.
STRUCTURE; 93345518.
MEDLIKE; 93345518.
CUTHBERTSON R.M.;
BARDEN J.A., CUTHBERTS1315-321(1993).
EUR. J. BIOCHEM. 215:315-321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRUCTURE BY NMR OF 32-68.
MEDLINE: 95318084.
MEDLINE: 95318084.
MOUNTED BY NMR OF 32-68.
MARX U.C., AUSTENANN S., BAYER P., ADERMANN K.,
STICHT H., WALTER S., SCHMID F.-X., JAENICKE R.,
STICHT H., WALTER S., SCHMID F.-X.,
STICHT H., WALTER S., SCHMID F.-X., JAENICKE R.,
STICHT H., WALTER S., SCHMID F., WALTER S., WALTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDB: 1ZWB: 12-MAR-97
PDB: 1ZWB: 12-MAR-97
PDB: 1ZWC: 12-MAR-97
PDB: 1ZWC: 12-MAR-97
PDB: 1ZWC: 12-MAR-97
PDB: 1ZWB: 12-MAR-97
PDB: 1ZWB: 16-JUN-97
PDB: 1ZWB: 16-JUN-97
PDB: 1ZWB: 16-JUN-97
100.0%; Query Match 100.0%; Best Local Similarity 100.0%; Best Local 10, Conservative Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BIOL. CHEM. 270:15194-15202(1995).
                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                  HORMONE;
                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                         VARIANT
                                                                                                                                                                                                                                                     'TE; PS00335; PARATHYROID; 1.
TE; PS00335; PARATHYROID; 1.
TE; SIGNAL; DISEASE MUTATION; 3L
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                                                                                                                                                                                                                              107
                                                                                                                                                                                           12861 MW;
                                                      Score 68; DB 1; Le
score No. 9.25e-06;
pred. No. 9.25e-06;
0; Mismatches 0;
                                                                                                                                                                                               PARATHYROID HORMONE.
C -> R (IN FIH; LEADS TO INEFFICIENT
C -> R (IN FIH; PRECURSOR).
PROCESSING OF THE PRECURSOR).
N -> D (IN REF. 5).
1243E87C7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KAMBER B., MAIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                    3D-STRUCTURE.
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                                                                                                                                                            Length 115;
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                                                                                                     Indels
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01-JAN-1988 (
01-FEB-1996 (
PARATHYROID H
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||||||||
1 SVSEIQLMHN 10
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SEQUENCE; 87316938.
MEDLINE; 87316938.
SCHMELZER H.-J., GR(
SCHMELZER H.-J., GR(
NUCLEIC ACIDS RES. 1
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA;
EUTHERIA; ARTIODACTYLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches
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SEQUENCE OF 26-115.
MEDILINE; 76018954.
CHU L.L.H., HUANG W.-Y., LITTLEDIKE E.T., HAMILTON J.W.,
BIOCHEMISTRY 14:3631-3635(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAUER R.T., NIALL H.D., HOGAN M.L., KEUTWANN H.T., O'RIORDAN J.L. SAUER R.T., NIALL H.D., HOGAN M.L., KEUTWANN H.T., O'RIORDAN J.L. POTTS J.T., JR.; 1994-1999(1974).

BIOCHEMISTRY 13:1994-1999(1974).

1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS ENCITOR.

1- FUNCTION: PTH ELEVATES CALCIUM LEVER BY DISSOLVING THE SALTS ENCITOR.

1- FUNCTION: PROSTE; PTPG.

PIR: A01535; PTPG.

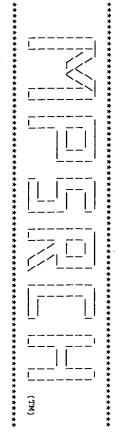
PIR: B26806: B26806.

PIR: B26806: B26806.

PIR: PSO0335; PARATHYROID; 1.
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Local Similarity 100.0%;
Local Similarity 100.0%;
Local Similarity 100.0%;
Local Similarity 100.0%;
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(REL. 06, LAST SEQUENCE UPDATE)
(REL. 33, LAST ANNOTATION UPDATE)
(REL. 33, CAST ANNOTATION (PPARATHYRIN) (P)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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S. 15:6740-6740(1987).
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12852 MW;
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31
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pred. No. 9.25e-06;
pred. No. 9.25e-06;
0; Mismatches 0;
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98B67F47 CRC32;
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Gaps

0



MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

on: bular output not generated. Thu Jul 30 09:56:12 1998; MasPar time 3.80 Seconds 110.885 Million cell updates/sec

Description: Perfect Score: Sequence: Scoring table: Title: PAM 150 Gap 15 >US-08-817-547A-1 (1-10) from US08817547A.pep 68 1 SVSEIQLMHN 10

Searched: 140542 segs, 42109429 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb15

Statistics: Mean 22.590; 1:sp\_fung1 2:sp\_human 3:sp\_invertebrate 4:sp\_mammal 5:sp\_mhc 6:sp\_organelle 7:sp\_phage 8:sp\_plant 9:sp\_bacteria 10:sp\_rodent 11:sp\_virus 12:sp\_vertebrate 13:sp\_unclassified Variance 21.849; scale 1.034

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

1 3 3 3 4 4 4 4 1 1 1 1 1 1 1 1 1 1 1 1	Result
04444444444444444444444444444444444444	Score
5544.20222225655651	% Query Match
105 248 445 266 465 266 465 266 476 405 1103 405 276 401 1440 1440 1440 1440 1440 1440 1440	Length
100 100 100 100 100 100 100 100 100 100	BB
Q63473 Q63473 Q58833 Q14581 Q14581 Q05708 Q05708 Q05707 Q61856 P73337 Q21996 P77215 Q31210 P70366 Q61202 Q61202 Q61202 Q61202 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q61203 Q6	SUMMARIES ID
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SUBMITTED (AUG-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
TO CATALYTIC ACTIVITY: ATP + N-ACETYL-L-GLUTAMATE 5-PHOSPHATE.
ADP + N-ACETYL-L-GLUTAMATE 5-PHOSPHATE.
EMBL; X99978; E284231; TRANSFERASE.
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Score 63; Pred. No.

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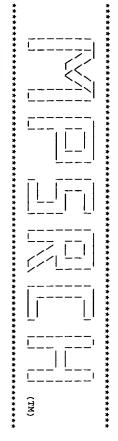
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prints of human parathyroid hormone 1-34 peptide - which DR WPI; 97-118819/11.

Present so f human parathyroid hormone 1-34 peptide - which PT stimulate bone growth and are used for treatment of osteoporosis and PT stimulate bone growth and are used for treatment of osteoporosis and PT bone fracture;

Probone fracture is a specific example of a human parathyroid probone fracture is a specific example of a human parathyroid of the present sequence is a specific example of a human parathyroid of the present sequence at positions 3, 12, 16, 17, 19 and 34 of the wild-type has been substituted by Aib. The hPTH cat appear analogues stimulate bone growth and so are useful in human or veterinary analogues stimulate bone growth and so are useful in human or veterinary completion for treatment of osteoporosis and bone fracture, optionally in calcitonin). With anti-resorptive therapy (bisphosphonates and conjunction with anti-resorptive therapy (bisphosphonates and conjunction
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30-JAN 1997.
30-JUL-1996; U11292.
03-JUL-1995; US-001105.
06-SEP-1995; US-003305.
29-MAR-1996; US-625186.
29-MAR-1996; US-625186.
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Human parathyroid hormone analogue [Aib34]hpTH(1-34)NH2.
Osteoporosis; agonist; PTH; human; anti-resorptive therapy;
bone fracture.
Homo sapiens.
Synthetic.
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

n on: Thu Jul 30 09:59:20 1998; MasPar time 3.14 Seconds 104.825 Million cell updates/sec

bular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-817-547A-2 (1-9) from US08817547A.pep 63 1 SVSEIQLMH 9

Scoring table: PAM 150 Gap 15

Searched: 120441 segs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 21.980; Variance 26.868; scale 0.818

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

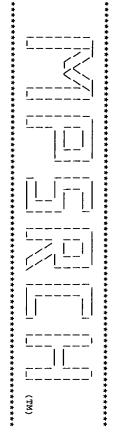
#### SUMMARIES

52 82.5 34 5 52 82.5 35 5 48 76.2 34 5 48 76.2 34 5 48 76.2 1015 2 47 74.6 383 2 47 74.6 448 2 46 73.0 445 2 46 73.0 1034 2 47 71.4 152 2	Sult No. 1 2 3 3 4 4 6 6 7 7 10	54	Query Match 100.0 100.0 100.0 100.0 96.8 93.7 93.7 93.7 93.7 93.7 93.7 93.7 93.7	Length34 37 315 115 115 115 115 115 115 115 115 115	-522552++55 <del>  B</del>	12WA 11WA 11HPH PTIPG A05091 12WB 15185 15185 15185 15187 A34937 744202 12WC PTBO	1	
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47 74.6 448 2 46 73.0 445 2 46 73.0 843 2 46 73.0 1034 2 45 71.4 152 2	18	47	74.6	383	N	B42377	acetyl	acetylornithine deace
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46 73.0 843 2 46 73.0 1034 2 45 71.4 152 2	20	46	73.0	445	N	B40970	undulin	2 - }
46 73.0 1034 2 45 71.4 152 2	21	46	73.0	843	N	A40970	undulin	1 -
45 71.4 152 2	22	46	73.0	1034	N	S36758	mgl1 p	53
	23	45	71.4	152	2	S14236	Ig gam	gamma-1 chain C re

45	44	43	42	41	40	39	38	37	36	<u>υ</u>	34	ω ω	32	31	30	29	28	27	26	25	24
42	42	42	42	42	43	43	43	43	43	43	43	43	43	43	44	44	44	45	45	45	40
66.7	66.7	66.7	•	66.7	•	•		•	•		68.3	•	•		•		69.8	•	71.4	71.4	71.4
619	579	176	176	116	2163	1136	1134	1057	651	402	247	225	167	103	557	553	99	1371	444	393	324
N	N	N	N	N	N	<b>,</b>	بر	N	N	N	N	N	N	Ν	ب	_	2	N	2	ب	٢
I59558	S54872	S10202	S27192	S22553	S50675	S57845	JN0711	138171	S47750	S76629	S60307	S77105	E69768	D64034	TLBPT3	TLBPF7	C64489	S77521	PC4436	G1MSM	GLMS
dopamine transporter	penicillin-binding pr		tinol-binding p	Ig heavy chain V regi	ıΩ	protein-tyrosine kina	protein-tyrosine kina		thetical p	thetical pr	3	ַק	thetical	hypothetical protein		fiber pr	hypothetical protein	sensory transduction	noclonal	Ig gamma-1 chain C re	ig gamma-i chain c re
	9.79e+01		9.79e+01			6.32e+01	6.32e+01	6.32e+01	6.32e+01	6.32e+01	6.32e+01	6.32e+01	6.32e+01	6.32e+01	4.05e+01	4.05e+01	4.05e+01	2.57e+01	2.57e+01	2.57e+0	2.5/e+U

ū Š	RESULT 2  ENTRY 1HPH #type complete  TITLE structures) - synthetic  ORGANISM #formal_name synthetic  REFERENCE A65802  # submission submitted to the Brookhaven Protein Data Bank, February 1995 # comment Resolution: not applicable COMMENT Resolution: not applicable COMMENT Resolution: not applicable COMMENT Revalue: no refinement KEYWORDS hormone FEATURE #region helix (right hand alpha)\	6-9 #region helix (right hand alpha)\ 19-30 #region helix (right hand alpha)\ SUMMARY #length 34 #molecular-weight 4118 #checksum 5629  Query Match 100.0%; Score 63; DB 5; Length 34; Best Local Similarity 100.0%; Pred. No. 2.58e-03; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  Db 1 SVSEIQLMH 9	RESULT  ENTRY  ENTRY  PARATHYROId hormone (residues 1-34) - human  ALTERNATE NAMES HPTH(1-34)  PDB_TITLE  ORGANISM structure of human parathyroid hormone fragment 1-34, NMR 10  REFERENCE Structures  ORGANISM #formal_name Homo sapiens #common_name man  ROP856
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	<pre>search completed: Thu Jul 30 09:59:39 1998 job time : 19 secs.</pre>	Query Macco Similarity 100.0%; Pred. NO. 2.50 0; Indels 0; Gaps Best Local Similarity 00; Mismatches 0; Indels 0; Gaps Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps Matches 1; Mismatches 0; Mismatches 0; Indels 0; Gaps Matches 1; Mismatches 0; Mismatches 0; Indels 0; Gaps Matches 1; Mismatches 0; Mismatches	plecular-weight 4401 #checksum 3791 score vo 2 58e-03:
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Thu Jul 30 09:58:20 1998; MasPar time 2.06 Seconds 109.762 Million cell updates/sec

bular output not generated.

Title: Description: Perfect Score: Sequence: >US-08-817-547A-2 (1-9) from US08817547A.pep 63 1 SVSEIQLMH 9

Scoring table: PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 22.879; Variance 22.094; scale 1.036

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

No. S	Score	Query Match	Length [	: B	ID	Description	Pred.
, <b>_</b>	5 3	100.0	115		PTHY_HUMAN	HORMONE	
2	63	100.0	115	٢	PIHY_PIG	HORMONE	
w	61		115	ш	PTHY_RAT	HORMONE	
4	58		119	μ.	PTHY_CHICK	HORMONE	
σı	56	88.9	115	<b></b>	PTHY_CANFA	HORMONE	
σ	54		115	ببر	PTHY_BOVIN	HORMONE	
7	50		369	μ	PROB_CORGL	GLUTAMATE 5-KINASE (EC	
00	47	74.6	383	<b> </b>	ARGE_ECOLI	ጸ.	
Q	47	74.6	435	μ	Y413_ARATH	HYPOTHETICAL 48.8 KD P	
10	45	71.4	324	۲	GC1_MOUSE	IG GAMMA-1 CHAIN C REG	
11	<b>4</b> 5		393	1	GC1M_MOUSE	IG GAMMA-1 CHAIN C REG	ر ن
12	44	69.8	151	_	LE14_GOSHI	LATE EMBRYOGENESIS ABU	9
13	44	69.8	553	٢	VTFP_BPT7	TAIL FIBER PROTEIN.	
14	44	69.8	557	1	VIFP_BPI3	TAIL FIBER PROTEIN.	
15	43	68.3	103	_	YF17_HAEIN	HYPOTHETICAL PROTEIN H	
16	43	68.3	651	μ	YHJK_ECOLI	HYPOTHETICAL 73.1 KD P	
17	43	68.3	1069	_	ENTK_MOUSE	ENTEROPEPTIDASE (EC 3.	
18	43	68.3	1134	μ	TIE1_MOUSE	TYROSINE-PROTEIN KINAS	
19	43	68.3	1136	۲	TIE1_BOVIN	TYROSINE-PROTEIN KINAS	μ.
20	43	68.3	2163	_	BRR2_YEAST	PRE-MRNA SPLICING HELI	
21	42	66.7	175	_	PTHR_MOUSE	PARATHYROID HORMONE-RE	
22	42	66.7	176	1	RET1_ONCMY	PLASMA RETINOL-BINDING	
23	42	66.7	176	_	RET2_ONCMY	PLASMA RETINOL-BINDING	

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
41	41	41	41	41	41	41	41	41	41	41	42	42	42	42	42	42	42	42	42	42	42
65.1	65.1	65.1	•	•	•	65.1	•		65.1	65.1	66.7	66.7		66.7	•	•	•	66.7	•	66.7	66.7
2109	1967	1443	835	726	628	626	481	360	312	259	1643	870	619	610	542	534	508	177	177	177	176
ب	<del> </del>	<b> </b> 4	μ	μ	سا	μ.	Н	Н	Н	<b>ب</b>	۳	س	μ	μ	μ	مبو	٢	۳	<u>س</u>	Н	ш
RRPL_VSVSJ	YG50_YEAST	DP31_MYCPN	VIRL_AGRT6	YCCC_ECOLI	TESK_RAT	TESK_HUMAN	KRCB_HUMAN	CWLL_BACLI	Y085_MYCPN	YZ24_METJA	RRPO_NMV	COPG_CAEEL	NTDO_RAT	CDP1_ARATH	CDP3_ORYSA	CDP1_ORYSA	CDPK_SOYBN	PTHR_RAT	PTHR_HUMAN	PTHR_CANFA	PTHR_CHICK
RNA POLYMERASE BETA SU	PUTATIVE RNA HELICASE	PUTATIVE DNA POLYMERAS	LIMITED HOST RANGE (LH	HYPOTHETICAL 81.2 KD P	TESTIS-SPECIFIC PROTEI	TESTIS-SPECIFIC PROTEI	RAC-BETA SERINE/THREON	N-ACETYLMURAMOYL-L-ALA	HYPOTHETICAL PROTEIN M	HYPOTHETICAL PROTEIN M	RNA REPLICATION PROTEI	PROBABLE COATOMER GAMM	SODIUM-DEPENDENT DOPAM	_	CALCIUM-DEPENDENT PROT	CALCIUM-DEPENDENT PROT	CALCIUM-DEPENDENT PROT	PARATHYROID HORMONE-RE	PARATHYROID HORMONE-RE	PARATHYROID HORMONE-RE	PARATHYROID HORMONE-RE
4.60e+01	4.60e+01	4.60e+01	4.60e+01	4.60e+01	4.60e+01	4.60e+01	4.60e+01	4.60e+01	4.60e+01	4.60e+01				2.76e+01					2.76e+01		2.76e+01

RN	25 E	RA A	RP R	잡	RA	R X	7 7	RN	RL	R A	RX	RP	RN	RL.	R.	RX	RP	2 7	3 3	RA	RX	RP	2 2	RA RA	RX	RP	R	88	S	GN	DE	Į,	3 5	3 2	šĖ	RESULT
(1975). [7]		KEUTMANN H.T., NIALL H.D., JACOBS J.W., BARLING P.M., HENDY G.N., O'RIORDAN J.L.H., POTTS J.T. JR.;		CHEMISTRY 1	r. JR.;	KEUTMANN H.T., SAUER M.M., HENDY G.N., O'RIORDAN J.L.H.,	SEQUENCE OF 61-83 AND 84-115.		SCI. U.S.A. 71:384-388(1974)	O'RIORDAN J.L.H., AURBACH G.D., POTTS J.T. JR.;		UENCE		249:155-157(1974).	JACOBS J.W. KEMPER B., NIALL H.D., HABENER J.F., POTTS J.T. JR.:		SEQUENCE OF 26-37.		G.N., POITS J.H. JR., RI	T.J., MCCEVITT B.E., FREEMAN M.W., FENNI	MEDLINE; 83169834.	SEQUENCE FROM N.A.	C. NAIH. ACAD. SCI. 0.S.A.	G.N., KRONENBERG H.M.	NE; 82150870.	SEQUENCE FROM N.A.	[1]	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	).		HORMONE PR	35, LAST	(RET. 05)	7-1771086 (BET. Ol. OBBATED)	THY HUMAN STANDARD; PRT; 115 AA.	1

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Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative
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MEDLINE: 7327467.

ANDREATTA R.H., HARRMANN A., JOEHL
ANDIKER B., RITTEL W., SIEBER P.;
RINIKER B., RITTEL W., SIEBER P.;
HELV. CHIM. ACTA 56:470-473(1973).
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MEDLINE; 75059220.

MEDLINE; 75059220.

TREGEAR G.W., VAN RIETSCHOTEN J., GREEN E., NIALL H.D.,

KEUTMANN H.T., PARSONS J.A., O'RIORDAN J.L.H., POTTS J.T.

KEUTMANN H.T., PARSONS J.A., 355:415-421(1974).

HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 355:415-421(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REVISIONS,
MEDLINE; 75146516.
KEUTMANN H.T., NIALL H.D., O'RIORDAN J.L.H.,
REJCHEMISTRY 14:1842-1847(1975).
                                                                                                                                                                                                                                                                EMBL: A29146;

PIR: A01536;

PIR: A01539;

PIR: A19339;

PDB: 1HPH; 10

PDB: 1HTH; 11

PDB: 1ZWA; 12

PDB: 1ZWB; 12

PDB: 1ZWB; 12

PDB: 1ZWD; 12

PDB: 1ZWB; 12

PDB: 1ZWB; 12

PDB: 1ZWB; 12

PDB: 1ZWB; 16

PDB: 1ZWB
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MEDLINE, 93345518.
BARDEN J.A., CUTHBERTSON R.M.;
EUR. J. BIOCHEM. 215:315-321(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KLAUS W., DIECKMANN T., WRAY V.,
BIOCHEMISTRY 30:6936-6942(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRUCTURE BY NMR OF 32-65.
MEDLINE; 91299748.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MARX U.C., AUSTERMANN S., BAYER P., ADERMANN K., STICHT H., WALTER S., SCHMID F.-X., JAENICKE R., ROESCH P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRUCTURE BY NMR OF 32-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BONE AND PREVENTING THEER REMAL EXCRETION.

-! DISEASE: DEFECTS IN PTH ARE A CAUSE OF FAN
HYPOPARATHYROIDISM (FIH).
EMBL; J00301; G190704;
EMBL; V00599; G37144;
EMBL; A29146; E186700;
-...
PIR; A01536; PTHU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 95318084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. CLIN. INVEST 86:1084-1087(1990).
-i- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 91009811.
ARNOLD A., HORST S.A., GARDELLA T.J.,
KRONENBERG H.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT ARG-18
                                                                                    CONFLICT
SEQUENCE
                                                                                                                                                                 PROPEP
CHAIN
                                                                                                                                                VARIANT
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                                                                                                                                                                                                                              HORMONE;
                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             вгог. снем. 270:15194-15202(1995).
                                                                                                                                              , PS00335;
; PS00335;
; SIGNAL; F
26
32
32
18
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12-MAR-97.
12-MAR-97.
12-MAR-97.
12-MAR-97.
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15-OCT-97.
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115
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                                                                                        ΑĄ;
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DISEASE MUTATION;
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12861
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31
115
18
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          Score 63; DB 1; 1
Pred. No. 7.43e-05;
0; Mismatches (
                                                                                        PARATHYROID HORMONE.

C -> R (IN FIH; LEADS TO INEFFICIENT C PROCESSING OF THE PRECURSOR).

N -> D (IN REF. 5).

; 243E87C7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCHOMBURG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:
                                                                                                                                                                                                                                      3D-STRUCTURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BABA H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KAMBER B.,
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                                                        Length 115;
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FORSSMANN W.-G.,
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                       Indels
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Search completed: Thu Job time: 7 secs.
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Best Local Similarity 100.0%;
Matches 9; Conservative
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P01269;
21-JUL-1986
01-JAN-1988
01-FEB-1996
PARATHYROID
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EUKARYOTA; METAZO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 26-115.

MEDLINE; 76018954.

CHU L.L.H., HUANG W.-Y., LITTLEDIKE E.T., HAMILTON J.W.,

BIOCHEMISTRY 14:3631-3635(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 32-115.

SEQUENCE OF 32-115.

MEDLINE; 74253317.

SAUER R.T., NIALL H.D., HOGAN M.L., KEUTMANN H.T., O'RI SAUER R.T., JR.;

POTTS J.T., JR.;

BIOCHEMISTRY 13:1994-1999(1974).

1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING DONE AND PREVENTING THEIR RENAL EXCRETION.

EMBL; X05722; G1839; T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDILINE; 87316938.
SCHWELZER H.-J., GROSS G., WIDERA G., MAYER
NUCLEIC ACIDS RES. 15:6740-6740(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUTHERIA; ARTIODACTYLA.
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SEQUENCE
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ITE; PS00335; PARATHYROID;
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(REL. 06, LAST SEQUENCE UPDATE)
(REL. 33, LAST ANNOTATION UPDATE)
HORMONE PRECURSOR (PARATHYRIN) (P
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32
115 /
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12852
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                                        09:58:27
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                                             1998
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Release 3.1A.John F. COILIANS, BLOCOMPUTING Research Unit. Copyright (c) 1931-1988 University of Edinburgh U. K. Copyright (c) 1931-1989 University Office U	11 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	10 H	Statistics: Pred. No score gr	Database:	Post-processing:	Scoring table: Searched:	Title: Description: Perfect Score: Sequence:	un on:		
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computing Research Unit.  yof Edinburgh, U.K.  ford Molecular Ltd.  ch, using Smith-Waterman alg  MasPar time 3.70 Seconds  102.472 Million cell update  103.472 Million cell update  103.472 Million cell update  104.5 Seconds  105.472 Million cell update  11.5 Parametrical 4: sp_mammal  12.5 Parametrical 4: sp_mammal  13.5 Callion cell update  14.5 Callion cell update  15.5 Callion cell update  15.5 Callion cell update  16.5 Callion cell update  16.5 Callion cell update  17.5 Callion cell update  18.6 Callion cell update  18.7 Callion ce		of the	Variance of result:	p_hur organ 10:sp	0.8 4.5 s	42109429 r	547A-2 US08817547A.pep 9	:58:46 1998	Collins, 998 Unive rights by	
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	ŝ	C49F5.2.		PENICILLIN-BINDING PRO		F47A4.3.		_			CALMODULIN-LIKE DOMAIN				NUCLEAR	EARLY BLASTULA	BASES 2347342	CONSERVED PROTEIN.	POLYPROTEIN.		TERMINAL PROTEIN.	HEXON PROTEIN.	45.8 KD	AGAMOUS PROTEIN.	

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RESULT
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Best Local Similarity 77.8%;
Matches 7; Conservative
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063473
063473
01-NOV-1996 (TREMBLREL 01, CREATED)
01-NOV-1996 (TREMBLREL 01, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL 05, LAST ANNOTATION UPDATE)
01-JAN-1998 (TREMBLREL 05, LAST ANNOTATION UPDATE)
PARATHYROLD HORMONE (FRAGMENT).
PTH.
                                                                                                                                                                                                                                                                                                                      LT 2
08320 PRELIMINARY; PRT; 248 AA.
008320;
01-JUL-1997 (TREMBLREL. 04, CREATED)
01-JUL-1997 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JUL-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
ACCETYLGLUTAMATE KINASE (EC 2.7.2.8).
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
[1]
                                                                                                                                                               ARGB.
LACTOBACILLUS PLANTARUM.
PROKARYOTA; FIRMICUTES; REGULAR ASPOROGENOUS ROD; LACTOBACILLACEAE.
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE-THYROID, AND PARATHYROID;
TISSUE-THERID, GROSS G., MAYER H.;
SCHMELZER H.J., GROSS G., MAYER H.;
ADV. GENE TECHNOL. 21:228-229(1984).
EMBL; M54875; G601933; -.

NON_TER 1 1 1
NON_TER 1 1746 MW; 6AC3163E CRC32;
SEQUENCE FROM N.A.
STRAIN-CCM 1904;
BRINGEL F., FREY L., BOIVIN S., HUBERT J.C.;
J. BACTERIOL. 179:0-0(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 AISEIQLMH 30
::||||||
1 SVSEIQLMH 9
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Pred. No. 6.56e-04;
2; Mismatches 0; Indels
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RN [2]

RD SEQUENCE FROM N.A.

RC STRAIN=CCM 1904;

RA BRINGEL F.;

RL SUBMITTED (AUG-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.

CC -!- CATALYTIC ACTIVITY: ATP + N-ACETYL-L-GLUTAMATE = CADP + N-ACETYL-L-GLUTAMATE 5-PHOSPHATE.

CR EMBL; X99978; E284231; -.

KW TRANSFERASE.

SQ SEQUENCE 248 AA; 26580 MW; 3E945D79 CRC32;

SQ SEQUENCE 248 AA; 26580 MW; 3E945D
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

n on: Thu Jul 30 10:02:44 1998; MasPar time 2.60 Seconds 47.195 Million cell updates/sec

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Description: Perfect Score: Title: >US-08-817-547A-3 (1-8) from US08817547A.pep 54 1 SVSEIQLM 8

Sequence:

Scoring table: PAM 150 Gap 15

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Mean 14.998; Variance 50.414; scale 0.298

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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R99981 R41565	W14312	R88829	R34357	R34359	W17955	W17954	R41559	R41560	W24273	W08131	W08130	W24276	R34360	R34361	W01610	R99978	R94192	Ĭ	
Porcine parathyroid h	c parathyroid	Human parathyroid hor				hyroid	<pre>{Gly27]hPTH (1-34).</pre>	[His27]hPTH (1-34).	Wild type parathyroid	Human PTH derivative,	Human PTH derivative,	Parathyroid hormone (	Human parathyroid hor	Human parathyroid hor	Parathryoid hormone a		Human parathyroid hor	Description	
	2.22e+01	2.22e+01	2.22e+01	2.22e+01	2.22e+01	2.22e+01	2.22e+01	2.22e+01	2.22e+01	2.22e+01	2.22e+01	2.22e+01	2.22e+01	2.22e+01	2.22e+01	2.22e+01	2.22e+01	Pred. No.	

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1 svseiqlm 8 |||||||| 1 svseiqlm 8

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3	⇁		Human parathyroid hor	-	מ		-	_	늪	PTH(1-36)-N	[D-Ser1]-hPTH(1-36)-N	[NMePhe34]-hPTH(1-36)	p30]-hPTH(1	]-hPTH(1-	[Ala16]-hPTH(1-36)-NH	ъ		rathyr	33, Ala34]-	ŝ	Human PTH derivative,	Human parathyroid hor	Human parathyroid hor	[F23,H25,H26,L27,I28,	[Glu16]hPTH (1-34).
	٠.				٠,			2.22e+01			٠		'n			2.22e+01		2.22e+01				2.22e+01		2.22e+01	2.22e+01

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Search completed: Thu Jul 30 10:03:01 1998 Job time: 17 secs.
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PF 10-MAR-1995; D08672.

PR 10-MAR-1995; D08672.

PR 10-MAR-1995; DE-008672.

PR (BOEF) BOENTRINGER MANNHEIM GMBH.

PA (BOEF) BOENTRINGER MANNHEIM GMBH.

PI Dony C. Esswein A. Hoffmann E. Honold K. Schaefer W;

PI Dony C. Esswein A. Hoffmann E. Honold K. Schaefer W;

PI Dony C. Esswein A. Hoffmann E. Honold K. Schaefer W;

PR WPI; 96-413519/42.

PR WPI; 96-413519/42.

PR WPI; 96-413519/42.

PR VIVO half life and are useful for treating osteoporosis and preventing epidermal cell proliferation

Disclosure; Page 9; 14pp; German.

New cyclic parathyroid hormone fragments (CPTH) have the amino acid sequence of h, b, p, r or cPTH(1-34), opt. extended by up to 4 amino acids (aa) at the C-terminus and opt. Shortened by up to 3 amino acids acids (aa) at the C-terminus and opt. Shortened by up to 3 amino acids the N-terminus, and are cyclised between positions 13 and 17. One of CC these positions is occupied by L- or D- Orn or Lys, and the other by L- or D- Glu or Asp. CPTH have calcium-regulating activity (esp. for CC treating psoriasis). The CPTH have an improved half life in vivo than CC capacity, reduced catabolic, calcium-mobilising activity and increased activity for calcium retention and incorporation into bone. The CC present sequence is that of human PTH peptide fragment (1-34).
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-APR-1997 (first entry)

Human parathyroid hormone peptide fragment (1-34).

cyclic parathyroid hormone fragment; calcium-regulating activity; osteoporosis; inhibit proliferation; epidermal cell; psoriasis; improved half life; calcium retention; bone.

Synthetic.

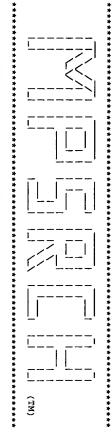
Synthetic.

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Synthetic.
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79978 standard; peptide; 34 AA.
R99978;
30-APR-1997 (first entry)
                                                                                                                                                                            1 svseiqlm 8
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1 SVSEIQLM 8
                                                                                                                                                                                                                                                                                                                                                             Match 100.0%;
Local Similarity 100.0%;
les 8; Conservative
                                                                                                                                                                                                                                                                                                                                                             Score 54; DB 20; Le
Pred. No. 2.22e+01;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 34;
                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                                                                                       0;
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Thu Jul 30 10:01:58 1998; MasPar time 3.10 Seconds 94.424 Million cell updates/sec

bular output not generated.

Title:
Description:
Perfect Score:
Sequence: >US-08-817-547A-3 (1-8) from US08817547A.pep 54 1 SVSEIQLM 8

Scoring table: PAM 150 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 21.117; Variance 23.944; scale 0.882

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

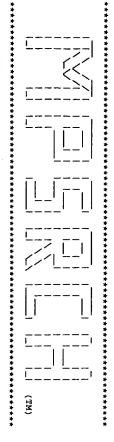
No.	500 re 544 554	0.0000 ith	Length 1 34 37 115 115	5 1 DB	ID 1ZWA 1HPH PTHU PTPG A05091		
л 🕰		100.0	115	٦ ٢	PTPG	parathyr	hormone
თს		96.3 92.6	115 36	υN	A05091	parathyroic parathyroic	hormone
7	50		105	Ņ	151851	parathyroid	
æ	49	•	119	Ν	A34937	parathyroid	_
9	47	•	115	N	JC4202	parathyroid	hormone
10	45	•	37	σ	1ZWC	parathyroid	yroid hormone (
11	45	•	115	Н	PTBO	parathyroid	yroid hormone p
12	43	79.6	34	Ŋ	1HTH	cyclic	thyroid h
13	43	•	35	ŲΙ	12WD	parathyroid	
14	43	•	167	N	E69768	hypotl	$\vdash$
15	43		1134	μ	JN0711	prote	ຜ
16	43	•	1136	Н	S57845	prote	protein-tyrosine kina
17	41	•	259	N	G64512	d ros	protein homolog -
18	41	•	260	N	A38114	reso	resolvase rsd – Salmo
19	41	•	312	N	S73934	MG085	mod
20	41	•	312	N	S66952	hypo	hypothetical protein
21	41	•	441	N	S41710	mito	mitosis-specific cycl
22	41		481	۲	A46288	protein	ein kinase (EC 2.
23	41	75.9	481	ν	JC2438	RAC F	tein kin

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	
39	39	39	39	39	40	40	40	40	40	40	40	40	41	41	41	41	41	41	41	41	;
72.2	72.2	72.2	72.2	72.2	74.1	74.1	74.1	74.1	74.1	74.1	74.1	74.1					75.9				
402	245	34	34	34	3124	1487	1150	1061	883	353	306	99	1371	896	896	835	605	591	591	590	000
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S76629	S75470	12WG	12WF	1ZWE	A40020	S62048	S49956	S37667	S31175	C69979	WMBE18	C64489	S77521	S76064	S59990	A27211	S36592	I52728	I38924	JC2468	
hypothetical protein	<pre>protein hglK - Synech</pre>	parathyroid hormone 4	parathyroid hormone 4	parathyroid hormone (	collagen alpha 1(XII)	probable membrane pro	probable membrane pro	traC-1 protein - Esch	hypothetical protein	conserved hypothetica	ribonucleoside-diphos	hypothetical protein	sensory transduction	hypothetical protein	e anchor	virA protein - Agroba	El protein - human pa	reduced folate carrie	reduced folate carrie	folate transporter -	TOTAL STREET, STOCK
1.52e+02	1.52e+02	1.52e+02	1.52e+02	1.52e+02	9.60e+01	9.60e+01	9.60e+01	9.60e+01	9.60e+01	9.60e+01	9.60e+01	9.60e+01	6.02e+01	6.02e+01	6.02e+01	6.02e+01	6.02e+01	6.02e+01	6.02e+01	6.02e+01	0.00

RESULT 2  ENTRY  IHPH  parathyroid hormone fragment 1 37 (hpth(1-37)) (NMR, 10  structures) - synthetic  ORGANISM  #formal_name synthetic  REFERENCE #authors #submission submitted to the Brookhaven Protein Data Bank, February 1995  #cross-references pDB:IHPH  COMMENT Resolution: not applicable COMMENT Resolution: NMR COMMENT R-value: no refinement KEYWORDS FEATURE #region helix (right hand alpha)\ #region helix (right hand alpha)\	Query Match 100.0%; Score 54; DB 5; Length 34; Best Local Similarity 100.0%; Pred. No. 6.75e-02; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Db 1 SVSETQLM 8	COMMENT Resolution: not applicable COMMENT Determination: NMR KEYWORDS hormone FEATURE #region helix (right hand alpha)\ 19-30 #region helix (right hand alpha)\ SUMMARY #length 34 #molecular-weight 4118 #checksum 5629	hors miss ss-r CE hors	RESULT 1  ENTRY TITLE  ALTERNATE_NAMES HPFH(1-34)  PDB_TITLE  Structure of human parathyroid hormone fragment 1-34, NMR 10  STRUCTURES  ORGANISM  REFERENCE  A67856
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Page 2

	Search completed: Thu Jul 30 10:02:26 1998 Job time : 28 secs.	Db 1 SVSEIQLM 8 0y 1 SVSEIQLM 8	17-28 #region helix (right hand alpha) SUMMARY #length 37 #molecular-weight 4401 #checksum 3791 Query Match 100.0%; Score 54; DB 5; Length 37; Query Match 100.0%; Pred. No. 6.75e-02; Best Local Similarity 100.0%; Pred. No. 6.75e-02; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps
			ω 0;



MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

n on: Thu Jul 30 10:00:33 1998; MasPar time 2.09 Seconds 95.854 Million cell updates/sec

bular output not generated.

Title:
Description:
Perfect Score:
Sequence: >US-08-817-547A-3 (1-8) from US08817547A.pep 54 1 SVSEIQLM 8

Scoring table: PAM 150 Gap 15

Searched: 69111 segs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 21.952; Variance 19.669; scale 1.116

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

45	44	43	42	41	40	39	38	37	36	35	34	3 3	32	31	30	29	28	27	26	25	24
39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	40	40	40
72.2	72.2	72.2	72.2	72.2	72.2	72.2	72.2	72.2	72.2	72.2	72.2	72.2	72.2	72.2	72.2	72.2	72.2	72.2	74.1	74.1	74.1
2109	1827	1436	1116	628	626	567	529	525	503	474	461	461	455	455	248	220	207	106	3124	1487	1150
ם	Ь	μ	Ь	مبر	<b>,</b>	H	H	Н	H	μ	ب	<b></b>	Н	<u>, , , , , , , , , , , , , , , , , , , </u>	щ	<u>, , , , , , , , , , , , , , , , , , , </u>	<u>س</u>	ш	ب	ب	ы
RRPL_VSVSJ	CUT1_SCHPO	WC11_BOVIN	RPOB_HETCA	TESK_RAT	TESK_HUMAN	CYDC_BACSU	HSF1_HUMAN	SP1_RARFA	HSF1_MOUSE	MEC3_YEAST	DCOR_MOUSE	DCOR_MUSPA	SYP_METJA	DCOR_CRIGR	LEP3_BACSU	GTC2_RAT	RR4_CHLEL	RPE_RHOCA	CA1C_CHICK	MDS3_YEAST	YIC6_YEAST
RNA POLYMERASE BETA SU	CUT1 PROTEIN.	ANTIGEN WC1.1.	DNA-DIRECTED RNA POLYM	TESTIS-SPECIFIC PROTEI	TESTIS-SPECIFIC PROTEI	TRANSPORT ATP-BINDING	HEAT SHOCK FACTOR PROT	SERINE PROTEASE I PREC	HEAT SHOCK FACTOR PROT	CHECKPOINT PROTEIN MEC	ORNITHINE DECARBOXYLAS	ORNITHINE DECARBOXYLAS	PROLYL-TRNA SYNTHETASE	ORNITHINE DECARBOXYLAS	TYPE 4 PREPILIN-LIKE P	GLUTATHIONE S-TRANSFER	CHLOROPLAST 30S RIBOSO	RIBULOSE-PHOSPHATE 3-E	COLLAGEN ALPHA 1(XII)	MDS3 PROTEIN (MCK1 DOS	HYPOTHETICAL 133.0 KD
4.60e+01	4.60e+01	4.60e+01	4.60e+01	4.60e+01	4.60e+01	4.60e+01	4.60e+01	4.60e+01	4.60e+01	4.60e+01	4.60e+01	4.60e+01	4.60e+01	4.60e+01	4.60e+01	4.60e+01	4.60e+01	4.60e+01	2.66e+01	2.66e+01	2.66e+01

REFERE	RRRR	2 5	R	R.P	R.F.	RA A	2 2	RP	2 2	P R	RX	RP	R	3	R.R.	RX	RP R	Z Z	R R	RX	R A	200	8	S	GN	J (	3 5	ğ	AC	ij	RESULT
(IN) CALCIUM-REGULATING HORMONES, TALMADGE R.V., OWEN M., PARSONS J.A., EDS., PP.9-14, EXCERPTA MEDICA FOUNDATION, AMSTERDAM, (1975). [7]	O. ALL H.D., J	FOITS J.T. JR.; BIOCHEMISTRY 17:5723-5729(1978).	KEUTMANN H.T., SAUER M.M., HENDY G.N., O'RIORDAN J.L.H.,	SEQUENCE OF 61-83 AND 84-115.	ACAD. SCI. U.S.A. 71:384-388(1	•		SEQUENCE OF 32-68.	2			SEQUENCE OF 26-37.	Č.	NAME ACAD COT II C A	EK T.J., MCCEVITI B.E., FREEMAN M.W., FENNICK B	83169	SEQUENCE FROM N.A.	FROC. NATL. ACAD. SCI. 0.5.A. /8:/365-/369(1981). [2]	G.N., KRONENBERG H.M	NE; 82150870.	SEQUENCE FROM N.A.	EOTHERIA; PRIMATES.	ME	HOMO SAPIENS (HUMAN).		HORMONE PRECIR	O1-NOV-1997 (REL. OS, LAGE ANNOTATION HUDDATE)	(REL. 01, CREA		PTHY_HUMAN STANDARD; PRT; 115 AA.	JLT 1

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REVISIONS; 75146516.
MEDLING; 75146516.
KEUTWANN H.T., NIALL H.D., O'RIORDAN J.L.H., POTTS J.T. JR.;
BIOCHEMISTRY 14:1842-1847(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 75059220.

MEDLINE; 75059220.

TREGERR G.W., VAN RIETSCHOTEN J., GREEN E., NIALL H.D., TREGERR G.W., PARSONS J.A., O'RIORDAN J.L.H., POTTS J.T. KEUTMANN H.T., PARSONS J.A., CHEM. 355:415-421(1974).

HOPPE-SEXLER'S Z. PHYSIOL. CHEM. 355:415-421(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANDREATTA R.H., HARTWANN A., JOEHL A., ANDREATTA R.H., SIEBER P.; RINIKER B., RITTEL W., SIEBER P.; HELV. CHIM. ACTA 56:470-473(1973).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRUCTURE BY NMR OF 32-65.
MEDLINE; 91299748.
KLAUS W., DIECKMANN T., WRAY V.,
BIOCHEMISTRY 30:6936-6942(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYNTHESIS OF 32-65.
MEDLINE: 73227467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRUCTURE BY NMR OF 32-65
                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE: 95318084.

MARX U.C., AUSTERMANN S., BAYER P., ADERMANN K., STICHT H., WALTER S., SCHMID F.-X., JAENICKE R., ROESCH P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUR. J. BIOCHEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRUCTURE, 93345518.
MEDLINE; 93345518.
CUTHBERTSON R.M.;
BARDEN J.A., CUTHBERTSON R.M.;
BARDEN J.A., 215:315-321(1993).
                                                                                                                                                   PIR; A01339; A1339.
PIR; A19339; A19339.
PIB; 1HPH; 10-JUL-95.
PDB; 1HTH; 15-OCT-97.
PDB; 1ZWB; 12-MAR-97.
PDB; 1ZWB; 11-MAR-97.
PDB; 1ZWB; 16-JUN-97.
PDB; 1ZWB; 16-JUN-97.
PDB; 1ZWB; 16-JUN-97.
PDB; 1ZWB; 16-JUN-97.
Query Match 100.0%; Plest Local Similarity 100.0%; Best Local Similarity Conservative Matches 8; Conservative
                                                                                                                PROSITE;
                                          CONFLICT
SEQUENCE
                                                                       VARIANT
                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                 CHEM. 270:15194-15202(1995).
                                                                                                                 PS00335; PARATHYROID; 1.
SIGNAL; DISEASE MUTATION;
                                           107
115
                                                                             1
26
32
18
                                               ΑA;
                                                                              25
31
115
18
                                                 107
12861 MW;
           Score 54; DB 1; Let pred. No. 4.02e-03; 0; Mismatches 0;
                                                 PARATHYROID HORMONE.
C -> R (IN FIH; LEADS TO INEFFICIENT C PROCESSING OF THE PRECURSOR).
N -> D (IN REF. 5).
1; 243E87C7 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KAMBER B., MAIER
                                                                                                                           3D-STRUCTURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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FORSSMANN W.-G.,
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                          Gaps
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Search completed: Thu Jul 30 10:00:40 Job time: 7 secs.
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21-JUL-1986 (REL. 05, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDAT O1-FEB-1996 (REL. 37, LAST ANNOTATION UPDAT O1-FEB-1996 (REL. 38, LAST ANNOTATION)
PARATHYROID HORMONE PRECURSOR (PARATHYRIN)
                                                                                         Query Match
Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE; 87316938.
SCHMELZER H.-J., GRO
NUCLEIC ACIDS RES. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTH.
SUS SCROPA (PIG).
EURARYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; ARTIODACTYLA.
                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 26-115.
SEQUENCE; 76018954.
MEDILNE; 76018954.
CHU L.L.H., HUANG W.-Y., LITTLEDIKE E.T., HAMILTON J.W.,
BIOCHEMISTRY 14:3631-3635(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32
                                                                                                                                                                                                                              SAUER R.T., NIALL H.D., HOGAN M.L., KEUTMANN H.T., O'RI SAUER R.T., NIALL H.D., HOGAN M.L., KEUTMANN H.T., O'RI POTTS J.T., J.R.;
BIOCHEMISTRY 13:1994-1999(1974).

1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING BONE AND PREVENTING THEIR RENAL EXCRETION.

EMBL: X05722: G1839; T.
                                                                                                                                                                                                                                                                                                SEQUENCE OF 32-115.
MEDLINE: 74253317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 SVSEIQLM 39
1 SVSEIQLM 8
                                                                                                                                                                                     HORMONE; SIGNAL.
                                                                                                                                                                                                       PIR; A01535; PTPG.
PIR; B26806; B26806.
PEOSTTE: PS00335; PARATHYROID;
                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                   PROSITE;
                                                                                                                                          SEQUENCE
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                                                32 SVSEIQLM 39
||||||||
1 SVSEIQLM 8
                                                                                          7 Match 100.0%; Local Similarity 100.0%; Local Similarity sees 8; Conservative
                                                                                                                                             26
32
115 AA;
                                                                                                                                                                                                                                                                                                                                                                                                GROSS G., WIDERA G., MAYER
S. 15:6740-6740(1987)
                                                                                                                                                 25
31
115
12852 MW;
                                                                                                      Score 54; DB 1; Le
pred. No. 4.02e-03;
0; Mismatches 0;
                                                                                                                                                    PARATHYROID HORMONE:
; 98B67F47 CRC32;
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                                                                                                                                    Length 115;
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                                                                                                                  Indels
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(MT)
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MPsrch\_pp in on: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 11:15:09 1998; MasPar time 2.61 Seconds 52.810 Million cell updates/sec

Title: Tabular output not generated. >US-08-817-547A-32 (1-9) from US08817547A.pep 68

Description: Perfect Score:

Sequence: 1 LRKKLQDVH 9

Scoring table: PAM 150 Gap 15

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match Listing first 0% 45 summaries

Database:

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 16.984; Variance 56.277; scale 0.302

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Re

sult Query	100.0	ᆸ	100.0	68 100.0	68 100.0	100.0	68 100.0	68 100.0	68 100.0	68 100.0	68 100.0	68 100.0	00 100 0	00 LUU.U	68 100.0	68 100.0 68 100.0	68 100.0 68 100.0	68 100.0 68 100.0 68 100.0	14 68 100.0 35 16 68 100.0 35 16 68 100.0 36 17 68 100.0 36 17 68 100.0 36
DB	4.	26	9	9	9	9	9	9	22	22	22	14	14	14	9	9	9	و	ø
IJ	R22072	R62432	R58079	R58081	R58049	R58048	R58291	R49697	W20002	W20003	W17962	R74516	R74457	R74458	R58275	R58249	R58285	R58069	
iptio	Modified [D-Trp_12, Ty	Accelerator peptide b	[L8, H10, Q18, R22, T33, A	[L8,E10,Q18,R22,T33,A	), K11,Q16,D1	[L8,Q16,R22,T33,A34]-	<pre>{Lys(For)26, Lys(For)</pre>	Sequence of variant o	Cyclised rat parathyr	Cyclised [Nle 8,18, T	Human PTH analogue [C	Parathyroid hormone p	Parathyroid hormone p	Parathyroid hormone p	[Ala16]-hPTH(1-36)-NH	[D-Ser1]-hPTH(1-36)-N	(Ala23]-hPTH(1-36)-NH	<pre>Isopropyl-[L8,K(Isopr</pre>	
Pred. No.	1.66e+00	1.66e+00	1.66e+00	1.66e+00	1.66e+00	1.66e+00	1.66e+00	1.66e+00	1.66e+00	1.66e+00	1.66e+00	1.66e+00	1.66e+00	1.66e+00	1.66e+00	1.66e+00	1.66e+00	1.66e+00	1 660+00

Best Loc Matches Query Match

y Match 100.0%; Local Similarity 100.0%; hes 9; Conservative

Score Pred. 0; M

Length 28; 0

Mismatches 68; DB 4; L No. 1.66e+00;

Indels

0 Gaps

0

68 100.0 36 9 R58238 [NMcPhe34]-hPFH(1-36) 68 100.0 36 9 R58237 [NMcPhe34]-hPFH(1-36) 68 100.0 38 9 R58028 [Thr1]-hPTH(1-38)-OH. 68 100.0 44 26 P30015 Human parathyroid hor 68 100.0 84 4 R21257 Human parathyroid hor 68 100.0 84 4 R23249 Porcine parathyroid hor 68 100.0 84 4 R23241 Human parathyroid hor 68 100.0 84 4 R23241 Human parathyroid hor 68 100.0 84 4 R23242 Human parathyroid hor 68 100.0 84 4 R23243 Bovine parathyroid hor 68 100.0 84 4 R23356 Bovine parathyroid hor 68 100.0 84 4 R23357 Bovine parathyroid hor 68 100.0 84 4 R23357 Bovine parathyroid hor 68 100.0 84 4 R23351 Bovine parathyroid hor 68 100.0 84 4 R2351 Bovine parathyroid hor 68 100.0 84 4 R23185 Human parathyroid hor 68 100.0 84 4 R23166 Human parathyroid hor 68 100.0 84 4 R211256 Human parathyroid hor 68 100.0 84 4 R21256 Human parathyroid hor 68 100.0 84 4 R21270 Human parathyroid hor	45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20
36 9 R58238 [D-Asg030]-hPTH(1:-30) 36 9 R580237 [Mesphe34]-hPTH(1:-30) 38 9 R58028 [Thr1]-hPTH(1:-38)- 44 26 P30015 Human parathyroid 42 4 P30015 Human parathyroid 44 26 P30015 Human parathyroid 44 27 W25687 Human parathyroid 44 R21257 Human parathyroid 44 R23496 Porcine parathyroid 44 R23380 Bovine parathyroid 44 R23241 Human parathyroid 44 R23356 Bovine parathyroid 44 R23356 Bovine parathyroid 44 R23351 Bovine parathyroid 44 R23519 Bovine parathyroid 44 R23521 Bovine parathyroid 44 R23521 Bovine parathyroid 44 R23453 Porcine parathyroid 44 R23453 Human parathyroid 44 R23166 Bovine parathyroid 44 R21206 Human parathyroid 44 R21206 Human parathyroid 44 R21206 Human parathyroid 44 R21276 Human parathyroid 44 R21177 Human parathyroid 44 R21170 Human parathyroid 44 R21170 Human parathyroid 44 R21279 Human parathyroid	68	68	68	83	68	83	68	83	83	83	68	83	83	83	68	68	68	68	68	68	83	68	83	68	68	68
9 R58238 [D-Asp30]-hPTH(1-9 R58237 [MmePhe34]-hPTH(1-38)- R58238 [Thx1]-hPTH(1-38)- R58237 [Thx1]-hPTH(1-38)- R58238 [Thx1]-hPTH(1-38)- R58238 [Thx1]-hPTH(1-38)- R58238 [Thx1]-hPTH(1-38)- R582342 Human parathyroid R23340 Bovine parathyroid R23341 Human parathyroid R23356 Bovine parathyroid R23357 Bovine parathyroid R23351 Bovine parathyroid R23521 Bovine parathyroid R23528 Human parathyroid R23368 Bovine parathyroid R23368 Bovine parathyroid R23368 Human parathyroid Human parathyroid R21170 Human parathyroid		•	•	•	•	•	•		٠	•					•	•			•				.0	.0	0	0
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[D-Asp30]-hPTH(1-38)-[NPEPh634]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1]-hPTH(1-38)-[Thr1	4	4	4	4	4	4	4	4	4	4	4	4							4	4	4	27	26	ø	9	ø
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Claim 1; Column 10; Gpp; English.

The peptide is modified at Lys13 (of the parent PTH) in the epsilon amino acid gp. by N.N-diisobutyl or 3-phenylpropancyl. The desamino form is also claimed. The PTH analogue binds with high affinity to the peptide hormone receptor without activating the 2nd messenger mol. The modification of the Lys residue stabilises the bloactive conformation of PTH to enhance the activity. The peptide may be used in in vitro bloassays to measure naturally occurring PTH and to diagnose the etiology of or to treat osteoporosis or hypercalcaemia. It may also be used to treat hyperthyroidism and diseases caused by abberrent prodn. of hormone-like substances, as inflammation. It may also be used to treat immune diseases such as inflammation. It is prepd. by solid phase synthesis.
                                                                                                                                                                                                                                                                                                                                                                                             US5093233-A.
03-MAR-1992.
                                                                                                                                                                                                                                        osteoporosis and hyperparathyroidism. Claim 1; Column 10; 6pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-JUL-1992 (first entry)
Modified [D-Trp_12,Tyr_34]rPTH(7-34)NH2.
Parathyroid hormone; analogue; osteoporosis; hyperthyroidism;
tumours; hypercalcaemia; renal failure; rat.
   Sequence
                                                                                                                                                                                                                                                                          New parathyroid hormone analogues - useful for treatment and vitro diagnosis of PTH-dependent tumours, immune disorders,
                                                                                                                                                                                                                                                                                                                WPI; 92-096233/12.
                                                                                                                                                                                                                                                                                                                              (MERI ) MERCK & CO INC. Rosenblatt M, Roubini E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R22072 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                             25-APR-1990; US-514394.
25-APR-1990; US-514394.
   28 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "OTHER
28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= NH2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ū
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     comments"
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Db 18 1rkKiddyh 26

Qy 1 LHKKLDDYH 9

RESULT 2

ID R62432 standard; peptide; 34 AA.

AC R62442.

AC R62442.

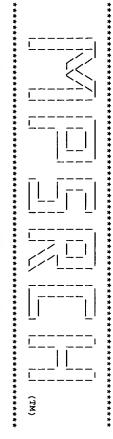
AC R624632 standard; peptide basic region peptide, p-8.

AC R62453 standard; peptide basic region peptide, p-8.

KW beriodontal tissue; regeneration; periodontitis; periodontal pocket; periodontal tissue; regeneration; periodontitis; periodontal pocket; professor, periodontal tissue; regeneration; periodontal tissue - comprises in 10-783-193; AC-9398.

BY 10-783-193; AC-9398.

FY 10-7
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MPsrch\_pp n on: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 11:14:22 1998; MasPar time 3.17 Seconds 103.833 Million cell updates/sec

Tabular output not generated.

Title: >US-08-817-547A-32 (1-9) from US08817547A.pep 68 1 LRKKLQDVH 9

Description: Perfect Score: Sequence:

Scoring table: PAM 150 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 23.542; Variance 35.708; scale 0.659

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

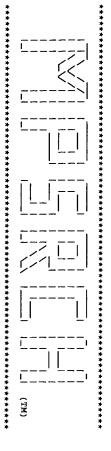
#### SUMMARIES

113 113 114 115 115 116 117 117 117 118 118 118 119 119 119 119 119 119 119	sult No.
	Score
100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0	% Query Match Le
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parathyroid hormone 4 parathyroid hormone 4 cyclic parathyroid hormone ( parathyroid hormone seril-trna synthetase seryl-trna synthetase seryl-trna synthetase seryl-trna synthetase seryl-trna synthetase	Description
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54 79.4 421 5 15EKB SETY1-TUNA Synthetase 53 77.9 348 2 845890 ODP1 protein - yeast 52 76.5 878 2 \$20486 paramyosin - fruit fl 52 76.5 879 2 \$22028 paramyosin, standard 52 76.5 2475 2 \$33306 paramyosin, standard 52 76.5 2475 2 \$33306 floral homeotic prote 51 75.0 317 2 \$45708 MSH receptor - bovine 51 75.0 1200 2 \$77524 chromosome segregatic 50 73.5 412 2 \$07537 myosin heavy chain, c 50 73.5 437 2 \$64113 Mc397 homolog DO2_orf 50 73.5 569 2 \$62851 Mc397 homolog DO2_orf 50 73.5 586 2 \$44850 K12H4.1 protein - Cae 50 73.5 586 2 \$44850 myosin heavy chain - 50 73.5 1938 2 \$755421 smooth muscle myosin 50 73.5 1938 2 \$755421 smooth muscle myosin 50 73.5 1972 2 JC5421 smooth muscle myosin 50 73.5 1972 2 JC5421 smooth muscle myosin 50 73.5 1972 2 JC5421 smooth muscle myosin 64 72.1 530 2 \$64302 hypothetical protein 64 70.6 154 2 \$03242 hypothetical protein 65 70.6 444 2 \$09681 citrate transport protein 66 70.6 1126 2 \$04716 DNA-directed RNA poly	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
9 348 2 S4589 ODP1 protein - yea   5 878 2 S20486 paramyosin - fruit   5 879 2 S22028 paramyosin - fruit   5 2475 2 S35307 polyprotein pp220   6 257 2 S35306 floral homeotic protein pp220   7 2 S45708 MSH receptor - bow   7 2 S44570 Myosin heavy chain   7 2 S44850 MSH Hypothetical protein   7 2 MSH receptor - bow   7 2 S44850 MSH receptor   7 2 S44850 MSH Hypothetical protein   7 3 MSH receptor - bow   7 3 MSH receptor - bow   7 472 S4457 Myosin heavy chain   7 5 4725 MA4357 Myothetical protein   7 6 154 2 S3342 Myothetical protein   7 6 154 2 S3342 Myothetical protein   7 7 8 MSH receptor   7 8 MSH receptor - bow   7 8 MSH receptor   7 8 MSH recept	48	48	48	48	49	49	50	50	50	50	50	50	50	50	51	51	51	52	52	52	53	54
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15ERB	1126	444	229	154	630	215	4725	1972	1938	621	586	569	437	412	1200	317	257	2475	879	878	348	421
o oppl protein - year o oppl protein - year o oppl protein - year o paramyosin - fruit paramyosin - standa paramyosin - standa paramyosin - standa polyprotein pp220 floral homeotic pr o myosin heavy chain tetrahydrofolylpol MG397 homolog D0- K12H4.1 protein - myosin heavy chain smooth muscle myos smooth muscle myos dynein heavy chain hypothetical prote pypothetical prote hypothetical prote	2	N	N	N	N	2	ب	N	N	N	N	N	N	N	N	N	N	N	N	N	N	U
protein yea yosin fruit yosin, standa rotein pp220 il homeotic pr eceptor bovo losome segrega n heavy chain hydrofolylpol hydrofolylpol homolog p02. I protein n heavy chain n heavy chain n heavy chain n heavy chain n heavy chain hetical protein hetical protein	S04716	S09681	G70073	S03242	C64302	S35640	A44357	JC5420	JC5421	S10450	S44850	S62851	C64113	S07537	S77524	S45708	S53306	S35307	S22028	S20486	S45890	LUEKE
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ATE NCE NCE NCE NCE NCE LThor bmis	Query Match Best Local Simila Matches 9; C Db 21 LRKKLODVH                     Oy 1 LRKKLODVH	#authors #book COMMENT Resol COMMENT Deter KEYWORDS FEATURE 2-9 15-25 SUMMARY	RESULT 1 12WG ENTRY 12WG TITLE 5ynthetic ALTERNATE_NAMES n-succinyl-h PDB_TITLE 5uccinyl-h PDB_TITLE 6uccinyl-h PD
parathyroid hormone 4 37 mutant N-TERMINAL ACETYLATED - synthetic n-acetyl-hpth(4-37) structure of n-terminal acetylated human parathyroid hormone, NMR, 10 structures 467742 ROCESCH, P.; Marx, U.C. submitted to the Brookhaven Protein Data Bank, June 1996 nces pDB:12WF TN003318 Marx, U.C. in Strukturen Verschiedener Parathormonfragmente in Loesung, in Strukturen Verschiedener Parathormonfragmente in Loesung,	100.0%; Score 68; DB 5; Length 34; Similarity 100.0%; Pred. No. 1.61e-02; 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0; (KLODVH 29 (KLODVH 9)	Marx, U.C.  Marx, U.C.  In Strukturen Verschiedener Parathormonfragmente in Loesung, pp.0, Bayreuth: University of Bayreuth (Thesis), 1996  Resolution: NMR  Determination: NMR  disease mutation; hormone; signal  #region helix (right hand alpha)\ #region helix (right hand alpha)\ #length 34 #molecular-weight 4128 #checksum 5508	12WG #type complete parathyroid hormone 4 37 mutant N-TERMINAL SUCCINYLATED - synthetic n-succinyl-hpth(4-37) succinyl human parathyroid hormone 4-37, NMR, 10 structures #formal_name synthetic A67743 Roesch, P.; Marx, U.C. submitted to the Brookhaven Protein Data Bank, June 1996 nees ppB:1ZWG TN003319

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COMMENT Resolution: not applicable COMMENT Determination: NATE DETERMINE DETERMINED PRICED PROPERTY DETERMINED PROPERTY DETERMINED PROPERTY DOLORS SUMMARY STORE S
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MPsrch\_pp : to d protein - protein database search, using Smith-Waterman algorithm

Thu Jul 30 11:13:17 1998; MasPar time 2.13 Seconds 105.752 Million cell updates/sec

abular output not generated.

Title: Description: Perfect Score: >US-08-817-547A-32 (1-9) from US08817547A.pep 68 1 LRKKLQDVH 9

Sequence:

Scoring table: PAM 150 Gap 15

Searched: 69111 segs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 24.742; Variance 29.653; scale 0.834

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

MONE MONE MONE MONE MONE MONE MONE MONE	.6 154 1 Y17K_SSV1 HYPOTHETICAL .6 229 1 YXDJ_BACSU HYPOTHETICAL .6 360 1 HISB LACLA HISTIDINOL-PH	48 70.6 154 1 Y17K_SSV1 HYPOTHETICAL 48 70.6 229 1 YXDJ BACSU HYPOTHETICAL	48 70.6 154 1 Y17K_SSV1 HYPOTHETICAL		49 72.1 630 1 YO19 METJA HYPOTHETICAL	49 72.1 209 1 VS10_ROTBS MINOR OUTER C	50 73.5 4725 1 DYHC_DICDI DYNEIN HEAVY	50 73.5 586 1 YM61_CAEEL HYPOTHETICAL	50 73.5 569 1 Y397_MYCPN HYPOTHETICAL	50 73.5 437 1 FOLC_HAEIN	51 75.0 317 1 MSHR_BOVIN	51 75.0 310 1 SYNK_ARATH	52 76.5 879 1 MYSP_DROME PARAMYOSIN,	52 76.5 621 1 Y04E_MYCTU HYPOTHETICAL 6	53 77.9 348 1 HMT1_YEAST HNRNP ARGININE	54 79.4 421 1 SYS_THETH	54 79.4 119 1 PTHY_CHICK PARATHYROID	68 100.0 115 1 PTHY_HUMAN PARATHYROID	68 100.0 115 1 PTHY_RAT PARATHYROID	68 100.0 115 1 PTHY_PIG PARATHYROID	100.0 115 1 PTHY_CANFA PARATHYROID	68 100.0 115 1 PTHY_BOVIN PARATHYROID	Score Match Length DB ID Descrip	enit Operv
		HISTIDINOL-PHOSPHA	U HYPOTHETICAL 26.6	HYPOTHETICAL 17.8	HYPOTHETICAL PROTE	MINOR OUTER C		, HYPOTHETICAL	HYPOTHETICAL PROTE		MELANOCYTE STIMU	SYNTAXIN-RELATED	•	J HYPOTHETICAL 6		SERYL-TRNA SYNTHETAS	PARATHYROID HORMONE	PARATHYROID HORMONE	HORMONE	PARATHYROID HORMONE	PARATHYROID HORMONE	- 1	Description	

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24
46	46	46	46	46	46	46	46	46	46	46	46	46	46	46	47	47	48	48	48	48	48
67.6	67.6	67.6	67.6	٠	67.6	•	67.6	67.6	67.6	67.6	67.6	•	67.6	67.6	69.1	69.1	70.6	70.6	70.6	70.6	70.6
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POLN_EEVV3	POLN_EEVVT	KIF4_MOUSE	YAN2_SCHPO	KATA_ARATH	KATC_ARATH	KATB_ARATH	PTMA_ECOLI	YM63_YEAST	CPT7_PIG	EMB8_PICGL	KCC2_YEAST	CAPM_STAAU	YIE1_YEAST	GLG2_ARATH	YI91_SHIDY	YI91_ECOLI	RPOB_SULAC	PQQL_HAEIN	YML1_YEAST	MEDB_GIALA	YMS2_YEAST
NONSTRUCTURAL POLYPROT	NONSTRUCTURAL POLYPROT	KINESIN-LIKE PROTEIN K	HYPOTHETICAL 117.4 KD	KINESIN-LIKE PROTEIN A	KINESIN-LIKE PROTEIN C	KINESIN-LIKE PROTEIN B	PTS SYSTEM, MANNITOL-S	HYPOTHETICAL 67.7 KD P	CYTOCHROME P450 XVIIA1	LATE EMBRYOGENESIS ABU	CALCIUM/CALMODULIN-DEP	CAPM PROTEIN.	36.7 KD PROTEIN IN CBR	GLUCOSE-1-PHOSPHATE AD	INSERTION ELEMENT IS91	INSERTION ELEMENT IS91	DNA-DIRECTED RNA POLYM	PROBABLE ZINC PROTEASE	HYPOTHETICAL 104.8 KD	MEDIAN BODY PROTEIN.	HYPOTHETICAL 76.2 KD P
4.57e+01	4.57e+01	4.57e+01	4.57e+01	4.57e+01	4.57e+01	4.57e+01	4.57e+01	4.57e+01	4.57e+01	4.57e+01	4.57e+01	4.57e+01	4.57e+01	4.57e+01	2.97e+01	2.97e+01	1.92e+01	1.92e+01	1.92e+01	1.92e+01	1.92e+01

RX RX	RR	RA	R S	장	RN	<b>2</b>	23	D R	망	Z	3 5	RX	₽.	RN	2 Z	2 2	장	RN	æ	RA	R A	g R	RL	RA	RA	æ :	9 2	8	გ	SO	GN	H	ij	3 5	7 2	ä	RESULT
SEQUENCE OF 32-115. MEDLINE; 71063634.		POTTS J.T. JR.;		SEQUENCE OF 32-115.		PROC. NATL. ACAD. SCI. U.S.A. 71:653-656(1974).	COHN D.V.:	TW NIATE HID TACONS TW KNIMMANN HIM DOWNS TH	SEQUENCE OF 26-115.	[5]	WEAVER C.A., GORDON D.F., KISSIL M.S., MEAD D.A., KEMPER B.;		UENCE		MCD: CELL: ENDOCRINOI: 28:411-424(1982).	COUNTY TO THE PERSON OF THE PE	SEQUENCE FROM N.A.		I. U.S.A. 78:40		SEKULANCE E NUMBER OF THE SEKULANCE OF T		PROC. NATL. ACAD. SCI. U.S.A. 76:4981-4985(1979).	JR., RICH A.;		MEDLINE; 80056617.	CEDITENCE EDOM N 2	EUTHERIA; ARTIODACTYLA.	٠.	BOS TAURUS (BOVINE).		HORMONE PR	(REL. 35,	3 5	PEL	PTHY_BOVIN STANDARD; PRT; 115 AA.	P

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RESULT
AC PE
AC PE
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Best Local S
Matches
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RA POTTS J.T. JR., TREGEAR G.W., KEUTMANN H.T., NIALL H.D., SAUER R., DEETOS L.J., DAWSON B.F., HOGAN M.L., AUBBACH G.D.;

RA DEETOS L.J., DAWSON B.F., HOGAN M.L., AUBBACH G.D.;

RL PROC. NATL. ACAD. SCI. U.S.A. 68:63-67(1971).

CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN COMMENT OF COMMENT OF CALCIUM LEVEL BY DISSOLVING THE SALTS IN COMMENT OF CAMBL; VO0106; G85; -.

CC EMBL; V00104; G163641; -.

CR EMBL; J00024; G163643; -.

CR EMBL; J00024; E18250; ALT_INIT.

CR EMBL; V001938; G163647; -.

CR EMBL; W1938; G163645; -.

CR EMBL; M25082; G163645; -.

CR PIR; A01534; PTBO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%;
Matches 9; Conservative
                                                                                                          PROPEP
CHAIN
SEQUENCE
                                                                                                                                                    SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

TISSUE-PARATHYROID;

MEDLINE; 95365666.

ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,

DEWILLE J.W., CAPEN C.C.;

GENE 160:241-243(1995).

-1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS

BONE AND PREVENTING THEIR RENAL EXCRETION.

EMBL; U15662; G558916; -.

PROSITE; PS00335; PARATHYROID; 1.

HORMONE; SIGNAL.

TS BY STWILDETTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                          CANIS FAMILIARIS (DOG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; CARNIVORA.
                                                                                                                                                                                                                                                                                                                                                                               JT 2
PTHY_CANFA STANDARD; PRT; 115 AA.
P52212;
01-0CT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
HORMONE;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BREWER H.B. JR., RONAN R.;
PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
[8]
             55 LRKKLQDVH 63
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LRKKLQDVH 9
                                                                   Similarity
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26
32
115 AA;
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26 31
32 115
106 V
115 AA; 12980 MW;
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ilarity 100.0%;
Conservative
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31
115
12957
                                                                                                          MW;
                                                  Score 68; DB 1; L
Pred. No. 8.13e-04;
0; Mismatches 0
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BY SIMILARITY.
PARATHYROID HORMONE.
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V -> G (IN REF. 4).
; 673EA5F2 CRC32;
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Search completed: Thu Jul 30 11:13:23 1998 Job time: 6 secs.

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Result
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113
114
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Copyright (c) 1993-1998 University of Edinburgh, U
Distribution rights by Oxford Molecular Ltd
         protein - protein database search, using Smith-Waterman algorithm
                                                                                                                                                                                                                                                                                                                                                                                           Query
Match
         PAM 150
Gap 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   >US-08-817-547A-32
(1-9) from US08817547A.pep
68
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1:sp_fung1 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mbc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified
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Listing first 45 summaries
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                                           LRKKLQDVH
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Q923768
Q92970
Q40790
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TARTAN PROTEIN PRECURS CHROMOSOME SEGREGATION MYOSIN HEAVY CHAIN (AA C14C10.1. MYOSIN HEAVY CHAIN 21 MYOSIN. MYOSIN. MYOSIN. MYOSIN. MYOSIN LIGHT CHAIN KIN MYOSIN LIGHT CHAIN KIN
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                                                                                                                                                                     BOX PROTEIN.
MELANOCYTE STIMULATING
MC1-R PROTEIN.
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POLYPROTEIN PP220.
MADS-BOX FAMILY TRANSC
PUTATIVE MADS-BOX FAMI
                                                                                                                                                                                                                                                                                                                 CO6G3.9 PROTEIN.
SIMILAR TO SACCHAROMYC
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STRAIN HB3 CG2 (CG2).	CHLOROQUINE RESISTANCE	CHLOROQUINE RESISTANCE	HYPOTHETICAL 119.1 KD	ATP-DEPENDENT RNA HELI	RABAPTIN-5.	RABAPTIN.	RAT RABAPTIN-5.	MOUSE RABAPTIN-5.	CHICKEN RABAPTIN-5.	ORF695.	ARA70.	C13A2.5 PROTEIN.	FISSION YEAST (FRAGMEN	CONSERVED HYPOTHETICAL	TPR HOMOLOG.	KIAA0336.	SIMILARITY TO MYOSIN H	HUNTINGTIN INTERACTING	COSMID C27D9.	HUNTINGTIN INTERACTING	C38C3.3 PROTEIN.	HISC.	POLYPEPTIDE DEFORMYLAS	MYOSIN LIGHT CHAIN KIN
3.99e+01	3.99e+01	•	3.99e+01		3.99e+01		٠,	3.99e+01	3.99e+01	3.99e+01	3.99e+01	3.99e+01		3.99e+01	2.56e+01	2.56e+01	2.56e+01		2.56e+01		2.56e+01	2.56e+01	-	1.64e+01

#### ALIGNMENTS

PRELIMINARY;

PRT;

105

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RESULT
AC OCC
AC
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TISSUE-THYROID, AND PARATHYROID;
SCHMELZER H.J., GROSS G., MAYER H.;
SCHMELZER H.J., GROSS G., MAYER H.;
ADV. GENE TECHNOL. 21:228-229(1984).
EMBL, M54875; G601933; -.
NON_TER
NON_TER
105 AA; 11746 MW; 6AC3163
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017750;
01-NOV-1996 (TREMBLREL. 0
01-NOV-1996 (TREMBLREL. 0
01-JAN 1998 (TREMBLREL. 0
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Q63473
Q63473;
Q63473;
01-NOV-1996
01-NOV-1996
01-JAN-1998
SEQUENCE FROM N.A.
STRAITH-BRISTOL N2;
LATREILLE P., STELLYES L.;
SUBMITTED (JUL-1996) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                        CAENORHABDITIS ELEGANS EUKARYOTA; METAZOA; ACC
                                                                                                                                                                                                                    C06G3.9 PROTEIN.
C06G3.9.
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
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||||||| |
1 LRKKLQDVH 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 88.9%
les 8; Conservative
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6 (TREMBLREL. 01, LAST
8 (TREMBLREL. 05, LAST
D HORMONE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                           ACOELOMATES;
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01, LAST SEQUENCE UPDATE)
05, LAST ANNOTATION UPDATE)
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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0; 1
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                                                                                                                                                        NEMATODA; SECERNENTEA; RHABDITIDA.
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2.16e-01;
                                                                                                                                                                                                                                                                                                                                                                                                      735 AA
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DR EMBL: U61947; G1397274; -W; 84A565CC CRC32;

QUERY MATCH 79.44; SCOTE 54; DB 3; Length 735;

Best Local Similarity 66.78; Pred. No. 1.57e+00;

Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Matches 1,111-11;

QY 1 LRKKLODVH 9

Search completed: Thu Jul 30 11:14:05 1998

Job time : 24 secs.
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                                                                                                                                                                                                                            (MT)
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MPsrch\_pp 900 protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 11:17:36 1998; MasPar time 2.58 Seconds 47.571 Million cell updates/sec

Sequence: Description: Perfect Score: Title: >US-08-817-547A-33 (1-8) from US08817547A.pep 59 1 LRKKLQDV 8

Tabular output not generated.

Scoring table: PAM 150 Gap 15

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 16.574; Variance 53.366; scale 0.311

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

1 3 3 3 4 4 4 4 4 1 1 1 1 1 1 1 1 1 1 1	Result No.
W G W G W G W G W G W G W G W G W G W G	Score
111111111111111111111111111111111111111	Query Match L
34 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Length DB
R22072 R52032 R58083 R58048 R58079 R580070 R58291 R49697 W220003 W17962 W20003 W17962 R74485 R74485 R74485 R58191 R58253 R58285 R58253	Ħ
Modified [D-Trp_12, Ty Accelerator peptide b [18,010,018,R22,T33,A34]- [18,010,R22,T33,A34]- [18,010,018,R22,T33,A [18,G10,018,R22,T33,A [18,G10,018,R [18,G10	Description
9.9200000000000000000000000000000000000	Pred. No.

Query Match 100.0%; Best Local Similarity 100.0%; Matches 8; Conservative

Score 59; DB 4; Length 28; Pred. No. 9.92e+00; 0; Mismatches 0; Indels

Indels

0

Gaps

0;

R22072 sta R22072; 142072; 1701-199 Modified   Parathyrol tumours; b Synthetic Key modified_s modified_s modified_s   Synthetic Key modified_s   Synthetic   Synthetic   Synthetic   Key   modified_s   modified   MERI   modified   wpi; 92-05   New parath   vitro dias   vitro dias   claim   continuo dias   contended of the peptide   amino acide   desamino i affinity the peptide amino acide   desamino acide affinity the peptide amino acide a	04000000000000000000000000000000000000
1 22072 standard; 22072; 22072; 22072; 22072; 22072; 22072; 23072; 2401fied [D-Trp_arathyroid horm mours; hyperca ynthetic: 2401fied_site 2401fied_site 2516231-A. 25ARR-1990; 25-ARR-1990; 26-ARR-1990;	
ABONS d. G O O O O O O O O O O O O O O O O O O	
tandard; Protein; 28 AA.  992 (first entry) [D-Trp_12,Tyr_34]rPTH(7) oid hormone; analogue; analog	2 WWW48888888888888888888888888888888888
lein; 28 entry) r_34]rp analogu nia; ren lion/Qua el OTHE el OTHE el Cho. le Cho. le Cho. led at Li redisob o claime of pri robioa on of pri robioa oney also oberrent nay also ols prepd	00000144444444400000114111111111111111
substance of the second	R58237 R58022 R58023 P30015 P30015 R23241 R23244 R23242 R23356 R23243 R23243 R23243 R23243 R23243 R23243 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R2345 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23453 R23
NH2.  Spoorosis  ure; rat  ure; rat  comment  comment  comment  f the pa  3-phen  m.  m.  f the pa  3-phen  grif anal  grif anal  grif anal  comment  to the pa  dro tre  d to tre	[NMe] [11e [Ala Huma Huma Huma Huma Huma Huma Huma Hum
iis; hyperthyro at.  ints"  [F;  [F;  If for treatmen immune disord parent PTH) in alogue binds without active treative treat operthyroreat typerthyroreat immune disord the activity.  Fireat osteoporeat typerthyroreat immune disord immune disord immune disordesses synthesis.	eephe34]- al,Abu2- an parat an parat inn parat inn parat inn parat ine parat
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psilon psilon gh gh gh is the pride ing ing ing	
<b>a</b> s	22 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

Qy Db

18 lrkklqdv 25 ||||||| 1 LRKKLQDV 8

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FF SOCOCOCO SP PP
Search completed: Thu Jul 30 11:17:51 1998 Job time : 15 secs.
                                                                            ğ
                                                                                                                                                                                                                              PP 13-AUG-1994.

PP 13-AUG-1994.

PP 10-FEB-1993; 045998.

PP 10-FEB-1993; 19-045998.

PP 110-FEB-1993; 19-045998.

Recelerator for regenerating periodontal tissue - comprises Accelerator for regenerating periodontal tissue onnected basic periodonsure; Page 3; 7pp; Japanese.

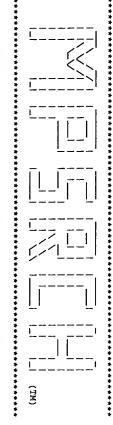
PI pisclosure; Page 3; 7pp; Japanese.

PI pisclosure; Page 3; 7pp; Japanese.

PI pisclosure; Page 3; 7pp; Japanese.

PI caccelerator contain at least two basic amino acids. The accelerator accelerator are periodontal tissue regeneration. The caccelerator in the growth of periodontal tissue regeneration. The accelerator is applied by opening the gingiva, treating the tissue constitution and accelerator reduces the down growth of the capithelium and accelerates fibre adhesion and regenerates cement.

So Sequence 34 AA;
                                                                                                                 용
                                                                                                                                                      Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ET 2
R62432 standard; peptide; 34 AA.
R62432;
31-JUL-1995 (first entry)
Accelerator peptide basic region peptide, P-8.
Accelerator; basic amino acid; cell growth factor; growth; gingiva; periodontal tissue; regeneration; periodontitis; periodontal pocket; down growth; epithelium; fibre adhesion; cement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06234653-A.
                                                                                                   24 lrkklqdv 31
                                                                                _
                                                                                LRKKLODV 8
                                                                                                                                                          Score 59; DB 26; Le
Pred. No. 9.92e+00;
0; Mismatches 0;
                                                                                                                                                                                                    Length 34;
                                                                                                                                                                     Indels
                                                                                                                                                                     0,
                                                                                                                                                                     Gaps
                                                                                                                                                                     0
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wesrch\_pp protein - protein database search, using Smith-Waterman algorithm

Thu Jul 30 11:16:07 1998; MasPar time 3.11 Seconds 93.824 Million cell updates/sec

labular output not generated.

Title: Description: Perfect Score: Sequence: >US-08-817-547A-33 (1-8) from US08817547A.pep 59 1 LRKKLQDV 8

Scoring table: PAM 150 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 22.968; Variance 34.253; scale 0.671

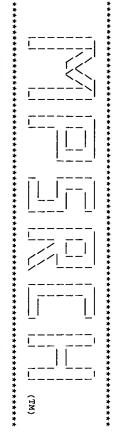
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

23	21	20	19	18	17	16	15	14	13	12	11	10	9	<b>&amp;</b>	7	σ	u	4	w	2	<u>سر</u>	No.
50	50	50	50	51	51	52	52	59	59	59	59	59	59	59	59	59	59	59	59	59	59	Score
84.7	84.7	84.7	84.7		86.4	88.1	88.1	100.0	100.0	100.0	100.0	100.0	100.0	100.0		100.0	100.0	•	100.0	•	100.0	Match
421 421	421	421	412	317	257	2475	105	115	115	115	115	115	37	37	36	35	34	34	34	34	34	Length
ທທ	ı Gı	N	N	N															տ	G	Ŋ	80
1SETA	1SRYA	S38948	S07537	S45708	S53306	S35307	I51851	A05091	PTHU	JC4202	PTBO	PTPG	1ZWC	1HPH	1ZWB	1ZWD	1ZWA	1ZWE	THTH	1 ZWF	1 ZWG	Ħ
Seryl-trna synthetase Seryl-trna synthetase		serinetRNA ligase (	myosin heavy chain, c	MSH receptor - bovine	otic pr	polyprotein pp220 pre	hormone	parathyroid hormone p	parathyroid hormone p	parathyroid hormone -	parathyroid hormone p	parathyroid hormone p	parathyroid hormone (	parathyroid hormone f	parathyroid hormone (	parathyroid hormone (	parathyroid hormone (		đ	parathyroid hormone 4	parathyroid hormone 4	Description
2.03e+01 2.03e+01	ر د		: 2.03e+01	1.36e+01	μ.	9.	9	4.	4.79e-01	4.79e-01	4.79e	4.79e-01	4.79e-01	Pred. No.								

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
47	47	47	47	47	47	47	47	48	48	49	49	50	50	50	50	50	50	50	50	50	50
79.7	79.7	79.7	79.7	79.7	79.7		79.7			83.1	83.1	84.7	84.7	84.7	84.7	84.7	84.7	84.7	84.7	84.7	84.7
1999	1200	614	360	199	134	133	100	1126	154	630	215	4725	1972	1938	621	586	437	421	421	421	421
<b>,_</b>	N	N	N	N	Ν	N	Ν	N	N	N	Ν	_	N	N	N	N	ν	U	σ	vi	Çī
S21801	S77524	S61532	F69342	E69539	G64750	S75121	S56508	S04716	S03242	C64302	S35640	A44357	JC5420	JC5421	S10450	S44850	C64113	1SERB	1SESB	1SESA	1SETB
myosin heavy chain, n	egregati	RET oncogene fusion p	DNA primase homolog -	conserved hypothetica	hypothetical protein	hypothetical protein	hypothetical 11.6K pr	DNA-directed RNA poly	hypothetical protein	hypothetical protein	hypothetical protein	dynein heavy chain, c	muscle	smooth muscle myosin	myosin heavy chain -	Kl2H4.1 protein - Cae	tetrahydrofolylpolygl	seryl-tRNA synthetase	Seryl-trna synthetase	Seryl-trna synthetase	Seryl-trna synthetase
6.49e+01	6.49e+01	6.49e+01	6.49e+01	6.49e+01	6.49e+01	6.49e+01	6.49e+01	4.43e+01	4.43e+01	3.01e+01	3.01e+01			2.03e+01	2.03e+01			2.03e+01	2.03e+01	2.03e+01	2.03e+01

#book		#cross-references PDB:12WF		Ħ	ORGANISM		ALTERNATE_NAMES			RESULT 2	QY 1 LRKKLQDV	Db 21 LRKKLQDV	Query Match Best Local Similarity Matches 8; Conse		15-25	C	S	Decerm			# # # # # # # # # # # # # # # # # # #		-referen	ion	rs	(1)	ORGANISM	NAMES	TITLE		RESULT 1
in Strukturen Verschiedener Parathormonfragmente in Loesung,	TN003318	CHE PROCESSIONES FRONTE PART PARTY CHIEF	to the Brookhawen Brotein Data Bank	A67742	NMR, 10 structures #formal_name synthetic	structure of n-terminal acetylated human parathyroid hormone,	synthetic n-acetyl-hpth(4-37)	thyroid	12WF #type complete		V-8	V 28	100.0%; Score 59; DB 5; Length 34; larity 100.0%; Pred. No. 4.79e-01; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	#length 34 #molecular-weight 4128 #checksum 5508	#region helix (right hand alpha)	#*/\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\	disease mutation; hormone; signal		plicable	ty of Bayreuth (Thesi	in strukturen Verschiedener Darathormonfragmente in Loesung.	INCOSSLY	ces PDB:12WG	ed to the	Roesch, P.; Marx, U.C.	A67743	succinyl numan paratnyroid normone 4-3/, NMK, iv structures #formal name synthetic		<pre>parathyroid hormone 4 37 mutant N-TERMINAL SUCCINYLATED -     synthetic</pre>	12WG #type complete	



MPsrch\_pp n on: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 11:15:44 1998; MasPar time 2.11 Seconds 95.235 Million cell updates/sec

Tabular output not generated.

Title:
Description:
Perfect Score:
Sequence: >US-08-817-547A-33 (1-8) from US08817547A.pep 59

1 LRKKLQDV 8

Scoring table: PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 24.101; Variance 28.427; scale 0.848

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	<b>&amp;</b>	7	o	51	4	ω	2	1	No.
46	46	46	46	47	47	48	48	48	49	49	50	50	50	50	50	51	51	59	59	59	59	59	Score
78.0	78.0		78.0	79.7	79.7	81.4	81.4	81.4	83.1	83.1	84.7	84.7	84.7	84.7	84.7	86.4	86.4	100.0		100.0	100.0	100.0	Query Match
326	229	224	100	112	100	1126	419	154	630	209	4725	621	586	437	421	317	310	115	115	115	115	115	Length
1		_	$\vdash$	μ.	Ь	$\vdash$	Ь	Ь	Н	Ь	_	μ.	Н	Ь	_	_	Ь	_	μ.	_	μ	μ	B B
YIE1_YEAST	YXDJ BACSU	TCTD SALTY	RR14_PORPU	YI91_SHIDY	YI91_ECOLI	RPOB_SULAC	PEXA_PICPA	Y17K_SSV1	Y019_METJA	VS10_ROTBS	DYHC_DICDI	Y04E_MYCTU	YM61_CAEEL	FOLC_HAEIN	SYS_THETH	MSHR_BOVIN	SYNK_ARATH	PTHY_HUMAN	PTHY_RAT	PTHY_PIG	PTHY_CANFA	PTHY_BOVIN	Ħ
EIN IN	•		CHLOROPLAST 30S RIBOSO	INSERTION ELEMENT IS91	INSERTION ELEMENT IS91	DNA-DIRECTED RNA POLYM	PEROXISOME ASSEMBLY PR	HYPOTHETICAL 17.8 KD P	HYPOTHETICAL PROTEIN M	MINOR OUTER CAPSID PRO	DYNEIN HEAVY CHAIN, CY	HYPOTHETICAL 69.2 KD P	HYPOTHETICAL 65.8 KD P	FOLYLPOLYGLUTAMATE SYN	SERYL-TRNA SYNTHETASE	MELANOCYTE STIMULATING	SYNTAXIN-RELATED PROTE	PARATHYROID HORMONE PR	Description				
2	2.86e+01		2.86e+01	1.83e+01	1.83e+01	1.16e+01	1.16e+01	1.16e+01	7.30e+00	7.30e+00	4.56e+00	4.56e+00	4.56e+00	4	4.56e+00	2.83e+00	2.83e+00	4.95e-02	4.95e-02	4.95e-02	4.95e-02	4.95e-02	Pred. No.

44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24
4 5 5	45	45	45	45	45	45	45	46	46	46	46	46	46	46	46	46	46	46	46	46
76.3 76.3	76.3	76.3	76.3	76.3	76.3	76.3	76.3	78.0	78.0	78.0	78.0	78.0	78.0	78.0	78.0	78.0	78.0	78.0	78.0	78.0
834 1978	565	554	430	430	428	314	119	2492	2492	2492	2161	1231	857	806	793	754	745	637	509	447
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SCD1_SCHPO	NO56_SOYBN	YER2_YEAST	GFAP_RAT	GFAP_MOUSE	GFAP_BOVIN	GCR_SHEEP	PTHY_CHICK	POLN_EEVV3	POLN_EEVVP	POLN_EEVVT	RRPL_CDVO	KIF4_MOUSE	MEDB_GIALA	SYFB_MYCGE	KATA_ARATH	KATC_ARATH	KATB_ARATH	PTMA_ECOLI	CPT7_PIG	KCC2_YEAST
SCD1 PROTEIN. MYOSIN HEAVY CHAIN, GI	LATE NODULIN 56 (N-56)	HYPOTHETICAL 62.3 KD P	GLIAL FIBRILLARY ACIDI	GLIAL FIBRILLARY ACIDI	GLIAL FIBRILLARY ACIDI	GLUCOCORTICOID RECEPTO	PARATHYROID HORMONE PR	NONSTRUCTURAL POLYPROT	NONSTRUCTURAL POLYPROT	NONSTRUCTURAL POLYPROT	RNA POLYMERASE BETA SU	KINESIN-LIKE PROTEIN K	MEDIAN BODY PROTEIN.	PHENYLALANYL-TRNA SYNT	KINESIN-LIKE PROTEIN A	KINESIN-LIKE PROTEIN C	KINESIN-LIKE PROTEIN B	PTS SYSTEM, MANNITOL-S	CYTOCHROME P450 XVIIA1	CALCIUM/CALMODULIN-DEP
4.44e+01 4.44e+01	4.44e+01	2.86e+01	2.86e+01	2.86e+01	2.86e+01	2.86e+01	2.86e+01	2.86e+01	2.86e+01		2.86e+01	2.86e+01	2.86e+01	2.86e+01						

R R R	R R	RA	RA	R R	RN	RL	RA	R	공	RN	P F	RX	RP :	Z 2	R R	RX	RΡ	RN	RĽ	₽3	7 7	RN	RL	₽	<b>R</b> 3	7 7	RN	8	გ	စ္တ	S 5	J 1	Į [	ij	ÃC	ij	RESULT
SEQUENCE OF 32-115. MEDLINE; 71063634.	70	POTTS J.T. JR.;	NIALL H.D., KEUTMANN H.T., SAUER R., HOGAN M.L., DAWSON B.F.,	SEQUENCE OF 32-115.				HAMILTON J.W., NIALL H.D., JACOBS J.W., KEUTMANN H.T., POTTS J.T. JR.,	SEQUENCE OF 26-115.		GENE 28:319-329(1984).	62483.	SEQUENCE FROM N.A.	ENDOCKTNOD.	WEAVER C.A., GORDON D.F., KEMPER B.;	05964.	DENCE		ACAD. SCI. U.S.A. 78	WEAVER C.A., GORDON D.F., KEMPER B.;	SECURICE FROM N.A.		NATL. ACAD	JR., RICH A.;	KRONENBERG H.W. MCDEVITT B.E., MAJZOUB J.A., NATHANS J., SHARP P.A.,	1 202 N		ARTIODACTY		TAURUS	PTH.	CAPT.	(NEL. O1,	(REL. 01, CREATED)		PTHY_BOVIN STANDARD; PRT; 115 AA.	

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Best Local Similarity 100.0%;
Matches 8; Conservative
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                                                                                                                                  Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 8; Conservative
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PIR; A01534; P
PIR; A24949; A
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PROC. NATL. ACAD. SCI. U.S.A. 67:1862-1869(1970).
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CONFLICT
SEQUENCE
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P52212;
01-OCT-1996
01-OCT-1996
01-OCT-1996
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PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00335;
HORMONE; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CANIS FAMILIARIS (DOG).
EUKARYOTA; METAZOA; CHORDATA;
EUTHERIA; CARNIVORA.
                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-PARATHYROID;

MEDLINE; 95369696.

ROSOL T.J., STEINMEYER C.L., MCCAULEY L.K., GRONE A.,

ROSOL T.J., STEINMEYER C.L.,

DEWILLE J.W., CAPEN C.C.;

GENE 160:241-243(1995).

GENE 160:241-243(1995).

-1- FUNCTION: FYH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS

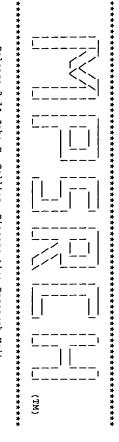
BONE AND PREVENTING THEIR RENAL EXCRETION.

EMBL; U15662; G558916; -.

EMBL; U15662; G558916; -.

EMBL; PS00335; PARATHYROID; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
                                                                                                                                                                                                                                                                    SIGNAL
PROPEP
CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                         HORMONE; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55 LRKKLQDV 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LRKKLQDV 8
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A24949; A24949.
A24949; A24949.
TTE: PS00335; PARATHYROID;
                                          55 LRKKLQDV 62
          \vdash
   LRKKLQDV 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1
26
32
106
115 AA;
                                                                                                                                                                                                                                                                       1
26
32
115 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25
31
115 P
106 V
12980 MW;
                                                                                                                                                                                                                                                                              25 B)
31 B)
115 P)
115 PW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 59; DB 1; Length 115; Pred. No. 4.95e-02; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PARATHYROID HORMONE.
V -> G (IN REF. 4).
; 673EA5F2 CRC32;
                                                                                                                                                                                                                                                                              BY SIMILARITY.
BY SIMILARITY.
PARATHYROID HORMONE.
W; 16ED0EBC CRC32;
                                                                                                                                            Score 59; DB 1; Length 115;
Pred. No. 4.95e-02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ۲
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 AA.
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                                                                                                                                                                     Gaps
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                                                                                                                                                                        0,
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Search completed: Thu Jul 30 11:15:51 1998 Job time : 7 secs.



MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 11:16:49 1998; MasPar time 3.69 Seconds 91.339 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: Title: >US-08-817-547A-33 (1-8) from US08817547A.pep 59 1 LRKKLQDV 8

Scoring table: PAM 150 Gap 15

Searched: 140542 segs, 42109429 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb15
1:sp\_fung1 2:sp\_human 3:sp\_invertebrate 4:sp\_mammal
5:sp\_mhc 6:sp\_organelle 7:sp\_phage 8:sp\_plant
9:sp\_bacteria 10:sp\_rodent 11:sp\_virus 12:sp\_vertebrate
13:sp\_unclassified

Statistics: Mean 23.168; Variance 27.952; scale 0.829

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

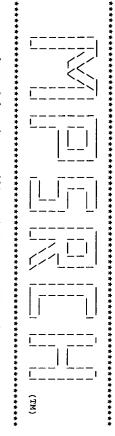
;	20	19	18	17	16	15	14	13	12	11	10	9	8	7	O	5	4	ω	2	۲,	Result
;	47	48	48	48	48	50	50	50	50	50	50	51	51	51	51	51	52	52	52	53	Score
	79.7	81.4	81.4	81.4	81.4	84.7	84.7	84.7	84.7	84.7	84.7				86.4	86.4	88.1	88.1	88.1	89.8	Query Match
	122	2346	481	385	164	1972	1938	1312	735	621	279	317	317	257	242	242	2475	929	105	398	Length
,	٥	w	ω	ω	9	10	10	N	w	10	10	4	4	œ	œ	œ	11	9	10	œ	BB
,	P71288	001385	Q18255	017076	P96113	008638	008639	Q92878	Q17750	Q63339	Q63338	019037	P79328	Q40700	P93468	Q40970	Q08358	032491	Q63473	004471	ID
	HYPOTHETICAL IS911 PRO	TPR HOMOLOG.	COSMID C27D9.	C38C3.3 PROTEIN.	POLYPEPTIDE DEFORMYLAS	MYOSIN.	MYOSIN.	RAD50.	C06G3.9 PROTEIN.	MYOSIN HEAVY CHAIN 21	MYOSIN HEAVY CHAIN (AA	MC1-R PROTEIN.	MELANOCYTE STIMULATING	BOX PROTEIN.	MADS-BOX FAMILY TRANSC	PUTATIVE MADS-BOX FAMI	POLYPROTEIN PP220.	PUTATIVE N6-ADEININE S	PARATHYROID HORMONE (F	SIMILAR TO SACCHAROMYC	Description
	2.386+01	1.50e+01	1.50e+01	1.50e+01	1.50e+01	5.84e+00	5.84e+00	5.84e+00	5.84e+00	5.84e+00	5.84e+00	3.61e+00	3.61e+00	3.61e+00	3.61e+00	3.61e+00	2.21e+00	2.21e+00	2.21e+00	1.35e+00	Pred. No.

975579 FROM BASES 263572 TO 2 027967 CONSERVED HYPOTHETICAL 040969 PUTATIVE MADS-BOX FAMI 029516 DNA PRIMASE, PUTATIVE. 978918 FISSION YEAST (FRAGMEN 013772 ARA70. 015307 RET FUSED GENE. 063618 CHICKEN RABAPTIN-5. 042351 CHICKEN RABAPTIN-5. 970609 MOUSE RABAPTIN-5. 970609 MOUSE RABAPTIN-5. 015276 RABAPTIN-5. 015276 CHROMOSOME SEGREGATION 035551 NEURONAL MYOSIN HEAVY 094658 CHLOROQUINE RESISTANCE 015791 CHLOROQUINE RESISTANCE 015792 CHLOROQUINE RESISTANCE 015792 CHLOROGUINE RESISTANCE 015792 CHACTONIN HB3 CG2 (CG2). 0166594 NONSTRUCTURAL POLYPROT 0966596 PUTATIVE REPLICASE. 066597 NONSTRUCTURAL POLYPROT 096806 PUTATIVE REPLICASE. 066597 NONSTRUCTURAL POLYPROT
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RROCCS	Qy RESULT	Qu Be Ma	RRA	RESULT O AC O AC O D T O O D O O O O O O O O O O O O O O
01-NOV-1996 (TREMBLREL. 01, CREATED) 01-NOV-1996 (TREMBLREL. 05, LAST SEQUENCE UPDATE) 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE) PARATHYROID HORMONE (FRAGMENT). PTH. RATTUS NORVEGICUS (RAT). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; RODENTIA. [1] SEQUENCE FROM N.A.	1 LRKKLQDV 8 1 LRKKLQDV 8 2 63473 PRELIMINA	Query Match 89.8%; Score 53; DB 8; Length 398; Best Local Similarity 62.5%; Pred. No. 1.35e+00; Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0; 328 LRKRLQEI 335	SEQUENCE FROM N.A. STRAIN-CV. COLUMBIA; STRAIN-CV. COLUMBIA; STRAIN-CV. COLUMBIA; SYSOTRAIA V.S., OSBORNE B.I., TORIUMI M., YU G., OJI O., VYSOTSKAIA V.S., OSBORNE B.I., TORIUMI M., YU G., OJI O., SHEN Y.K., BUBELLER E., CONWAY A.B., CONWAY A.R., DEWAR K., FENG J., KIM C., KURTZ D., LI Y., SHINN P., SUN H., DAVIS R.W., ECKER J.R., FEDERSPIEL N.A., THEOLOGIS A.; SUBMITTED (APR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS. EMBL; ACOO1229; G2190544; SEQUENCE 398 AA; 45629 MW; 2DF59F1E CRC32;	JT 1  O4471;  O1-JUL-1997 (TREMBLEEL. 04, CREATED) O1-JUL-1997 (TREMBLEEL. 04, LAST SEQUENCE UPDATE) O1-JUL-1997 (TREMBLEEL. 04, LAST SEQUENCE UPDATE) O1-JUL-1997 (TREMBLEEL. 04, LAST SEQUENCE UPDATE) SIMILAR TO SACCHAROMYCES HYPOTHETICAL PROTEIN P9642.2. F5114.7. ARABIOLOFIS THALIANA (MOUSE-EAR CRESS). EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE; CAPPARALES; CRUCIFERAE.

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RC TISSUE-THYROID, AND PARATHYROID;
RA SCHELZER H.J. GOSS G., MAKER H.;
RL ADV. CENE TECHNOL. 21:288-225(1884).

DR EMBL. M54875; G601933;
FT NON_TER NO. TER NO. TERNO. TER NO. TERNO. TER NO. TERNO. T
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MPsrch\_pp 9 :: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 11:20:11 1998;

MasPar time 2.56 Seconds 41.969 Million cell updates/sec

**Tabular output not generated** 

Title: Sequence: Description: Perfect Score: (1-7) from US08817547A.pep 1 LRKKLQD 7 >US-08-817-547A-34

Scoring table:

PAM 150 Gap 15

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Statistics: Mean 15.842; Variance 50.654; scale 0.313

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Result
11111111111111111111111111111111111111	1
5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	Score
100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0	Query
	Query Match Length
333333333333333333333333333333333333333	
26 27 27 27 27 27 27 27 27 27 27 27 27 27	BG.
R62432 R58230 R58231 R58231 R58231 R20003 W20003 W20003 W17963 R74446 R74446 R74448 R74448 R74448 R74448 R74448 R74443 R74443 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R7438 R74439 R7438 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R74439 R744	ij
Accelerator peptide b Human parathyroid hor [Lys(For)26, Lys(For) [Lys32]-hPTH(1-34)-NH Human parathyroid hor Cyclised [Nle 8,18, T Cyclised [Nle 8,18, T Cyclised [Nle 8,18, T Human PTH analogue (C Parathyroid hormone p	Description
3.78e+01 3.78e+01 3.78e+01 3.78e+01 3.78e+01 3.78e+01 3.78e+01 3.78e+01 3.78e+01 3.78e+01 3.78e+01 3.78e+01 3.78e+01 3.78e+01 3.78e+01 3.78e+01 3.78e+01 3.78e+01 3.78e+01 3.78e+01 3.78e+01 3.78e+01 3.78e+01 3.78e+01 3.78e+01 3.78e+01 3.78e+01 3.78e+01 3.78e+01 3.78e+01	Pred. No.

52 100.0 36 9 K58285   Alaz2j-hPH(1-36)-NH 52 100.0 36 9 R58069   Isopropyl-[LB,K(Isopropyl-100.0 38 9 R58136   Arg19]-hPH(1-38)-OH 52 100.0 38 9 R58136   Arg19]-hPH(1-38)-OH 52 100.0 84 426 P30015   Human parathyroid hor 52 100.0 84 4 R23356   Bovine parathyroid hor 52 100.0 84 4 R23357   Bovine parathyroid hor 52 100.0 84 4 R23241   Human parathyroid hor 52 100.0 84 4 R23242   Bovine parathyroid hor 52 100.0 84 4 R23242   Bovine parathyroid hor 52 100.0 84 4 R23243   Porcine parathyroid hor 52 100.0 84 4 R23251   Bovine parathyroid hor 52 100.0 84 4 R23253   Bovine parathyroid hor 52 100.0 84 4 R23253   Bovine parathyroid hor 52 100.0 84 4 R23273   Bovine parathyroid hor 52 100.0 84 4 R23273   Bovine parathyroid hor 52 100.0 84 4 R23256   Bovine parathyroid hor 52 100.0 84 4 R23235   Bovine parathyroid hor 52 100.0 84 4 R23235   Bovine parathyroid hor 52 100.0 84 4 R23235   Bovine
.0 36 9 R58695 [ALA23]-NPTH([-3] .0 36 9 R58059 ISOPROSPI-[LB,K] .0 36 9 R58136 [Arg19]-hPTH([-3] .0 38 9 R58136 [Arg19]-hPTH([-3] .0 38 9 R58136 [Arg19]-hPTH([1-3] .0 38 9 R58136 [Arg19]-hPTH([1-3] .0 44 26 P30015 Human parathyrol .0 44 27 W25687 Human parathyrol .0 84 4 R23357 Bovine parathyrol .0 84 4 R23241 Human parathyrol .0 84 4 R23242 Human parathyrol .0 84 4 R23243 Porcine parathyrol .0 84 4 R23243 Human parathyrol .0 84 4 R23243 Human parathyrol .0 84 4 R23251 Bovine parathyrol .0 84 4 R23253 Howan parathyrol .0 84 4 R23253 Howan parathyrol .0 84 4 R23273 Bovine parathyrol .0 84 4 R23273 Bovine parathyrol .0 84 4 R23256 Human parathyrol
9 R58285 [Ala2J]-nPTH([-3] 9 R58026 Isopropy]-[IB,K] 9 R58026 [D-Gln29]-hPTH([-3] 9 R58136 [Arg19]-hPTH([-3] 9 R58108 [Arg14]-hPTH([-3] 126 P30015 Human parathyroi 4 R2356 Bovine parathyroi 4 R23241 Human parathyroi 4 R23242 Bovine parathyroi 4 R23453 Porcine parathyroi 4 R23519 Bovine parathyroi 4 R23519 Bovine parathyroi 4 R23273 Human parathyroi 4 R23273 Human parathyroi 4 R23256 Bovine parathyroi 4 R23256 Bovine parathyroi 4 R23522 Human parathyroi 4 R23527 Human parathyroi 4 R23539 Human parathyroi 6 R23239 Human parathyroi 6 R23245 Human parathyroi 7 R34339 Human parathyroi 6 R23245 Human parathyroi
9 K58285   K18285   [Ala23] - nPTH(1-3) 9 K58069   Isopropyl - [18, K] 9 K580136   [Arg19] - hPTH(1-3) 9 K58136   [Arg14] - hPTH(1-3) 16 P30015   Human parathyroi 17 W25687   Human parathyroi 18 R23357   Bovine parathyroi 18 R23242   Human parathyroi 18 R23243   Human parathyroi 18 R23243   Human parathyroi 18 R23273   Human parathyroi 19 K58070   R23273   Human parathyroi 19 K58070   R23273   Human parathyroi 19 K58070   R23273   Human parathyroi 10 K78070   R23273   Human parathyroi
IABAZJ - NPIH (1-3 ISOPTORY) - [LB, K (1 ISOPTORY] - [LB, K (2 ISO
opyl-[18,K] n29]-hPTH(19) p]-hPTH(1-3) 4]-hPTH(1-3) 4]-hPTH(1-3) parathyroi parathyroi parathyroi e parathyroi e parathyroi e parathyroi e parathyro e parathyroi e parathyroi e parathyroi e parathyroi parathyroi parathyroi parathyroi parathyroi parathyroi parathyroi

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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SUNZ) SUNSTAR CHEM IND CO LTD. WPI; 95-157631/21.
R08300 standard; protein; 34 AA.
R08300;
18-FEB-1991 (first entry)
Human parathyroid hormone analogue, Trp12 hPTH(7-34).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               accelerator is applied by opening the ginglva, treating the tissue destroyed by periodontitis and applying the accelerator in the periodontal pocket. The accelerator reduces the down growth of the epithelium and accelerates fibre adhesion and regenerates cement. Sequence 34 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-JUL-1995 (first entry)
Accelerator peptide basic region peptide, P-8.
Accelerator; basic amino acid; cell growth factor; growth; gingiva;
periodontal tissue; regeneration; periodontitits; periodontal pocket
down growth; epithelium; fibre adhesion; cement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 3; 7pp; Japanese.

The sequences in R62425-36 are peptide fragments of an accelerator protein which contain at least two basic amino acids. The accelerate also comprises a cell growth factor. The accelerator may be used to accelerate the growth of periodontal tissue regeneration. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
J06234653-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aminoacid residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Accelerator for regenerating periodontal tissue - comprises peptide having 3-34 aminoacid residues having connected basic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R62432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R62432 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-FEB-1993; 045998.
10-FEB-1993; JP-0459
                                                                                                                                                                                                                                                                                                                                  24 lrkklqd 30
                                                                                                                                                                                                                                                                                        1 LRKKLQD 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 52; DB 26;
Pred. No. 3.78e+01;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 34;
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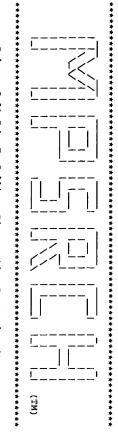
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Steoporosis; hypercalcemia; hyperparathyroidism; hypertension.

Steoporosis; hypercalcemia; hyperparathyroidism; hypertension.

Steoporosis; hypercalcemia; hyperparathyroidism; hypertension.

Steoporosis; hypercalcemia; hyperparathyroidism; hypertension.

Proceedings of the process of the p
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MPsrch\_pp on: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 11:19:28 1998; MasPar time 3.06 Seconds 83.440 Million cell updates/sec

Title: Tabular output not generated.

Description: Perfect Score: Sequence: >US-08-817-547A-34 (1-7) from US08817547A.pep 52 1 LRKKLQD 7

Scoring table: PAM 150 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 21.946; Variance 32.007; scale 0.686

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

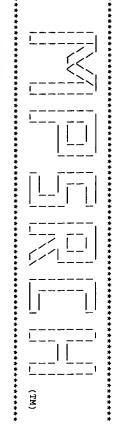
#### SUMMARIES

NO.	Score 52				1	Pred. No. 4.07e+00
ω κ	52	100.0	34 4 5	1HTH	parathyroid normone 4 cyclic parathyroid ho	4.07e+00
4	52					4.07e+00
G	52	•	34		parathyroid hormone (	4.07e+00
თ	52	100.0			parathyroid hormone (	4.07e+00
7	52	100.0	36		_	4.07e+00
8	52	100.0	7		_	4.07e+00
9	52	100.0	~		parathyroid hormone (	4.07e+00
10	52	100.0			parathyroid hormone -	4.07e+00
11	52	100.0				4.07e+00
12	52	100.0		2 A05091	parathyroid hormone p	4.07e+00
13	52	100.0		L PTHU	parathyroid hormone p	4.07e+00
14	52	100.0		L PTPG	parathyroid hormone p	4.07e+00
15	52	100.0		L PTBO	parathyroid hormone p	4.07e+00
16	51	98.1		2 853306	otic prot	6.22e+00
17	47	90.4	133 :	2 875121	hypothetical protein	3.23e+01
18	47	90.4			hypothetical protein	3.23e+01
19	47	•			DNA primase	3.23e+01
20	46	88.5		2 S56508	hypothetical	4.80e+01
21	46	•			hypothetical protei	4.80e+01
22	46	•		ര	-	4.80e+01
23	46				7	4.80e+0

46 88.5 509 2 S22339 StearOid ITalpha-monood 66 88.5 745 2 S48019 kinesin-related prote 68.5 745 2 S48020 kinesin-related prote 68.5 754 2 S48020 kinesin-related prote 68.5 754 2 S48020 kinesin-related prote 69.5 806 2 E64221 phenylalaninetRNA 1 69.5 89.9 2 S51441 probable membrane prote 79.0 1 C44213 probable membrane prote 88.5 1231 2 A54803 microtubule-associate 88.5 2492 1 A44213 probable membrane prote 88.5 2492 1 A44213 prostructural polyprote 88.5 2492 1 MNWVID protection algorithms of 88.5 2492 1 MNWVID protection protein 75.5 2 S2577 phypothetical protein 75.5 2 S2577 phypothetical protein 75.5 2 S57398 protein Emeric 86.5 430 1 VEMSGF 91.1 Testriction—Emeric 86.5 443 2 S57338 uvsH protein - Emeric 65.5 443 2 S57338 uvsH protein finge 75.5 2 S5494 type I restriction—no 86.5 1999 1 S21801 myosin heavy chain, m 65.5 2475 2 S35307 polyportein pp220 pre	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	**
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2 S22399 2 Steroid 17athba-mm 2 S22399 2 Steroid 17athba-mm 2 S48019 2 S48020 2 S48020 2 S48020 2 S48200 2 S4821 2 S51341 2 S51341 3 Probable membrane 2 A54803 3 Probable membrane 2 A54803 1 C44213 2 Probable membrane 2 A54803 3 Probable membrane 2 A54803 1 Probable membrane 2 A54803 2 Probable membrane 2 A54803 3 Probable membrane 2 A54803 3 Probable membrane 2 A54803 4 Probable membrane 2 A54801 5 Probable membrane 2 Probable membrane 2 A54801 5 Probable membrane 2 Probable			σ.		σ.		5	σ.		ς,	8	8	8	8	8	8	8	ω.	ω.	8	8	
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steroid 17alpha-ma steroid 17alpha-ma kinesin-related py kinesin-related py kinesin-related py kinesin-related py kinesin-related py kinesin-related py phenylalaninetRI probable membrane microtubuleassoc nonstructural poly nonstructural poly nonstru	N	Н	Ŋ	N	N	ب	N	N	N	N	Ь	بر	Н	N	N	N	N	N	N	Н	N	٨
Zait fa to oll the	S35307	S21801	C69463	S55494	5732	VEMSGF	v	JC5492	S57793	S22577	MNWVTD	A44213	C44213	A54803	S51341	E64221	S34830	S48020	S48019	WQEC2M	22	4007
	protein p	in heavy chain,	I restriction-	type zinc fing	protein - Emeri	fibrillary	protein -		tein		tructural polypr	l polypr	l polypr	ssoci	membrane	÷	in-related pro	-related prot	prot	ase s	steroid 17alpha-monoo	₹

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COMMENT Resolution: not applicable
COMMENT RETWORDS
COMMENT RETWORDS
COMMENT RETWORDS
COMMENT RETWORDS
COMMENT RETWORDS
COMMENT RETWORDS
COMMENT RESOLUTION: Not applicable
DATE:

BARTURE #region helix (right hand alpha) #region hel
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srch\_pp protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 11:18:09 1998; MasPar time 2.07 Seconds 84.981 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Title: >US-08-817-547A-34 (1-7) from US08817547A.pep 52 1 LRKKLQD 7

Sequence:

Scoring table: PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 23.054; Variance 26.515; scale 0.869

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

222223	No.
V U U U U U 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Score
11000 11000 11000 11000 11000 11000 11000 11000 11000 11000 11000 11000 11000 11000 11000 11000 11000 11000 11000 11000 11000	Query Match
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	B
PTHY_BOVIN PTHY_CAWFA PTHY_PIG PTHY_HIVAN Y04E_MYCTU Y191_ECOLI Y191_SALTY KCC2_YEAST CPT7_PIG PTMA_ECOLI KATE_ARATH KATC_ARATH KATC_ARATH KATC_ARATH KATA_MOGGE FOLN_EEVVT POLN_EEVVT POLN_EEVVI POLN	ID
PARATHYROID HORMONE PR PARATHYROID HORMONE PR HYPOTHETICAL 17.8 KD INSERTION ELEMENT IS91 INSERTION ELEMENT IS91 INSERTION ELEMENT IS91 INSERTION ALEMENT IS91 INSERTION ALEMENT IS91 INSERTION ALEMENT IS91 CALCIUM/CALMODULIN-DEP CYTOCHROME P450 XVIIA1 PTS SYSTEM, MANNITOL-S KINESIN-LIKE PROTEIN A KINESIN-LIKE PROTEIN A PHENYLALANYL-TRABA SYNT KINESIN-LIKE PROTEIN K NONSTRUCTURAL POLYPROT NONSTRUCTURAL POLYPROT	Description
6.49e-01 6.49e-01 6.49e-01 6.49e-01 6.49e-01 7.85e-00 1.26e+00 1.26e+00 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.26e+01 1.2	Pred. No.

44	43	4 4	39	38	37	36	<u>3</u> 5	34	<u>ω</u>	32	31	30	29	28	27	26	25	24
44	4 4 4 4	44	44	44	44	44	44	44	44	44	44	44	44	44	44	45	45	45
84.6	84. 66.	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	84.6	86.5	86.5	86.5
752 2843	630 669	617	470	463	461	458	453	450	444	335	314	310	182	110	100	4725	430	430
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HPR1_YEAST APC_HUMAN	Y019_METJA	ASMA_ECOLI	BFR1_YEAST	VIM4_XENLA	VIME_ONCMY	IF3T_TORCA	OP2_MAIZE	VIMB_CARAU	CIT1_KLEPN	HIS9_YEAST	GCR_SHEEP	SYNK_ARATH	Y922_HAEIN	PTCA_BACSU	RR14_PORPU	DYHC_DICDI	GFAP_MOUSE	GFAP_RAT
POLYPC	HYPOTHETICAL PROTEIN M HYPOTHETICAL 76.2 KD P	ASMA PROTEIN PRECURSOR	BAR SEGREGAT	VIMENTIN 4.	•	TYPE III INTERMEDIATE	OPAQUE-2 REGULATORY PR	VIMENTIN BETA.	CITRATE-PROTON SYMPORT	HISTIDINOL-PHOSPHATASE	GLUCOCORTICOID RECEPTO	SYNTAXIN-RELATED PROTE	HYPOTHETICAL LIPOPROTE	PTS SYSTEM, CELLOBIOSE	CHLOROPLAST 30S RIBOSO	DYNEIN HEAVY CHAIN, CY	FIBRILLARY	GLIAL FIBRILLARY ACIDI
3.20e+01 3.20e+01	3.20e+01 3.20e+01	3.20e+01	3.20e+01	3.20e+01	3.20e+01	3.20e+01	3.20e+01	3.20e+01	3.20e+01	3.20e+01	3.20e+01	3.20e+01	3.20c+01	3.20e+01	3.20e+01	2.02e+01	2.02e+01	2.02e+01

SU	1171/BOVIN 01268; 1-JUL-1986 (RE 1-JUL-1986 (RE 1-NOV-1997 (RE ARATHYROID HOR TH. TH. TAURUS (BOV UKARYOTA; META UTHERIA; ARTIO 1 EQUENCE FROM N	ATED) I SEQ I ANN RSOR ATA; ATA;	RT; 115 A ENCE UPDATE TATION UPDA PARATHYRIN) ERTEBRATA; ERTEBRATA; 6:4981-4985	A. (PTH). TETRAPODA; MAMMALIA; A., NATHANS J., SHARP
	(REL.	1, LAST 5, LAST PRECUR	UENCE UPDATE) OTATION UPDAT (PARATHYRIN)	E) (PTH).
3 X X X 3	TAURUS RYOTA; ERIA;	RDATA;		
\$ £ %	SEQUENCE FROM N.A. MEDLINE; 80056617.			
55	KRONENBERG H.M., MC	, B	, MAJZOUB J.A	THANS J.,
Z F	PROC. NATL. ACAD. S	U.S.A.	76:4981-4985(	1979).
7 X X			KEMPER B.;	
R R	PROC. NATL. ACAD. S	5. A.	78:4073-4077(1981).	1981).
RX X	SEQUENCE FROM N.A. MEDLINE; 83105964.			
₽₽	₽.	H	28:411-424(1982).	
R R V	[4] SEQUENCE FROM N.A.			
R R	MEDLINE; 84262483	7)	TT. M S MEAD	א א א א א א א א א א א א א א א א א א א
R P.	GENE 28:319-329(1984).			
R R X	SEQUENCE OF 26-115.			
RA	NOL	L H.D., JACOBS	J.W.,	KEUTMANN H.T., POTTS J.T.
R P 3	PROC. NATL. ACAD. S	SCI. U.S.A.	71:653-656(1974)	74).
R R	SEQUENCE OF 32-115. MEDLINE; 71076162.			
R.P.	NIALL H.D., KEUTMANN H.T.,	N H.T., SAUER	R., HOGAN	M.L., DAWSON B.F.,
2 P 3	HOPPE-SEYLER'S Z. PHYSIOL. CHEM.	HYSIOL. CHE	M. 351:1586-1588(1970).	588(1970).
R R	SEQUENCE OF 32-115. MEDLINE; 71063634.			

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RN C E E C
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Best Local S
Matches
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                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; V00106; G85; -.

EMBL; J00023; G163641; -.

EMBL; J00024; G163643; A.T.SEQ.

EMBL; J00024; E18249; ALT_INIT.

EMBL; J00024; E18250; ALT_INIT.

EMBL; K01938; G163647; -.

EMBL; M25082; G163645; -.
                                             Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BREWER H.B. JR., RONAN PROC. NATL. ACAD. SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 71091588.

POTTS J.T. JR., TREGEAR G.W., KEUTMANN H.T., NIALL H.D., SAUER R., POTTS J.T., DAWSON B.F., HOGAN M.L., AURBACH G.D.;

DEFTOS L.J., DAWSON B.F., HOGAN M.L., AURBACH G.D.;

PROC. NATL ACAD. SCI. U.S.A. 68:63-67(1971).

PROC. NATL ACAD. SCI. U.S.A. 68:63-67(1971).

-:- FUNCTION. PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN BONE AND PREVENTING THEIR RENAL EXCRETION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYNTHESIS OF 32-65. MEDLINE; 71091588.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HORMONE; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                                                                                       PTHY_CANFA STANDARD; PRT; 115 AA.

P52212;

P52212;

01-OCT-1996 (REL. 34, CREATED)

01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)

01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)

PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                          SIGNAL
PROPEP
CHAIN
SEQUENCE
                                                                                                                                                            CANIS FAMILIARIS (DOG).
EUKARYOTA; METAZOA; CHORDATA;
EUTHERIA; CARNIYORA.
                                                                                                                                      PROSITE; PS00335; PARATHYROID; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 LRKKLQD 61
                                                                                                                                                                                                                                                                                                                                                                                                                           1 LRKKLOD 7
               55 LRKKLQD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A01534; PTBO.
A24949; A24949.
SITE; PS00335; PARATHYROID;
  LRKKLQD 7
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Similarity 100.0%;
7; Conservative
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115 AA;
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26
32
115 AA;
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31
9ARATHYROID HORMONE.
115
106
V -> G (IN REF. 4).
12980 MW; 673EA5F2 CRC32;
                                                                                            25 B)
31 B)
115 P/
; 12957 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R.;
U.S.A. 67:1862-1869(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 52; DB 1; Length 115;
Pred. No. 6.49e-01;
0; Mismatches 0; Indels
                                                                                             BY SIMILARITY.
BY SIMILARITY.
PARATHYROID HORMONE.
W; 16ED0EBC CRC32;
                                                  Score 52; DB 1; L
Pred. No. 6.49e-01;
0; Mismatches 0
                                                                                                                                                                                                                                                                                         VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                      115 AA
                                                                          Length 115;
                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                        0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                        Gaps
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Search completed: Thu Jul 30 11:18:16 1998 Job time : 7 secs.

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Result
                                                                                                                                                                                                                                                              Statistics:
                                                                                                                                                                                                                                                                                                                  Database:
                                                                                                                                                                                                                                                                                                                                          Post-processing:
                                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                            Description:
Perfect Score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Tabular output
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                on:
 Pred. No.
                                                                                                                                                                                   Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Release 3.1A John F. Collins, Biocomputing Research Copyright (c) 1993-1998 University of Edinburgh, U Distribution rights by Oxford Molecular Ltd
 No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed. s derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein - protein database search, using Smith-Waterman algorithm
                                                                                                                                                                                   Match
                                                                                                                                                                                                                                                                                                                                                                                                                                              not generated.
 Minimum I
                                                                                                                                                                                                                                                                                                                                                                           PAM 150
Gap 15
                                                                                                                                                                                                                                                              Mean 22.212;
                                                                                                                                                                                                                                                                                                                sptremb15
                                                                                                                                                                                                                                                                                                                                                           140542 seqs, 42109429 residues
                                                                                                                                                                                                                                                                                                                                                                                                             >US-08-817-547A-34
(1-7) from US08817547A.pep
52
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thu Jul 30 11:18:33 1998;
                                                                                                                                                                                                                                                                              1:sp_fung1 2:sp_human 3:sp_invertebrate 4:sp_mammal 5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant 9:sp_bacter1a 10:sp_rodent 11:sp_virus 12:sp_vertebrate 13:sp_unclassified
                                                                                                                                                                                                                                                                                                                                                                                                     LRKKLQD 7
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1034
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first
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032491
Q40970
P93468
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004471
Q18255
P73917
Q40969
029516
Q63618
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075679
P75679
Q05436
P96187
Q56689
P78918
Q06132
Q17117
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                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                  summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MasPar time 3.62 Seconds
81.362 Million cell updates/sec
TRANSMEMBRANE TRANSCRI
FISSION YEAST (FRAGMEN
CHROMOSOME XII COSMID
M151.4 PROTEIN.
                                                             YXZC
                                                                  DNA PRIMASE, PUTATIVE.
ESPIN.
HYPOTHETICAL IS911 PRO
                                                                                                                                      PARATHYROID HORMONE (F
PUTATIVE N6-ADEININE S
PUTATIVE MADS-BOX FAMI
MADS-BOX FAMILY TRANSC
                                                                                             COSMID C27D9.
HYPOTHETICAL 15.4 KD P
PUTATIVE MADS-BOX FAMI
                                           FROM BASES 263572 TO 2
CAM KINASE II (FRAGMEN
                                                                                                                        SIMILAR TO SACCHAROMYC
                                                                                                                                BOX PROTEIN.
                                                                                                                                                                                  Description
                                                   PROTEIN.
                                                                                                                                                                                                                                                              scale 0.849
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                                           1.46e+00
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1.07e+01
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46 88.5 2493 11 Q66592 NONSTRUCTURAL POLYPROT 46 88.5 2493 11 Q86594 NONSTRUCTURAL POLYPROT 46 88.5 2497 11 Q86978 NONSTRUCTURAL POLYPROT 46 88.5 2497 11 Q86978 NONSTRUCTURAL POLYPROT 45 86.5 139 Q52560 ORF WITHIN IS1240. 45 86.5 129 P96373 KDPE. 45 86.5 226 P96373 KDPE. 45 86.5 275 P96373 KDPE. 45 86.5 276 P96373 MADS-BOX PROTEIN AGL3. 46 86.5 356 1 Q0018 DNA REPAIR AND RECOMBI 47 10 Q002398 DNA REPAIR AND RECOMBI 48 86.5 1393 Q17750 C0663.9 PROTEIN. 49 86.5 1393 Q46545 TYPE I RESTRICTION-MOD 40 86.5 1390 Q46545 ORF1130. 41 84.6 237 3 Q21772 POLYPROTEIN (FRAG 42 84.6 237 3 Q21772 R06C7.2. 43 84.6 237 8 Q041835 DNA BOX PROTEIN (FRAG 44 84.6 237 8 Q041835 DNA BOX PROTEIN (FRAG 44 84.6 237 8 Q041835 DNA BINDING PROTEIN OP 45 86.5 931 2 P79042 MADS BOX PROTEIN (FRAG 46 84.6 237 8 Q04191 HUNTINGTIN INTERACTING 47 84.6 914 2 Q00291 HUNTINGTIN INTERACTING 48 84.6 914 12 Q00291 ADENOMATOUS POLYPOSIS
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11 Q66592 NONSTRUCTURAL POLYPH 11 Q88978 NONSTRUCTURAL POLYPH 11 Q88978 NONSTRUCTURAL POLYPH 11 Q88978 NONSTRUCTURAL POLYPH 1240 ORF WITHIN IS1240. 1240 Q4797 INSERTION SEQUENCE I 1240 P96373 KDPE. 1241 P96373 P96781 RAND RECON 1241 P96373 DNA REPAIR AND RECON 1241 P96373 DNA REPAIR AND RECON 1241 P96373 DNA REPAIR AND RECON 1241 P96373 CO663.9 PROTEIN PP220. 1241 P96373 NEURONAL WOSIN HEAV 1241 P96373 P96211.1. 1241 P96373 P96211.1. 1241 P96373 P96211.1. 1341 P96373 P96211.1. 1441 P96373 P96211.1. 1441 P96373 P96211 P96220. 1441 P96373 P96373 P96220. 1441 P96373 P9637
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TRUCTURAL POLYPR TRUCTURAL POLYPR TRUCTURAL POLYPR MITHIN IS1240.  MITHIN IS1240.  RITION SEQUENCE I  FROM PROTEIN AGI TIVE TRANSPOSAST REPAIR AND RECON REPAIR AND RECON 3.9 PROTEIN. I RESTRICTION-N 1030. I RESTRICTION-N 111.1. 11.1. 11.1. 11.1. 11.1. 11.1. 12. 13. 13. 13. 14. 15. 16. 17. 17. 18. 18. 18. 18. 18. 18. 18. 18. 18. 18

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01-NOV-1996
01-JAN-1998
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                                                                                                                                                                                         032491
032491
032491
01-JAN 1998 (TREMBLREL 05, CREATED)
01-JAN 1998 (TREMBLREL 05, LAST SEQUENCE UPDATE)
01-JAN 1998 (TREMBLREL 05, LAST ANNOTATION UPDATE)
PUTATIVE NOF-ADEININE SPECIFIC METHYLTRANSFERASE.
BACTEROIDES NODOSUS (DICHELOBACTER NODOSUS).
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; ANAEROBIC
SEQUENCE FROM N.A.
STRAIN-A198;
MEDLINE; 96118688.
HARING V., BILLINGTON S.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-THYROID, AND PARATHYROID; SCHMELZER H.J., GROSS G., MAYER H.; ADV. GENE TECHNOL. 21:228-229(1984). EMBL; M54875; G601933; -. NON_TER 1 1 1
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
                                                                                                                                                                     BACTEROIDACEAE.
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Local Similarity 100.0%;
les 7; Conservativo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45 LRKKLQD 51
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
   WRIGHT C.L., HUGGINS A.S., KATZ M.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 52; DB 10;
Pred. No. 8.70e-01;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 105
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RA ROOD J.L.
RI MICROBIOLOGY, (22317805; -
DR SHELL 20243; (22317805; -
NW TANKSPERASE, METHYLTRANSSERRSE.
SO SEQUENCE 929 AA, 106474 MW; 4085E117 CRC32;
SQ SEQUENCE 929 AA, 106474 MW; 4085E117 CRC32;
Best Local Similarity 100.0%; Pred No. 8.70e-01;
Best Local Similarity 100.0%; Pred No. 8.70e-01;
METCHES 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

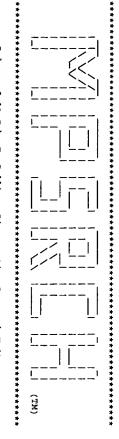
METCHES 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 42 LRKHLOD 48

Qy 1 LRKHLOD 7

Search completed: Thu Jul 30 11:19:10 1998

JOB time: 37 secs.
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. 9n.: Thu Jul 30 11:22:40 1998; MasPar time 2.49 Seconds 30.840 Million cell updates/sec

Sequence: Perfect Score: Description: >US-08-817-547A-36 (1-5) from US08817547A.pep 39 1 LRKKL 5

Title:

Scoring table: PAM 150 Gap 15

Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq31-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27

Statistics: Mean 14.364; Variance 43.704; scale 0.329

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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R2
R23473
R2
7 W.
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R5
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RESULT
ID RI
AC RI
DT 20
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                                                                                                                                                                                                                                                     Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                Disclosure; Page 3; 7pp; Japanese.

The sequences in R62425-36 are peptide fragments of an accelerator protein which contain at least two basic amino acids. The accelerator also comprises a cell growth factor. The accelerator may be used to accelerate the growth of periodontal tissue regeneration. The accelerator is applied by opening the gingliva, treating the tissue destroyed by periodontitis and applying the accelerator in the periodontal pocket. The accelerator reduces the down growth of the epithelium and accelerates fibre adhesion and regenerates cement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-JUL-1995 (first entry)
Accelerator peptide basic region peptide, P-8.
Accelerator; basic amino acid; cell growth factor; growth; gingiva;
periodontal tissue; regeneration; periodontitis; periodontal pocket;
down growth; epithelium; fibre adhesion; cement.
R58040;
20-SEP-1994 (first entry)
[L8,Q18,A29,E30,I31]-hPTH(1-34)-OH
                                                R58040 standard;
                                                                                                                                                                                                                                                    epithelium and ac
Sequence 34 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                   Accelerator for regenerating periodontal tissue - comprises peptide having 3-34 aminoacid residues having connected basic aminoacid residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-FEB-1993; 045998.
10-FEB-1993; JP-045998.
(SUMZ) SUNSTAR CHEM IND CO LTD.
WPI; 95-157631/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
J06234653-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R62432 standard;
R62432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-AUG-1994.
                                                                                                                                                   24 lrkkl 28
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                                                   peptide;
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Pred. No. 3.76e+02;
0; M1smatches 0
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                                                                                                                                                                                                               Length 34;
                                                                                                                                                                                     Indels
                                                                                                                                                                                    0;
                                                                                                                                                                                     Gaps
                                                                                                                                                                                     0
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KW Human parathyroid hormone; hPTH; variant; analogue;
KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
KW hypoparathyroidism.

OS 971676-A,
PN 6276776-A,
PN 6276
```

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\* (MI)

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

"srch\_pp protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 11:22:05 1998; MasPar time 2.97 Seconds 61.502 Million cell updates/sec

Tabular output not generated.

Title: Description: Perfect Score: Sequence: >US-08-817-547A-36 (1-5) from US08817547A.pep 39 1 LRKKL 5

Scoring table: PAM 150 Gap 15

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nr13d

Statistics: Mean 20.005; Variance 26.164; scale 0.765

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

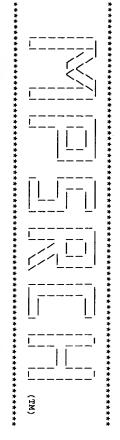
#### SUMMARIES

1 3 3 3 4 4 4 5 5 5 6 5 7 6 5 7 7 8 8 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Sult No.
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500	500	492	492	273	273	273	273	273	273	273	273	273	273	273	273	273	273	273	273	273	
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1ECGB	1ECFB	1ECFA	1ECGA	1R08A	1HRIA	1RUIA	2RR1A	2HWCA	2R04A	1R09A	2HWBA	2R06A	2RS3A	2RS5A	4 RHVA	2RM2A	2RS1A	2R07A	1RUJA	1RUDA	1
glutamine phosphoribo	glutamine phosphoribo	glutamine phosphoribo	glutamine phosphoribo	coat protein VP1 (wit	coat protein VP1 (wit	4 mut	coat protein VP1 (wit	VP1 n	coat protein VP1 (wit	coat protein VP1 (wit	coat protein VP1 muta	coat protein VP1 (wit	coat protein VP1 (wit	coat protein VP1 (wit	VP1,	coat protein VP1 (wit	VP1	coat protein VP1 (wit	rhinovirus 14 mutant	rhinovirus 14 mutant	***************************************
1.53e+02	1.53e+02	1.53e+02	1.53e+02	1.53e+02	1.53e+02	1.53e+02	1.53e+02	1.53e+02	1.53e+02	1.53e+02	1.53e+02	1.53e+02	1.53e+02	1.53e+02	1.53e+02	1.53e+02	1.53e+02	1.53e+02	1.53e+02	1.53e+02	1.000

Ъ COMMENT
KEYWORDS
FEATURE
2-9
15-25
SUMMARY δÔ Query Match 100.0%; Score 39; DB 5; Length 34; Best Local Similarity 100.0%; Pred. No. 1.53e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 21 LRKKL 25 ||||| 1 LRKKL 5 Determination: NMR disease mutation; hormone; signal #region helix (right hand alpha)\
#region helix (right hand alpha)
#length 34 #molecular-weight 4128 #checksum 5508 0;

Search completed: Thu Jul 30 11:22:22 1998 Job time : 17 secs.



Psrch\_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Jul 30 11:20:45 1998; MasPar time 2.01 Seconds 62.459 Million cell updates/sec

Tabular output not generated.

Description:
Perfect Score:
Sequence: Title: >US-08-817-547A-36 (1-5) from US08817547A.pep 39 1 LRKKL 5

Scoring table: PAM 150 Gap 15

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 21.052; Variance 21.024; scale 1.001

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

2	No.	Score	Query Match	Query Match Length	DB	Ħ	Description	Pred. No.
	_	39	100.0	86	۳ ا	FIS_ECOLI	FACTOR-FOR-INVERSION S	4.38e+01
	Ν	39	100.0	100	<b>-</b>	YI91_ECOLI	INSERTION ELEMENT IS91	4.38e+01
	ω	39	100.0	112	ᆫ	YI91_SHIDY	ELEMENT	4.38e+01
	4	39	100.0	115	_	PTHY_CANFA	PARATHYROID HORMONE PR	4.38e+01
	თ	39	100.0	115	_	PTHY_HUMAN	PARATHYROID HORMONE PR	4.38e+01
	σ	39	100.0	115	⊢	PTHY_BOVIN	HORMONE	4.38e+01
	7	39	100.0	209	Ъ	VS10_ROTBS	MINOR OUTER CAPSID PRO	4.38e+01
	œ	39	100.0	209	_	RR3_GRATE	CHLOROPLAST 30S RIBOSO	4.38e+01
	ဖ	39	100.0	213	ᆫ	URK_MYCPN	URIDINE KINASE (EC 2.7	4.38e+01
	10	39	100.0	224	_	TCTD_SALTY	TRANSCRIPTIONAL REGULA	4.38e+01
	11	39	100.0	229	_	YXDJ_BACSU	HYPOTHETICAL 26.6 KD S	4.38e+01
	12	39	100.0	242	_	RSTA_ECOLI	TRANSCRIPTIONAL REGULA	4.38e+01
	3	39	100.0	310	_	SYNK_ARATH	SYNTAXIN-RELATED PROTE	4.38e+01
	14	39	100.0	330	_	YXAQ_BACSU	HYPOTHETICAL 37.5 KD P	4.38e+01
	15	39	100.0	334	Ь	YHO5_YEAST	HYPOTHETICAL 37.9 KD P	4.38e+01
	16	39	100.0	353	ب	Y613_METJA	PUTATIVE ENDONUCLEASE	4.38e+01
	17	39	100.0	360	Ь	HIS8_LACLA	HISTIDINOL-PHOSPHATE A	4.38e+01
	18	39	100.0	366	Ь	SYY_SULSO	TYROSYL-TRNA SYNTHETAS	4.38e+01
	19	39	100.0	435	ш	MRP_MYCLE	MRP PROTEIN HOMOLOG.	4.38e+01
	20	39	100.0	437	Ь	SECY_STRGB	PREPROTEIN TRANSLOCASE	4.38e+01
	21	39	100.0	437	ы	SECY_STRGR	PREPROTEIN TRANSLOCASE	4.38e+01
	22	39	100.0	437	μ.	SECY_STRSC	PREPROTEIN TRANSLOCASE	4.38e+01
	23	39	100.0	437	٢	SECY_STRLI	PREPROTEIN TRANSLOCASE	4.38e+01

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39
100.0	100.0	100.0	•	100.0		100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0		100.0	100.0	100.0	100.0	100.0	100.0	100.0
2492	2492	2492	1032	1031	926	806	800	754	745	744	517	517	504	501	496	496	479	459	455	451	444
μ	Н	ب	μ	H	بر	ш	Н	ب	ب	بر	ب	ب	ш	ب	ب	بر	۲	μ	Н	Н	Н
POLN_EEVVT	POLN_EEVV3	POLN_EEVVP	YQ53_CAEEL	RAD2_YEAST	PQQL_HAEIN	SYFB_MYCGE	RR3_CHLEU	KATC_ARATH	KATB_ARATH	NU85_YEAST	PUR1_RAT	PUR1_HUMAN	PUR1_ECOLI	UVS2_NEUCR	RECQ_BACSU	SRM_MOUSE	ICE8_HUMAN	NU4M_HYLLA	YNU6_YEAST	TRPC_BUCAP	PURA_SYNY3
NONSTRUCTURAL POLYPROT	NONSTRUCTURAL POLYPROT	NONSTRUCTURAL POLYPROT	HYPOTHETICAL 117.1 KD	DNA REPAIR PROTEIN RAD	PROBABLE ZINC PROTEASE	PHENYLALANYL-TRNA SYNT	ъ	PROTEIN	KINESIN-LIKE PROTEIN B	NUCLEOPORIN NUP85 (NUC	AMIDOPHOSPHORIBOSYLTRA	AMIDOPHOSPHORIBOSYLTRA	AMIDOPHOSPHORIBOSYLTRA	UVS-2 PROTEIN.	ATP-DEPENDENT DNA HELI	TYROSINE-PROTEIN KINAS	CASPASE-8 PRECURSOR (E	NADH-UBIQUINONE OXIDOR	HYPOTHETICAL 51.6 KD P	INDOLE-3-GLYCEROL PHOS	ADENYLOSUCCINATE SYNTH
4.38e+01	4.38e+01	4.38e+01	4.38e+01	4.38e+01	4.38e+01	4.38e+01	4.38e+01	4.38e+01	4.38e+01	4.38e+01	4.38e+01		4.38e+01	4.38e+01		4.38e+01			4.38e+01	4.38e+01	4.38e+01

## ALIGNMENTS

RESULT

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RA RA	R R R R R	R R R R R R R R R R R R R R R R R R R	RRRRRRR	R R R R R R R	R R R R R R R	28888 8888		58
EUNCTION.  SPECIES-E.COLI;  MEDLINE; 91006075.  ROSS W., THOMPSON J.F., NEWLANDS J.T., GOURSE R.L.;  EMBO J. 9:3733-3742(1990).	SEQUENCE FROM N.A.  SPECIES-S.TYPHIMURIUM; STRAIN-LT2;  MEDLINE; 95238273.  OSUNA R., LIENAU D., HUGHES K.T., JOHNSON R.C.;  J. BACTERIOL. 177:2021-2032(1995).	SEQUENCE FROM N.A.  SPECIES-E.COLI; STRAIN-K12 / MG1655; BLATTNER F.R., PLUNKETT G. III, MAYHEW G.F., PERNA N.T., GLASNER F.D.; SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS. [5]	UENCE FROM N.A. CIES=E.COLI; LINE; 93094136. L C.A., OSUNA R., F BACTERIOL. 174:8043	SEQUENCE FROM N.A. SPECIES-E.COLI; SPECIES-E.COLI; MEDLINE; 88247997. KOCH C., VANDERKERCKHOVE J., KAHMANN R.; PROC. NATL. ACAD. SCI. U.S.A. 85:4237-4241(1988).	SEQUENCE FROM N.A., AND SEQUENCE. SPECIES-E.COLI; MEDLINE; 88217925. JOHNSON R.C., BALL C.A., PFEFFER D., SIMON M.I.; PROC. NATL. ACAD. SCI. U.S.A. 85:3484-3488(1988).	ESCHERICHIA COLI, AND SALMONELLA TYPHIMURIUM. PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; ENTEROBACTERIACEAE. [1]	01-JUL-1989 (REL. 11, CREATED) 01-JUL-1989 (REL. 11, LAST SEQUENCE UPDATE) 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE) FACTOR-FOR-INVERSION STIMULATION PROTEIN (HIN RECOMBINATIONAL ENHANCER BINDING PROTEIN) (FIS PROTEIN).	FIS_ECOLI STANDARD; PRT; 98 AA.

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RESULT 2
ID YI91_ECOLI
AC P39212;
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                                                                                               Query Match
Best Local S
Matches
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-!- SUBUNIT: HOMODIMER.
EMBL; J03245; G145971; -.
EMBL; J03245; G145973; -.
EMBL; J03816; G14973; -.
EMBL; M95784; G14977; -.
EMBL; M95784; G165202; -.
EMBL; M18997; G606202; -.
EMBL; M18997; G606202; -.
EMBL; M18997; G424092; -.
EMBL; U03101; G424092; -.
EMBL; U03101; G424092; -.
PIR; A28207; A28207;
PIR; A28207; A28207;
PIR; S15344; S15344.
PIR; C47043; C47043.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 96433150.
WOLD S., CROOKE E., SKARST!
NUCLEIC ACIDS RES. 24:3527
[8]
NUTAGENESIS, AND DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M.EDLINE; 92319362.

M.EDLINE; 92319362.

J. MOL. BIOL. 226:209-226(1992).

J. MOL. BIOL. 226:209-226(1992).

-1- FUNCTION: ACTIVATES RIBOSOMAL RNA TRANSCRIPTION. PLAYS A DIRECT ROLE IN UPSTREAM ACTIVATION OF RRNA PROMOTERS. BINDS TO A RECOMBINATIONAL ENHANCER SEQUENCE THAT IS REQUIRED TO STIMULATE HIN-MEDIATED DNA INVERSION. PREVENTS INITIATION OF DNA REPLICATION
                                                                                                                                                    TURN
HELIX
TURN
HELIX
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HELIX
TURN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES-E.COLI;
MEDLINE; 9195026.
KOSTREWA D., GRANZIN J., KOCH C., CHOE H.-W., RAGHUNATHAN S., WOLF W.,
LABAHN J., KAHMANN R., SAENGER W.;
NATURE 349:178-180(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [7]
FUNCTION.
                                                                                                                                                                                                                                                    DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 91224111.
OSUNA R., FINKEL S.E., JOHNSON R.C.;
EMBO J. 10:1593-1603(1991).
                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                 STYGENE; SG1
DNA-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES-E.COLI;
                                                                                                                                                                                                                                           HELIX
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                                                                                                                                                                                                                                                                                                       ECOGENE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   K-RAY CRYSTALLOGRAPHY
                                                    88 LRKKL 92
|||||
1 LRKKL 5
                                                                                                         Match 100.0%;
Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                  4FIS;
                                                                                                                                                                                                                                                                                                                             1FIP; 14-FEB-95.
3FIS; 31-OCT-93.
                                                                                                                                                                                                                                                                   ; EG10317; FIS.
; SG10100; FIS.
>ING; 3D-STRUCTURE.
17 44
                                                                                                ű
                                                                                                Conservative
                                                                                                                                                      74
27
41
43
50
71
71
74
82
95
                                                                                                                                         AA;
            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , SKARSTAD K.;
24:3527-3532(1996).
                                                                                                                                         11240 MW;
                                                                                                                                                      93
40
41
70
70
72
81
82
94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (2.0 ANGSTROMS).
                                                                                                         Score 39; DB 1; L
Pred. No. 4.38e+01;
                                                                                                0
                                                                                                                                                                                                                                                   REQUIRED FOR THE STIMULATION OF HINMEDIATED RECOMBINATION.
H-T-H MOTIF.
            PRT;
                                                                                                                                         6AE88082 CRC32;
                                                                                               Mismatches
            100
            A
                                                                                                                    Length 98;
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                                                                                                                                                                                       Query Match
Best Local S
Matches
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NUCLEIC ACIDS RES. 23:2105-2119(1995).

EMBL; U14003; G537124; -.

EMBL; AE000499; G1790735; -.

HYPOTHETICAL PROTEIN; TRANSPOSABLE ELEMENT.

SEQUENCE 100 AA; 11558 MW; 3827E6B9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANOTATION UPDATE)
01-SERTION ELEMENT IS911 HYPOTHETICAL 11.6 KD PROTEIN (0100).
ESCHERICHIA COLI.
ESCHERICHIA COLI.
ENCARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE; 95334365;
BURLAND V.D., PLUNKETT G. III,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENTEROBACTERIACEAE.
82 LRKKL 86
|||||
1 LRKKL 5
                                                                                                                                                                                                 / Match 100.0%;
Local Similarity 100.0%;
nes 5; Conservative
                                                                                                                                                                                                 Score 39; DB 1; 1
Pred. No. 4.38e+01;
0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFIA H.J., DANIELS D.L.,
                                                                                                                                                                                                                                                                                                     Length 100;
                                                                                                                                                                                                            0;
                                                                                                                                                                                                       Indels
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Search completed: Thu Jul 30 11:20:51 1998 Job time : 6 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch\_pp on: protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 11:21:10 1998; MasPar time 3.54 Seconds 59.507 Million cell updates/sec

Title: Tabular output not generated. >US-08-817-547A-36 (1-5) from US08817547A.pep 39

Description:
Perfect Score:
Sequence: 1 LRKKL 5

Scoring table: PAM 150 Gap 15

Searched: 140542 seqs, 42109429 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb15
1:sp\_fung1 2:sp\_human 3:sp\_invertebrate 4:sp\_mammal
5:sp\_mhc 6:sp\_organelle 7:sp\_phage 8:sp\_plant
9:sp\_bacteria 10:sp\_rodent 11:sp\_virus 12:sp\_vertebrate
13:sp\_unclassified

Statistics;

re 4-cacer than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

20.197; Variance 20.875; scale 0.968

#### SUMMARIES

20	19	18	17	16	15	14	13	12	11	10	9	80	7	o	را ن	4	ω	2	1	Result No.
39	39	39		39	39		39	39	39	39	39	39	39	39	39	39	39	39	39	Score
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	Query Match I
480		459	459	459	459		434	398	360	346		289	259	231	231	218	199	105	65	Length 1
2	5	σ	σ	σ	σ	11	ب	0	ø	9	11	H	ø	$\vdash$	9	ဖ	9	5	ω	. B
015519	008854	021714	021698	021706	021845	036416	P78918	Q63701	034130	029648	Q84775	Q84737	028703	Q05436	034951	029263	027967	Q63473	Q24890	IJ
CASPER.	TRAF-INTERACTING PROTE	NADH DEHYDROGENASE SUB	NADH DEHYDROGENASE SUB	NADH DEHYDROGENASE SUB	NADH DEHYDROGENASE SUB	ORF66.	FISSION YEAST (FRAGMEN	CATHEPSIN E PRECURSOR.	HISC.	LPS GLYCOSYLTRANSFERAS	14 (HRV-14) RNA SEQUEN	TYPE 14 (HRV14), COMPL	CONSERVED HYPOTHETICAL	CAM KINASE II (FRAGMEN	SIGNAL TRANSDUCTION RE	HYPOTHETICAL 24.6 KD P	CONSERVED HYPOTHETICAL	PARATHYROID HORMONE (F	ANTIGEN B (FRAGMENT).	Description
5.95e+01	5.95e+01	5.95e+01	5.95e+01	5.95e+01	5.95e+01	5.95e+01	5.95e+01	5.95e+01	5.95e+01	5.95e+01	5.95e+01	5.95e+01	5.95e+01	5.95e+01	5.95e+01	5.95e+01	5.95e+01	5.95e+01	5.95e+01	Pred. No.

4.4 5.4	43	42	41	40	39	38	37	36	35	34	<b>ω</b>	32	31	30	29	28	27	26	25	24	23	22	21
39	υ 9	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39
100.0	•	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
2493	2493	1616	1338	1335	1282	1115	1005	954	939	938	929	899	885	880	855	836	808	775	764	627	529	495	481
11	: 1	11	N	ω	N					2				10	11	10	9	ш	w	9	N	9	10
Q88978	Q66594	P90211	014765	Q17250	Q14692	Q83484	Q13625	015326	Q62784	Q13187	032491	Q06132	Q13122	P97693	Q82081	Q63618	Q5893 <b>7</b>	013971	Q22598	030244	Q12892	027663	035707
NONSTRUCTURAL POLYPROT	-	180K PROTEIN.	ALDEHYDE OXIDASE.	XANTHINE DEHYDROGENASE	KIAA0187 PROTEIN.	130K PROTEIN.	BBP/53BP2.		INOSITOL POLYPHOSPHATE	INOSITOL POLYPHOSPHATE	PUTATIVE N6-ADEININE S	CHROMOSOME XII COSMID	~	P105 COACTIVATOR.	COAT PROTEIN (FRAGMENT	ESPIN.	95.6 KD	ICAL	Т19Н5.1.	HYPOTHETICAL 72.0 KD P	P53-BINDING PROTEIN (F	PHOSPHOSERINE PHOSPHAT	FLICE-LIKE INHIBITORY
5.95e+01	· .					:.		5.95e+01		5.95e+01					5.95e+01			5.95e+01	5.95e+01	5.95e+0	5.95e+01	5.95e+01	٠

## ALIGNMENTS

RX MEDLINE; 94359533.  RX MEDLINE; 94359533.  RI MOL. BIOCHEM. PARASITOL. 64:171-175(1994).  DR EMBL; Z26483; G452853;  FT NON.TER 1 1 10.0%; SCOIE 39; DB 3; Length 65; SEQUENCE 65 AA; 7617 MW; 3F256666 CRC32;  Query Match 100.0%; SCOIE 39; DB 3; Length 65; Best Local Similarity 100.0%; Pred. No. 5.95e+01; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps DB 45 LRKL 49  DD 45 LRKL 49  1 LRKKL 5  RESULT 2 (1111)  Qy 1 LRKKL 5  RESULT 2 (263473) PRELIMINARY; PRT; 105 AA.  AC Q63473 PRELIMINARY; PRT; 105 AA.  BO 101-NOV-1996 (TREMBLREL. 01, CREATED)  DT 01-VAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)  DT 01-VAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)  DT 01-VAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)  GO PTH.  GO PTH.  GO EUTHERIA; RODENTIA.  RO EUTHERIA; RODENTIA.  RO EUTHERIA; RODENTIA.  RC EUTHERIA; RODENTIA.  RC EUTHERIA; RODENTIA.  RC EUTHERIA; RODENTIA.  RC TISSUE-THYROID, AND PARATHYROID;  RC SCHELEZER H. J., GROSS G., MAYER H.;  RA ADV. GENE TECHNOL. 21:228-229(1984).	RESULT 1 10 Q24890; AC Q24890; AC Q24890; DT 01-NOV-1996 (TREMBLREL. 01, CREATED) DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE) DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE) DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE) DE ANTIGEN B (FRAGMENT). OS ECHINOCOCCUS MULTILOCULARIS. OC EUKARYOTA; METAZOA; ACOELOMATES; PLATYHELMINTHES; CESTODA. RP SEQUENCE FROM N.A. RC STRAIN-H90;
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FT
SQ
Search completed: Thu Jul 30 11:21:47 1998 Job time : 37 secs.
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                                                                                                                       Query Match 100.0%; Score 39; DB 10; Length 105; Best Local Similarity 100.0%; Pred. No. 5.95e+01; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
                                                                                                                                                                               EMBL; M54875; G601933; -.
NON_TER 1 1
SEQUENCE 105 AA; 11746 MW; 6AC3163E CRC32;
                                                           45 LRKKL 49
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1 LRKKL 5
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